SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ ___ Examiner # : _____ Date: _____

Art Unit: _____ Phone Number 30_____ Serial Number: _____

Mail Box and Bldg. Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.
Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or
utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if
known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the
appropriate serial number.

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

- -

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher _____ Jan	NA Sequence (#) ✓	STN _____
Searcher Phone # ____ 4498	AA Sequence (#) ____	Dialog _____
Searcher Location ____	Structure (#) ____	Questel Orbit _____
Date Searcher Received 7/15/03	Bibliographic ____	On Line _____
Date Completed 7/19/03	Litigation ____	Lexis Nexis _____
Searcher Prep & Review Time ____	Fulltext ____	Sequence Systems ✓
Claims Prep Time 15	Patent Family ____	WWW Internet _____
Time ____ +10	Other ____	Other specify _____

pr____

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 18, 2003, 04:46:48 ; Search time 5485.97 Seconds
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                                         10397.705 Million cell updates/sec

Title: US-09-627-896B-21
Perfect score: 1960
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
           1: gb_ba:*
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          38: em_sy:*
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          41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1611.8	82.2	8858	6	AR176315	AR176315 Sequence
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5	1514.2	77.3	2737	9	HSU72063	U72063 Human immun
6	1514.2	77.3	7810	9	AF178581	AF178581 Homo sapi
7	1512.6	77.2	68790	9	AF017732	AF017732 Homo sapi
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22	698	35.6	8068	6	AX011131	AX011131 Sequence
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ALIGNMENTS

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LOCUS   AR176315   8858 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6312693.
ACCESSION   AR176315
VERSION   AR176315.1 GI:17918670
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 8858)
  AUTHORS   Aruffo,A.A., Hollenbaugh,D., Siadak,A.W., Berry,K.K., Harris,L.,
            Thorne,B.A., Bajorath,J., Huse,W.D., Wu,H. and Watkins,J.D.
  TITLE   Antibodies against human CD40
  JOURNAL   Patent: US 6312693-A 6 06-NOV-2001;

Pred. No. is the number of results predicted by chance to have a

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                     /organism="unknown"
BASE COUNT   2396 a    2124 c   1950 g   2387 t    1 others
ORIGIN

Query Match       82.2%;   Score 1611.8;   DB 6;   Length 8858;
Best Local Similarity   90.6%;   Pred. No. 0;
Matches 1783;   Conservative   0;   Mismatches   137;   Indels   49;   Gaps   4;

Qy         9  ACCATGGGATTCACAGGCCCAGGTTCTTATATTGCTGCTATGGGTATCTGGCACCTGT    68
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Qy       129  ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAACTACTTG   188
              |||  || || |||||||||  ||  | ||| ||||||   |   |    | |||||
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Qy       189  GCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACT   248
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Qy       309  ACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA--   366
              |||||||| ||||||||  | || |||  ||||||||||||||||||   |   | |
Db      1284  AGTATCAACAGTGTGGAACCTGAAGATGTTGGAATTTATTACTGTCAACATGGTCACAGC  1343

Qy       367  -ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGT--------   414
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Qy       415  ------------AGTCTTCTCAACTCTAGAAATTCTAAACTCTAGAGGGGGTCGGATGACG   462
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Db      1464  TGGCCATTCTTTGCCTAAAGCATTGAGTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC  1523

Qy       523  TCAGAATGGCTGCAAAGAGCTCCAACAAACAATTTAGAACTTTATTAAGAATAGGGGG   582
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Qy       583  AAGCTAGGAAGAAGAACTCAAAACATCAAGATTTAAATACGCTTCTTGGTCTCCTGCTAT   642
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  AUTHORS   Shimizu,N. and Kawasaki,K.
  TITLE     Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos141
  JOURNAL   Published Only in Database (2000)
REFERENCE   2  (bases 1 to 37201)
  AUTHORS   Shimizu,N. and Kawasaki,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2000) Nobuyoshi Shimizu, Keio University, School
            of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
            160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370, Fax:81-3-3351-2370)
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BASE COUNT   11316 a   7697 c   7764 g   10424 t
ORIGIN

Query Match       77.4%;   Score 1517.4;   DB 9;   Length 37201;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 1518;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

 433 Qy AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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5441 Db AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 5500

 493 Qy ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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5501 Db ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 5560

 553 Qy CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAAATCAAGAT 612
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5561 Db CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAAACATCAAGAT 5620

 613 Qy TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTTCTG 672
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5621 Db TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTTCTG 5680

 673 Qy TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCAAGGGCAGAAACTTTGT 732
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5681 Db TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCAAGGGCAGAAACTTTGT 5740

 733 Qy TACTTAAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTCGGAAATCTGGAACTGTCTT 792
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5741 Db TACTTAAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTCGGAAATCTGGAACTGTCTT 5800

 793 Qy CATCTTCCCGCCATCTGATGAGCAGTTGAAATCGGAACTGGAACTGTCTT 852
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 853 Qy GAATAACTTCTATCCCAGAGAGAGTGTCACAGAGCAGGAGCAGCAAGACAGCCTTCCAATC 912
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 973 Qy CAGCACCCCTGACGCTGAGCAAAGCAGCTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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1153 Qy TGACCCTTTTCCACAGGGACCTACCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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1273 Qy GTGAATCTTTGCACCTGGTTTCTCTCTTCCTCATTTAATAATTATTATTATCTGTTGTTT 1332
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1333 Qy TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 1392
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1393 Qy CCATTTATAAAAATCATCCTTCATTCTATTTACCCTATCATCCTCTGCAAGACAGTCCT 1452
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1453 Qy CCCTCAAACCCACAAGCCTTCTGTCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGTCTT 1512
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6521 Db CTTCCTGTGTTTCCCCTCCTCAGCAAGCCCTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 6580

1573 Qy ACAGTCATATATCCTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 1632
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6581 Db ACAGTCATATATCCTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 6640

1633 Qy AAGAAACCTGCTATAAAGAGAATCATTGCAACATGATATAAAATAACAACACAATA 1692
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6641 Db AAGAAACCTGCTATAAAGAGAATCATTGCAACATGATATAAAATAACAACACAATA 6700

1693 Qy AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
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1753 Qy AATGGAATGTCATGCCCTTATTTACATTTTTAAACAGGTACTGAGGGACTTCCTGTCTGCCA 1812
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1813 Qy AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACAACCTAATTTAATCCACTATACTGTGAGATTAAA 1872
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6821 Db AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACAACCTAATTTAATCCACTATACTGTGAGATTAAA 6880

1873 Qy AACATTCATTAAAATGTTGCAAAGTTCTATAAAGCTGAGAGACAAATATTCTATAAC 1932
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1933 Qy TCAGCAATCCCACTTCTAG 1951
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6941 Db TCAGCAATCCCACTTCTAG 6959
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TITLE      The sequence of Homo sapiens clone
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 166276)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (13-DEC-2001) Genome Sequencing Center, Washington
           University School of Medicine, 4444 Forest Park Parkway, St. Louis,
           MO 63108, USA
COMMENT    ----------------- Genome Center -----------------
           Center: Washington University Genome Sequencing Center
           Center code: WUGSC
           Web site: http://genome.wustl.edu/gsc/index.shtml
           Contact: submissions@watson.wustl.edu
           ----------------- Project Information -----------------
           Center project name: H_NH1435C03
           ----------------- Summary Statistics -----------------
           Sequencing vector: M13; 0%
           Sequencing vector: plasmid; 100%
           Chemistry: Dye-primer ET; 0% of reads
           Chemistry: Dye-terminator Big Dye; 100% of reads
           Assembly program: Phrap; version 0.990319
           Consensus quality: 164631 bases at least Q40
           Consensus quality: 165062 bases at least Q30
           Consensus quality: 165346 bases at least Q20
           Insert size: 166000; agarose-fp
           Insert size: 165976; sum-of-contigs
           Quality coverage: 6.84 in Q20 bases; agarose-fp
           Quality coverage: 6.81 in Q20 bases; sum-of-contigs
           ----------------------------------------------
         * NOTE: This is a 'working draft' sequence. It currently
         * consists of 4 contigs. The true order of the pieces
         * is not known and their order in this sequence record is
         * arbitrary. Gaps between the contigs are represented as
         * runs of N, but the exact sizes of the gaps are unknown.
         * This record will be updated with the finished sequence
         * as soon as it is available and the accession number will
         * be preserved.
         *       1       21011: contig of 21011 bp in length
         *   21012       21111: gap of unknown length
         *   21112       63536: contig of 42425 bp in length
         *   63537       63636: gap of unknown length
         *   63637      152378: contig of 88742 bp in length
         *  152379      152478: gap of unknown length
         *  152479      166276: contig of 13798 bp in length.
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                   /clone="RP11-1435C3"
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                   vector_side:right"
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BASE COUNT   51344 a  32704 c  32660 g  49267 t       301 others
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Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1518;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      433 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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Db 144744 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 144803
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Qy    493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA 552
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 144804 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA 144863
Qy    553 CAATTTAGAACTTTATTAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT 612
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Db 144864 CAATTTAGAACTTTATTAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT 144923
Qy    613 TTTAAATACGCTTCTTGGTCTTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG 672
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Db 144924 TTTAAATACGCTTCTTGGTCTTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG 144983
Qy    673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
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Db 144984 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 145043
Qy    733 TACTTAAACACCATCCTGTTTGCTTCTTTGTTCTTTCCTCAGGAACTGTGGCTGCACCATC 792
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Db 145044 TACTTAAACACCATCCTGTTTGCTTCTTTGTTCTTTCCTCAGGAACTGTGGCTGCACCATC 145103
Qy    793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGGTGTTTGTGTGTGCCTGCT 852
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Db 145104 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGGTGTTTGTGTGTGCCTGCT 145163
Qy    853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Db 145164 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 145223
Qy    913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACAGGACACCTACAGCCTCAG 972
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Db 145224 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACAGGACACCTACAGCCTCAG 145283
Qy    973 CAGCACCTGACGCTGAGCAAAGCAGACTACGGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Qy   1033 CACCCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db 145344 CACCCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 145403
Qy   1093 GGAGAAGTGCCCCCACCTGCTCCTCCTCAGTTCCAGCCTGACCCCCATCCTTTGGCCTC 1152
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 145404 GGAGAAGTGCCCCCACCTGCTCCTCCTCAGTTCCAGCCTGACCCCCATCCTTTGGCCTC 145463
Qy   1153 TGACCCTTTTTCCACAGGGGACCTACCCGTTCCCAGCTCCATCTTCCACCTC 1212
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Db 145464 TGACCCTTTTTCCACAGGGGACCTACCCGTTCCCAGCTCCATCTTCCACCTC 145523
Qy   1213 ACCCCCCTCCTCCTTGCTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 145524 ACCCCCCTCCTCCTTGCTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 145583
Qy   1273 GTGAATCTTTGCACCTGTGTTTCTTCCTTTCCTCATTTAATAATTATAATATCTGTTGTTT 1332
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Db 145584 GTGAATCTTTGCACCTGTGTTTCTTCCTTTCCTCATTTAATAATTATAATATCTGTTGTTT 145643
Qy   1333 TACCAACTACTCAATTTCTTCTTATAAGGACTAAAATATGTAGTCATCGGCCGCATAA 1392
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Db 145644 TACCAACTACTCAATTTCTTCTTATAAGGACTAAAATATGTAGTCATCGGCCGCATAA 145703
Qy   1393 CCATTTATAAAAATCATCTCTCATTTCATTTTACCCTATCATCCTTCGCAAGACAGTCCT 1452
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Db 145704 CCATTTATAAAAATCATCTCTCATTTCATTTTACCCTATCATCCTTCGCAAGACAGTCCT 145763
Qy   1453 CCCTCAAACCCACAAGCTTCGTCCTCCACAGTTCCCCATGGGCCATGGGCCATTG 1512
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Qy   1513 CTTCCTTGTTTCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
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Db 145824 CTTCCTTGTTTCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 145883
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Qy   1573  ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 1632
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Db 145884  ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAATTTTTCAAAAG 145943

Qy   1633  AAGAAACCTGCTATAAAGAGAATCATTCATTCGAACATGATATAAAATAACAACACAATA 1692
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Db 145944  AAGAAACCTGCTATAAAGAGAATCATTCATTCGAACATGATATAAAATAACAACACAATA 146003

Qy   1693  AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
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Db 146004  AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 146063

Qy   1753  AATGGAAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 1812
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Db 146064  AATGGAAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 146123

Qy   1813  AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
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Qy   1873  AACATTCATTAAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1932
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Qy   1933  TCAGCAATCCCACTTCTAG 1951
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Db 146244  TCAGCAATCCCACTTCTAG 146262
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RESULT 4

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AC096579/c
LOCUS       AC096579              176555 bp    DNA     linear   PRI 01-MAR-2002
DEFINITION  Homo sapiens BAC clone RP11-601N4 from 2, complete sequence.
ACCESSION   AC096579 AC023416
VERSION     AC096579.1  GI:15638889
KEYWORDS    HTG.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 176555)
AUTHORS     Sulston,J.E. and Waterston,R.
TITLE       Toward a complete human genome sequence
JOURNAL     Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE     99063792
PUBMED      9847074
REFERENCE   2  (bases 1 to 176555)
AUTHORS     Grewal,N. and Abbott,A.
TITLE       The sequence of Homo sapiens BAC clone RP11-601N4
JOURNAL     Unpublished (2001)
REFERENCE   3  (bases 1 to 176555)
AUTHORS     Waterston,R.H.
TITLE       Direct Submission
JOURNAL     Submitted (18-SEP-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 176555)
AUTHORS     Waterston,R.
TITLE       Direct Submission
JOURNAL     Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Sep 18, 2001 this sequence version replaced gi:7705152.
            ------------------ Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@watson.wustl.edu
            ------------------ Summary Statistics
            Center project name: H_NH0601N04
            Drafting Center: WIBR
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NOTICE:  This sequence may not represent the entire insert of this
clone.  It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-450E9; the clone sequenced
to the right is RP11-685N3.  Actual start of this clone is at base
position 1 of RP11-601N4; actual end is at base position 176555 of
RP11-601N4.

Data from AC062029 and AC060807 was used to finish this clone,
AC023416.  Polymorphisms have been identified between AC023416 and
AC062029.

The sequence of AC023416 has been incorporated into AC096579.
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     repeat_region   1102..1153
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     repeat_region   1207..1364
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     repeat_region   1425..1774
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     repeat_region   1942..2293
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Db  132041 AATTCTAAACTCTGAGGGGTCGATGACGTCGGCCATTCTTGCCTAAAGCATTGAGTTT 131982

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Qy     613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTTCTG 672
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Db  131861 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTTCTG 131802

Qy     673 TCTGTCCCTAAACATGCCCTGTGATTATCCGCAAACACACACCAAGGGCAGAACTTGT 732
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Qy     733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGGAAATCTGATGAGCAGTTG 792
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Qy     853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGATAACGCCCTCCAATC 912
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Qy     913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAGACAGCACCTACAGCCTCAG 972
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Matches 1516;    Conservative 0;    Mismatches 0;    Indels 3;    Gaps 0;
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Db   242  TCTGTCCCTAACATGCCCTGTGATTATCCGCAAAACACACAACACACCAAGGGCAGAACTTTGT  301

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Qy  1153  TGACCCTTTTCCACAGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC  1212
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Qy  1333  TACCAACTACTCAATTCTCTATAAGGGACTAAAATATGTAGTCATCCTAAGGCGCCATAA  1392
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Qy  1873  AACATTCATTAAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATTCTATAAC  1932
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VERSION     U72063.1   GI:1619959
KEYWORDS    .
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
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REFERENCE   1  (bases 1 to 2737)
AUTHORS     Hu,W.X., Cao,Y., Li.X.Y., Lee,L.M. and Yao.K.T.
TITLE       Comparison of NPC Transforming Gene Tx to Ig Kappa Constant Region
            Gene and Their Expression in Different Cell Lines (Chinese with
            English Abstract)
JOURNAL     Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 27, 215-221 (1995)
REFERENCE   2  (bases 1 to 2737)
AUTHORS     Hu,W.X.
TITLE       Direct Submission
JOURNAL     Submitted (21-SEP-1996) Medicine/Hematology, UTHSCSA, 7703 Floyd
            Curl Drive, San Antonio, TX 78284, USA
FEATURES             Location/Qualifiers
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TITLE　　　An analysis of EcoRI/XhoI 3 kb fragment sequence of Nasopharyngeal
　　　　　　carcinoma transforming gene
JOURNAL　　Unpublished
REFERENCE　3 (bases 1 to 7810)
AUTHORS　　Wei,R., Ming,L., Linqing,X., Xinxian,W., Wei,L. and Ya,C.
TITLE　　　Nucleotide sequence analysis of Tx, a transforming gene isolated
　　　　　　From a nasopharyngeal carcinoma cell line CNE2
JOURNAL　　Unpublished
REFERENCE　4 (bases 1 to 7810)
AUTHORS　　Xinxian,W.
TITLE　　　An analysis of the full sequence of Nasopharyngeal carcinoma
　　　　　　transforming gene
JOURNAL　　Unpublished
REFERENCE　5 (bases 1 to 7810)
AUTHORS　　Ming,L., Wei,R., Wei,L., Xinxian,W., Linqing,X. and Ya,C.
TITLE　　　Direct Submission
JOURNAL　　Submitted (19-AUG-1999) Molecular Biology Laboratory, Cancer
　　　　　　Research Institute of Hunan Medical University, 88 Xiangya Road,
　　　　　　Changsha, Hunan 410078, People's Republic of China
REFERENCE　6 (bases 1 to 7810)
AUTHORS　　Wei,L., Ming,L., Wei,R., Xinxian,W., Linqing,X. and Ya,C.
TITLE　　　Direct Submission
JOURNAL　　Submitted (13-OCT-2000) Molecular Biology Laboratory, Cancer
　　　　　　Research Institute of Hunan Medical University, 88 Xiangya Road,
　　　　　　Changsha, Hunan 410078, People's Republic of China
REMARK　　　Sequence update by submitter
REFERENCE　7 (bases 1 to 7810)
AUTHORS　　Wei,L., Ming,L., Wei,L. and Ya,C.
TITLE　　　Direct Submission
JOURNAL　　Submitted (10-APR-2002) Molecular Biology, Cancer Research
　　　　　　Institute, Xiangya Medical School of Central South University, 88
　　　　　　Xiangya Road, Changsha, Hunan 410078, People's Republic of China
REMARK　　　Sequence update by submitter
COMMENT　　On Jun 26, 2002 this sequence version replaced gi:10800410.
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Best Local Similarity　99.8%;　Pred. No. 0;
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Qy　1693 AAAGCAATTAAATAAACAACAACATAGGGAAATGTTAAGTTCATCATGGTACTTAGACTT 1752
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Qy　1813 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
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Db　1382 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1441

Qy　1873 AACATTCATTAAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGCAAATATATTCTATAAC 1932
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Db　1442 AACATTCATTAAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1501

Qy　1933 TCAGCAATCCCACTTCTAG 1951
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Db　1502 TCAGCAATCCCACTTCTAG 1520

RESULT 6
LOCUS　　　　AF178581　　　　　7810 bp　　DNA　　　linear　　PRI 26-JUN-2002
DEFINITION　Homo sapiens nasopharyngeal carcinoma gene sequence.
ACCESSION　AF178581 AF276073 AF500623
VERSION　　AF178581.3　GI:21592476
KEYWORDS　　.
SOURCE　　　Homo sapiens
ORGANISM　　Homo sapiens
　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　1 (bases 1 to 7810)
AUTHORS　　Ming,L., Wei,R., Xinxian,W., Linqing,X., Wei,L. and Ya,C.
TITLE　　　Nucleotide sequence analysis of a transforming gene isolated from
　　　　　　nasopharyngeal carcinoma cell line CNE2: an aberrant human
　　　　　　immunoglobulin kappa light chain which lacks variable region
JOURNAL　　DNA Seq. 15, 1-5 (2002)
REFERENCE　2 (bases 1 to 7810)
AUTHORS　　Ming,L., Wei,R., Wei,L., Xinxian,W., Linqing,X. and Ya,C.

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Qy  1633  AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACACACAATA  1692
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Qy  1693  AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT  1752
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Db  6515  AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC  6574

Qy  1933  TCAGCAATCCCACTTCTAG  1951
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Db  6575  TCAGCAATCCCACTTCTAG  6593


RESULT 7
AF017732
LOCUS       AF017732            68790 bp    DNA     linear   PRI 24-OCT-1997
DEFINITION  Homo sapiens chromosome 2 cosmids cos111 and cos 607/6 containing
            immunoglobulin Vk-JkCk region, complete sequence.
ACCESSION   AF017732
VERSION     AF017732.1  GI:2558844
KEYWORDS    HTG.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 68790)
AUTHORS     Brandt,P., Jaerke,D., Scharfe,M., Dose,S., Schoen,O. and
            Bloecker,H.
TITLE       Human DNA sequence from cosmids cos111 and cos607/6 on chromosome
            II containing ESTs
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 68790)
AUTHORS     Brandt,P., Jaerke,D., Scharfe,M., Dose,S., Schoen,O. and
            Bloecker,H.
TITLE       Direct Submission
JOURNAL     Submitted (08-AUG-1997) Genomanalyse, Genomanalyse Gesellschaft
            fuer Biotechnologische Forschung mbH, Mascheroder Weg 1, 38124
            Braunschweig, Germany
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Qy   1513 CTTCCTTGTTTTCCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
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Db 63206 CTTCCTTGTTTTCCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 63265

Qy   1573 ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTCAAAAG 1632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 63266 ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTCAAAAG 63325

Qy   1633 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 63326 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 63385

Qy   1693 AAAGCAATTAAATAAACAAACAAACAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 63386 AAAGCAATTAAATAAACAAACAAACAAATGTTTAAGTTCATCATGGTACTTAGACTT 63445

Qy   1753 AATGGAAGTGCATGCCTATTTACATTTTAAACAGGTACTGAGGGACTCCTGTCTCGCCA 1812
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 63446 AATGGAAGTGCATGCCTATTTACATTTTAAACAGGTACTGAGGGACTCCTGTCTCGCCA 63505

Qy   1813 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCACTATACTGTGAGATTAAA 1872
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 63506 AGGGCCGTATTGAGTACTTTCCACAACGTAATTTAATCACTATACTGTGAGATTAAA 63565

Qy   1873 AACATTCATTAAAATGTTGCAAAGGTTCATAAAGCTGAGAGACAAATATATTCTATAAC 1932
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 63566 AACATTCATTAAAATGTTGCAAAGGTTCATAAAGCTGAGAGACAAATATATTCTATAAC 63625

Qy   1933 TCAGCAATCCCACTTCTAG 1951
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Db 63626 TCAGCAATCCCACTTCTAG 63644

RESULT 8
AR035237
LOCUS   AR035237   1701 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION   Sequence 54 from patent US 5871732.
ACCESSION   AR035237
VERSION   AR035237.1   GI:5951905
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1701)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE   Anti-CD4 antibody homologs useful in prophylaxis and treatment of
             AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 54 16-FEB-1999;
FEATURES   Location/Qualifiers
     source 1..1701
             /organism="unknown"
BASE COUNT   435 a   468 c   361 g   437 t
ORIGIN

Query Match   72.9%; Score 1429.4; DB 6; Length 1701;
Best Local Similarity   93.1%; Pred. No. 0;
Matches 1534; Conservative 0; Mismatches 96; Indels 17; Gaps 3;

Qy   11 CATGGATTCAGAGGCCCAGGTTCTTATATTGCTATGGTATCTGCACCTGTGG 70
          |||| |||||||||||||||||||||||||||||||||||||||||||||
Db   40 CATGAGGGTCCCCGCTCCAGCTCGTGGGGCTCCTGGCTGCTGCCAGTGCCAGAGG 99

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Qy   71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC 130
           || ||||||||||| ||||||||| |||||| ||| ||| |||| ||||||||||||| |
Db  100 TGATATCGTAATGACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGGCTAC 159

Qy  131 TATTAGTCGAAATCGAAATCAGTCAGAGTCTGCTGACACAGTAGAACCCGAGAGAACTACTTGGC 190
Db  160 TATAAACTCGAAGTCCAGTGTGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGC 219

Qy  191 TTGGTACCAGCAGAAACCAGGGACAGCCTCCTAAAACTGCTGATCTACTGGGCATCCACTAG 250
Db  220 CTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAAACTGCTGATTTACTGGGCATCCACTAG 279

Qy  251 GGAATCTGGGGTCCCTGATCGGTTCAGTGGCAGTGGATCGGGGACAGATTTCACTCTCAC 310
Db  280 GGAATCTGGGGTCCCTGATCGGTTCAGTGGCAGTGGATCTGGGGACAGATTTCACTCTCAC 339

Qy  311 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCGAGCCAATCTTATAATCT 370
Db  340 CATCAGCAGTTTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGCTA 399

Qy  371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCCAACTCTA 430
Db  400 TCGGACGTTCGGTCGAGGGACCAAGGTCGAGATCAAAGTAAGTGCACT----------- 448

Qy  431 GAAATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGT 490
Db  449 ----TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGT 504

Qy  491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGATGGCTGCAAAGAGCTCCAACAA 550
Db  505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGATGGCTGCAAAGAGCTCCAACAA 564

Qy  551 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAGAGAAACTCAAAACATCAAG 610
Db  565 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAGAGAAACTCAAAACATCAAG 624

Qy  611 ATTTTAAATACGCTTCCTTCCTTGCTATAATTATCTCGGATAAGCATGCTGTTTTC 670
Db  625 ATTTTAAATACGCTTCCTTGCTATAATTATCTCGGATAAGCATGCTGTTTTTC 684

Qy  671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGGCAAACACACAACACCCAGGGCAGAACTTT 730
Db  685 TGTCTGTCCCTAACATGCCCTGTGATTATCCGGCAAACACAACACACCCAGGGCAGAACTTT 744

Qy  731 GTTACTTAAACACCATCCTGTTTGCTTCTTCTTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 790
Db  745 GTTACTTAAACACCATCCTGTTTGCTTCTTCTTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 804

Qy  791 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGATGACTTTGTTGTGCCTG 850
Db  805 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGATGACTTTGTTGTGCCTG 864

Qy  851 CTGAATAACTTCTATCCCAGAGAGAGAGTGACAGTGGAAGTGGATAACGCCCTCCAA 910
Db  865 CTGAATAACTTCTATCCCAGAGAGAGAGTGACAGTGGAAGTGGATAACGCCCTCCAA 924

Qy  911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 970
Db  925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 984

Qy  971 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAĀCACAAAGTCTACGCCTGCGAA 1030
Db  985 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1044

Qy 1031 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACACAGGGGGAGAGCTTGTTAG 1090
Db 1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACACAGGGGGAGAGCTTGTTAG 1104

Qy 1091 AGGGAGAAGTGCCCCCACCCTGCTTCCTCAGCCTGACCCCCTCCATCCTTTGGCC 1150
Db 1105 AGGGAGAAGTGCCCCCACCCTGCTTCCTCAGCCTGACCCCCTCCATCCTTTGGCC 1164

Qy 1151 TCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1210
Db 1165 TCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1224

Qy 1211 TCACCCCCTCCTCCTGGCTTAATATGCTAATGTTGAGGAATGAATAATATTATCTGTTT 1270
Db 1225 TCACCCCCTCCTCCTGGCTTAATATGCTAATGTTGAGGAATGAATAATATTATCTGTTT 1284

Qy 1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTTTTCCTC-ATTTAATAATATTATCTGTTG 1329
Db 1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTTTTCCTCAATTTAATAATATTATCTGTTG 1344

Qy 1330 TTTTACCAACTACTCAATTTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCCCA 1389
Db 1345 -TTTACCAACTACTCAATTTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCA 1403

Qy 1390 TAACCATTTATAAAAATCATCCTTCATTCATTTACCCTATCTATTTACCCTATCCTCTGCAAGCACAGT 1449
Db 1404 TAACCATTTATAAAAATCATCCTTCATTCATTTACCCTATCCTCTGCAAGCAGT 1463

Qy 1450 CCTCCCTCAAACCCACCACAGCCTTCTGTCCTCACAGTCCCCTGCCCATGGTAGGAGAGAC 1509
Db 1464 CCTCCCTCAAACCCACCACAGCCTTCTGTCCTCACAGTCCCCTGGGCCCGTGGTAGGAGAGAC 1523

Qy 1510 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGT 1569
Db 1524 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1583

Qy 1570 CTTACAGTCATATATCCTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTCAA 1629
Db 1584 CTTACGGTCATATATCCTTGATTCATTCCCTGGGAATCAACCAAGGCAAATTTTCAA 1643

Qy 1630 AAGAAGAAACCTGCTATAAAGAGAATC 1656
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Db 1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670
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RESULT 9
AR035238
LOCUS   AR035238   1701 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 55 from patent US 5871732.
ACCESSION   AR035238
VERSION   AR035238.1 GI:5951906
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1701)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE   Anti-CD4 antibody homologs useful in prophylaxis and treatment of
            AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 55 16-FEB-1999;
FEATURES   Location/Qualifiers
     source 1..1701
            /organism="unknown"
BASE COUNT   435 a   468 c   361 g   437 t
ORIGIN

Query Match   72.9%; Score 1429.4; DB 6; Length 1701;
Best Local Similarity   93.1%; Pred. No. 0;
Matches 1534; Conservative 0; Mismatches 96; Indels 17; Gaps 3;

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Qy   11 CATGGATTCACAGGCCCAGGTTCTTATATTGTTCTTATATTGTTGCTGCTGTATGGTATGGTATGGTGG 70
Db   40 CATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGG 99

Qy   71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC 130
Db  100 TGATATCGTAATGACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGGCTAC 159

Qy  131 TATTAGTCGCAAATCAGTCAGAGTCTGCTGACACAGTTCACAGGGGAGAGTGTTAG 190
Db  160 TATAAACTCGAAGTCCAGTGTGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGC 219
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Qy   191 TTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACGGGCATCCACTAG      250
         ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db   220 CTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATTTACTGGGCATCCACTAG      279

Qy   251 GGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC      310
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   280 GGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC      339

Qy   311 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCT      370
         ||||||||||||||||||||||||||||||||||||||||||  |||||   ||||| ||
Db   340 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGCTA      399

Qy   371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTGTTCTCAACTCTA----      430
         |||| |||||||   |||||||||||| ||||| | |||||||||||         |
Db   400 TCGGACGTTCGGTCGAGGGACCAAGGTCGGAGATCAAACGTAAGTGCACT--------      448

Qy   431 GAAATTCTAAACTCTGAGGGGTTCGGATGAGTGGCCATTCTTGCCTAAAGCATTGAGT      490
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   449 ---TTTAAACTCTGAGGGGTTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGT      504

Qy   491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGATGGCTGCAAAGAGCTCCAACAA      550
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGATGGCTGCAAAGAGCTCCAACAA      564

Qy   551 AACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAACTCAAAACATCAAG      610
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 AACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAACTCAAAACATCAAG      624

Qy   611 ATTTTAAATACGCTTCTTGGTCTCCTGCTATAATTATCTGGGATAAGCATGCTGTTTTC      670
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 ATTTTAAATACGCTTCTTGGTCTCCTGCTATAATTATCTGGGATAAGCATGCTGTTTTC      684

Qy   671 TGTCTGTCCCTAACATGCCCTGATTATCCGCAAACACACACCAAGGCAGAACTTT      730
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 TGTCTGTCCCTAACATGCCCTGATTATCCGCAAACACACACACCAAGGCAGAACTTT      744

Qy   731 GTTACTTAAACACCATCCATCCTGTTGCTTCTTCTTGCTTCTTGTTTCCTCAGGCTGACCATCTGTC      790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 GTTACTTAAACACCATCCATCCTGTTGCTTCTTCTTGCTTCTTGTTTCCTCAGGCTGACCATCTGTC      804

Qy   791 TTCATCTTCCGCCATCTGATGAGCAGTGAAATCTGAAATCTGGTGTCCTCGTGTGTGCCTG      850
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Db   805 TTCATCTTCCGCCATCTGATGAGCAGTGAAATCTGAAATCTGGTGTCCTCGTGTGTGCCTG      864

Qy   851 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA      910
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Db   865 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA      924

Qy   911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACACCTACAGCCTC      970
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACACCTACAGCCTC      984

Qy   971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA     1030
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA     1044

Qy  1031 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAGGGGAGCTTCAACAGGGAGAGTGTTAG     1090
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAGGGGAGCTTCAACAGGGAGAGTGTTAG     1104

Qy  1091 AGGGAAGTGCCCCCACCTCCTCTCCACAGTTCCAGTTCCAGTTCCCATCCTTTGGCC     1150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105 AGGGAAGTGCCCCCACCTCCTCTCCACAGTTCCAGTTCCAGTTCCCATCCTTTGGCC     1164

Qy  1151 TCTGACCCTTTTCCACAGGGGGACTTCCACAGGGGGACTTCGCGGTCCTCCCAGTCATCTTTCACC     1210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165 TCTGACCCTTTTCCACAGGGGGACTTCCACAGGGGGACTTCGCGGTCCTCCCAGTCATCTTTCACC     1224

Qy  1211 TCACCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA     1270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225 TCACCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA     1284
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Qy  1271 AAGTGAATCTTTGCACCTGTGGTTTCTCCTTCCTC-ATTTAATAATAATTATTATCTGTTG     1329
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Db  1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTCCTCAATTTAATAATTATTATCTGTTG     1344

Qy  1330 TTTTACCAACTACTCAATTTCTCTTATAAGGACTAAAATATGTAGTCATCCTAAGGCGCA     1389
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Db  1345 -TTTACCAACTACTCAATTTCTCTTATAAGGACTAAAATATGTAGTCATCCTAAGGCGCA     1403

Qy  1390 TAACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT     1449
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Db  1404 TAACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT     1463

Qy  1450 CCTCCCTCAAACCCACAAAGCCTTCGTCCTGTCCTCACAGTCCCCTGGGCCATCGTAGGAGAGAC     1509
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Db  1464 CCTCCCTCAAACCCACAAAGCCTTCGTCCTGTCCTCACAGTCCCCTGGGCCGTGTGGAGGAGAC     1523

Qy  1510 TTGCTTCCTTGTTTCCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGT     1569
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Db  1524 TTGCTTCCTTGTTTTCCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGT     1583

Qy  1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA     1629
         ||||| |||||||||||||||||||||||||||||||||||||||||  |||||||||||
Db  1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA     1643

Qy  1630 AAGAAGAAACCTGCTATAAAGAGAATC     1656
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Db  1644 AAGAAGAAACCTGCGCGCCGATCGATTC     1670
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RESULT 10
HSIGKA.
LOCUS       HSIGKA                  5364 bp    DNA     linear   PRI 16-OCT-1992
DEFINITION  H.sapiens DNA for IG kappa JC region.
ACCESSION   X67858
VERSION     X67858.1  GI:33217
KEYWORDS    Ig kappa light chain.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5364)
AUTHORS     Garrard,W.T.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1992) W.T. Garrard, UT Southwestern Medical
            Centre, Department of Biochemistry, 5323 Harry Hines Blvd., Dallas
            TX 7525, USA
REFERENCE   2  (bases 1 to 5364)
AUTHORS     Whitehurst,C., Henney,H.R., Max,E.E., Schroeder,H.W. Jr.,
            Stuber,F., Siminovitch,K.A. and Garrard,W.T.
TITLE       Nucleotide sequence of the intron of the germline human kappa
            immunoglobulin gene connecting the J and C regions reveals a matrix
            association region (MAR) next to the enhancer
JOURNAL     Nucleic Acids Res. 20 (18), 4929-4930 (1992)
MEDLINE     93027217
PUBMED      1408808
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                     /note="J2 region"
     misc_feature    917..955
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                     /note="matrix association region (MAR)"
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misc_feature   4491..4993
                /note="constant region"

BASE COUNT   1623 a   1035 c   1114 g   1592 t
ORIGIN

Query Match   60.4%;   Score 1183.2;   DB 9;   Length 5364;
Best Local Similarity   99.6%;   Pred. No. 2.8e-270;
Matches 1207;   Conservative 0; Mismatches 3;   Indels 2;   Gaps 2;

Qy   433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT   492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4154 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT   4213

Qy   493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA   552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4214 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA   4273

Qy   553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAGAT   612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4274 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAGAT   4333

Qy   613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG   672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4334 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG   4393

Qy   673 TCTGTCCCTAAACATGCCCTGTGATTATCCGCAAACAACACACCCAGGGCCAGAACTTTGT   732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4394 TCTGTCCCTAAACATGCCCTGTGATTATCCGCAAACAACACACCCAGGGCCAGAACTTTGT   4453

Qy   733 TACTTAAACACCATCCTCGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT   792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4454 TACTTAAACACCATCCTCGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT   4513

Qy   793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT   852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4514 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT   4573

Qy   853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCCTCCAATC   912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4574 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCCTCCAATC   4633

Qy   913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAGCAAGGACAGCACCTAGCCTCAG   972
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4634 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAGCAAGGACAGCACCTAGCCTCAG   4693

Qy   973 CAGGACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT   1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4694 CAGGACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT   4753

Qy   1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG   1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4754 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG   4813

Qy   1093 GGAGAAGTGCCCCACCTGCCTCCCAGTTCAGCTGACCTGACCCCCATCCTTTGGCCTC   1152
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4814 GGAGAAGTGCCCCACCTGCCTCCCAGTTCAGCTGACCTGACCCCCATCCTTTGGCCTC   4873

Qy   1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGCTCCCTATTGCGGTCTTCACCTC   1212
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Db   4874 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGCTCCCTATTGCGGTCTTCACCTC   4933

Qy   1213 ACCCCCCTCCTCCTTGGCTTTAATATGCTAATGTTGGAGGAATGAATAAATAAA   1272
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Db   4934 ACCCCCCTCCTCCTTGGCTTTAATATGCTAATGTTGGAGGAATGAATAAATAAA   4993

Qy   1273 GTGAATCTTTGCACCGTGTGTTTCTCTCTTCCTC-ATTTAATAATTATTATCTGTTGTT   1331
           ||||||||||||||| |||||||||||||||||| |||||||||| |||||||||||||
Db   4994 GTGAATCTTTGCACCGTGTGTTTCTCTCTTCCTTCAATTTAATAATTAATTATCTGTTG-T   5052

Qy   1332 TTACCAACTACTCAATTTCTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCATA   1391
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Db   5053 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA   5112

1392 ACCATTTATAAAAATCATCCTTCATTCATTTACCCATCATCATCCTCTGCAAGACAGTCC   1451
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
5113 ACCATTTATAAAAATCATCCTTCATTCATTTACCCATCATCATCCTCTGCAAGACAGTCC   5172

1452 TCCCTCAAACCCACAAGCCTTCGTCCTCCTCCTCACAGTCCCTGGCCATGGCAGTAGGAGACTT   1511
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
5173 TCCCTCAAACCCACAAGCCTTCGTCCTCCTCCTCACAGTCCCTGGCCGTGGTAGGAGAGACTT   5232

1512 GCTTCCTTCGTTTCCCCTCCTCAGACAAGCCCTCATAGTCCTTTTAAGGTGACAGGTCT   1571
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
5233 GCTTCCTTCGTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGTGACAGGTCT   5292

1572 TACAGTCATATATCCTTTGATTCAATTCAATTCCTGGAATCAACCAAAGCAAATTTTTCAAAA   1631
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
5293 TACGGTCATATATCCTTTGATTCAATTCAATTCCTGGGAATCAACCAAGGCAAATTTTTCAAAA   5352

1632 GAAGAAACCTGC   1643
      ||||||||||||
5353 GAAGAAACCTGC   5364

RESULT 11
AR035236
LOCUS   AR035236   1276 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION   Sequence 53 from patent US 5871732.
ACCESSION   AR035236
VERSION   AR035236.1   GI:5951904
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1276)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE   Anti-CD4 antibody homologs useful in prophylaxis and treatment of
             AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 53 16-FEB-1999;
FEATURES   Location/Qualifiers
     source   1..1276
                     /organism="unknown"
BASE COUNT   340 a   352 c   244 g   340 t
ORIGIN

Query Match   60.3%;   Score 1181.4;   DB 6;   Length 1276;
Best Local Similarity   98.9%;   Pred. No. 6.4e-270;
Matches 1210;   Conservative 0; Mismatches 11;   Indels 2;   Gaps 2;

Qy   435 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC   494
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Db   24 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC   83

Qy   495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA   554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA   143

Qy   555 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAGATT   614
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Db   144 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAGATT   203

Qy   615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTGTC   674
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Db   204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTGTC   263

Qy   675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACACACCCAGGGCGAACTTTGTTA   734
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Db   264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCGAGAACTTTGTTA   323

Qy   735 CTTAAACACCATCCTCGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA   794
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Db   324 CTTAAACACCATCCTCGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA   383

Qy   795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA   854
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Db   384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA   443

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                                    genes conserve homology in functional segments
                        JOURNAL      Cell 22 (1 Pt 1), 197-207 (1980)
                        MEDLINE      81042304
                        PUBMED       6775818
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                                        /organism="Homo sapiens"
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                                        the conceptual translation"
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                                        /protein_id="CAA23823.1"
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                             polyA_site 833
                                        /note="poly adenylation site"
                        BASE COUNT      320 a      330 c      234 g      325 t
                        ORIGIN
                        Query Match            60.3%;       Score 1181.2;   DB 9;   Length 1209;
                        Best Local Similarity  99.6%;       Pred. No. 7.1e-270;
                        Matches 1205;  Conservative 0;  Mismatches 3;  Indels 2;  Gaps 2;
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Qy    855  ATAACTTCTATCCAGAGAGGAGGCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG  914
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444  ATAACTTCTATCCAGAGAGGAGGCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG  503

Qy    915  GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGCAAGGACAGCACCTACAGCCTCAGCA  974
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Db    504  GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGCAAGGACAGCACCTACAGCCTCAGCA  563

Qy    975  GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA  1034
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Db    564  GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA  623

Qy   1035  CCCATCAGGGCCTGAGCTCGCCCGTCACAAGGGGAGTGTTAGAGGG  1094
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Db    624  CCCATCAGGGCCTGAGCTCGCCCGTCACAAGGGGAGTGTTAGAGGG  683

Qy   1095  AGAAGTGCCCCACCTGCTCCAGTTCCAGCTGACCCCCTCCCATCCTTGGCCTCTG  1154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    684  AGAAGTGCCCCACCTGCTCCAGTTCCAGCTGACCCCCTCCCATCCTTGGCCTCTG  743

Db   1155  ACCCTTTTCCACAGGGGACCTACCCCCATTGCGGTCCTCCAGCTCATCTTTCACCTCAC  1214
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    744  ACCCTTTTCCACAGGGGACCTACCCCCATTGCGGTCCTCCAGCTCATCTTTCACCTCAC  803

Qy   1215  CCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT  1274
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Db    804  CCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT  863

Qy   1275  GAATCTTTGCACCTGTGGTTTCTCTCTTCCTC-ATTTAATAATTAATTATTATTCTGTTGTTT  1333
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Db    864  GAATCTTTGCACCTGTGGTTTCTCTCTTCCTCAATTTAATAATTAATTATTATTCTGTTGTTT  923

Qy   1334  ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC  1393
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Db    924  ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTACTCCTAAGGCG-ATAAC  982

Qy   1394  CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC  1453
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Db    983  CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC  1042

Qy   1454  CCTCAAACCCACAAGCCTTCTGCTCCTCTGTCCTCCACAGTCCCCTGGGCCATGTGAGGAGACTTGC  1513
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Db   1043  CCTCAAACCCACAAGCCTTCTGCTCCTCTGTCCTCCACAGTCCCCTGGGCCATGTGAGGAGACTTGC  1102

Qy   1514  TTCCTTGTTTCCCCTCCTCCTCAGCCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGTCTTA  1573
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Db   1103  TTCCTTGTTTCCCCTCCTCCTCAGCCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGTCTTA  1162

Qy   1574  CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA  1633
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Db   1163  CAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGA  1222

Qy   1634  AGAAACCTGCTATAAAGAGAATC  1656
           ||||||||||||||||||||||
Db   1223  AGAAACCTGCGCGGCCATCGATTC  1245
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RESULT 12
HSIGK1
LOCUS         HSIGK1             1209 bp    DNA        linear       PRI 07-JAN-1995
DEFINITION    C-terminal part of human kappa-immunoglobulin gene coding for amino
              acids 109 to 214.
ACCESSION     V00557 J00241
VERSION       V00557.1  GI:33140
KEYWORDS      germ line; Ig kappa light chain; immunoglobulin.
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 1209)
AUTHORS       Hieter,P.A., Max,E.E., Seidman,J.G., Maizel,J.V.Jr. and Leder,P.
TITLE         Cloned human and mouse kappa immunoglobulin constant and J region
```

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                                key            from    to       description
                                POLYA           833    833      poly adenylation site
                                CDS             336    653      reading frame.

FEATURES        Location/Qualifiers
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                    /map="2p12"
                    /tissue_type="placenta"
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                    /note="C region"
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                    /product="immunoglobulin kappa chain"
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                    ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
                    RGEC"

BASE COUNT     320 a     330 c     234 g     325 t
ORIGIN         Chromosome 2p12; about 700 bp after <humigkc2>.

Query Match          60.3%;     Score 1181.2;  DB 9;     Length 1209;
Best Local Similarity 99.6%;     Pred. No. 7.1e-270;
Matches 1205;   Conservative   0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    435 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 60

Qy    495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTCAAAGAGTCCAACAAAACA 554
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTCAAAGAGTCCAACAAAACA 120

Qy    555 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAAACTCAAAACATCAAGATT 614
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAAACTCAAAACATCAAGATT 180

Qy    615 TAAATACGCTTCTTGGTCCTTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTCTGTC 674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TAAATACCGCTTCTTGGTCCTTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTCTGTC 240

Qy    675 TGTCCCTAACATGCCCTGTGATTATCCGCAAAGAACACACCCAAGGGCAGAACTTTGTTA 734
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGTCCCTAACATGCCCTGTGATTATCCGCAAAGAACACACACCCAAGGGCAGAACTTTGTTA 300

Qy    735 CTTAAACACCATCCTCGTTTGCTTCTTTCCTCAGGAACGTGGCTGCACCATCTGTCTTCA 794
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Db    301 CTTAAACACCATCCTCGTTTGCTTCTTTCCTCAGGAACGTGGCTGCACCATCTGTCTTCA 360

Qy    795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTGTTGTGTGCCTGCTGA 854
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Db    361 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTGTTGTGTGCCTGCTGA 420

Qy    855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
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Db    421 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 480

Qy    915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
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Db    481 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 540

Qy    975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
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Db    541 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 600
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Db   661 AGAAGTGCCCCACCTGCTCCTCAGTTCAGCTGACCCCTCCATCCTTGGCCCTG 720
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Qy  1155 ACCCTTTTCCACAGGGGACTACCCCTTATTGCGGTCCTTCCAGCTCACTTCACCTCAC 1214
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Db   721 ACCCTTTTCCACAGGGGACTACCCCTTATTGCGGTCCTTCCAGCTCACTTTCACCTCAC 780

Qy  1215 CCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGATGAATAAATAAAGT 1274
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Db   781 CCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGATGAATAAATAAAGT 840

Qy  1275 GAATCTTTGCACCTGTGGTTTCTCCTTCCTC-ATTTAATAATTAATTATTCTGTTGTTTT 1333
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Db   841 GAATCTTTGCACCTGTGGTTTCTCCTTCCTCCTCAATTTAATAATTAATTATTCTGTTG-TTT 899

Qy  1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAAATATGTAGTCATCCTAAGGGCCATAAC 1393
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Db   900 ACCAACTACTCAATTTCTCTTATAAGGGACTAAAATATGTAGTCATCCTAAGGGCCATAAC 959

Qy  1394 CATTTATAAAAATCATCCTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
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Db   960 CATTTATAAAAATCATCCTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1019

Qy  1454 CCTCAAACCCCACAAGCCTTCTGTCTCCACAGCCTTCCCTGGGGCCATGTGGAGTAGGAGACTTGC 1513
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Db  1020 CCTCAAACCCCACAAGCCTTCTGTCTCCACAGCCTTCCCTGGGGCCGTGGTAGGAGAGACTTGC 1079

Qy  1514 TTCCTGTGTTTCCCCCTCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGTCTTA 1573
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1080 TTCCTGTGTTTCCCCCTCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1139

Qy  1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTCAAAAGA 1633
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Db  1140 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1199

Qy  1634 AGAAACCTGC 1643
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Db  1200 AGAAACCTGC 1209
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RESULT 13
HUMIGKC3
LOCUS       HUMIGKC3                1209 bp    DNA      linear    PRI 05-JAN-1995
DEFINITION  Human Ig germline kappa-L chain, C region (inv3 allele).
ACCESSION   J00241
VERSION     J00241.1  GI:185938
KEYWORDS    C-region; germline; immunoglobulin light chain;
            immunoglobulin-kappa.
SEGMENT     3 of 3
SOURCE      Homo sapiens placenta DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Hieter,P.A., Max,E.E., Seidman,J.G., Maizel,J.V. Jr. and Leder,P.
  TITLE     Cloned human and mouse kappa immunoglobulin constant and J region
            genes conserve homology in functional segments
  JOURNAL   Cell 22 (1 Pt 1), 197-207 (1980)
  MEDLINE   81042304
  PUBMED    6775818
REFERENCE   2  (bases 1 to 1209)
  AUTHORS   Hieter,P.A., Maizel,J.V. Jr. and Leder,P.
  TITLE     Evolution of human immunoglobulin kappa J region genes
  JOURNAL   J. Biol. Chem. 257 (3), 1516-1522 (1982)
  MEDLINE   82120090
  PUBMED    6276389
COMMENT     Compared in [1] with the mouse C-kappa gene. There is a short
            stretch containing a highly conserved, repeated pentanucleotide
            sequence 'cagca' (bases 511-550). The authors [1] show that there
            is probably only one C-kappa locus in the human genome, instead of
            three as was previously assumed. They also present a physical map of
            the J-C region. [1] also reported the sequences for the active
            V-J1 region and the human J4 gene. [1] compared with NBRF data.
            EMBL features not translated to GenBank features:
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Qy  1035  CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG  1094
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Db   601  CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG   660

Qy  1095  AGAAGTGCCCCCACCTGCTCCTCCCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG  1154
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Db   661  AGAAGTGCCCCCACCTGCTCCTCCCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG   720

Qy  1155  ACCCTTTTTCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTCAC  1214
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Db   721  ACCCTTTTTCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTCAC   780

Qy  1215  CCCCTCCTCCTCCTGGCTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT  1274
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Db   781  CCCCTCCTCCTCCTGGCTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT   840

Qy  1275  GAATCTTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATTAATTATTATTATCGTTGTTT  1333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GAATCTTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATTATTATTATTATCGTTG-TTT   899

Qy  1334  ACCAACTACTCAATTTCTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCATAAAC  1393
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Db   900  ACCAACTACTCAATTTCTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCATAAAC   959

Qy  1394  CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCGAAGACAGTCCTC  1453
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Db   960  CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCGAAGACAGTCCTC  1019

Qy  1454  CCTCAAACCCACAAGCCTTCGTCTCCTCCTCCCTGGGCCATGGTAGGAGAGACTTGC  1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1020  CCTCAAACCCACAAGCCTTCGTCTCCTCCTCCCTGGGCCATGGTAGGAGAGACTTGC  1079

Qy  1514  TTCCTTGTTTCCCCTCCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA  1573
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Db  1080  TTCCTTGTTTCCCCTCCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA  1139

Qy  1574  CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA  1633
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Db  1140  CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGCAAATTTTTCAAAAGA  1199

Qy  1634  AGAAACCTGC  1643
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Db  1200  AGAAACCTGC  1209
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RESULT 14

AR035234

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LOCUS       AR035234                1241 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 51 from patent US 5871732.
ACCESSION   AR035234
VERSION     AR035234.1  GI:5951902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1241)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE     Anti-CD4 antibody homologs useful in prophylaxis and treatment of
            AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 51 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..1241
                     /organism="unknown"
BASE COUNT      329 a    340 c    242 g    330 t
ORIGIN

Query Match      60.3%;  Score 1181.2;  DB 6;  Length 1241;
Best Local Similarity 99.6%;  Pred. No. 7.1e-270;
Matches 1205;  Conservative 0;  Mismatches 3;  Indels 2;  Gaps 2;
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Qy   435  TTCTAAACTTCGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC  494
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Db    24  TTCCTTGTTTCCCCTCCAGCAAGCCCTCATAGTCCTTTTTGCCTAAAGCATTGAGTTTAC  83
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Qy   495  TGCAAGGTCAGAAAAGCATGCAAAAGCCTCAGAATGCGCTGCAAAGAGCTCCAACAAAACA  554
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Db    84  TGCAAGGTCAGAAAAGCATGCAAAAGCCTCAGAATGCGCTGCAAAGAGCTCCAACAAAACA  143

Qy   555  ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGAGGAAGAAACTCAAAACATCAAGATTT  614
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Qy   615  TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTCTGTC  674
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Db   204  TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTCTGTC  263

Qy   675  TGTCCTAACATGCCCTGTGATTATCCGCAAACAACACCAAGGGCAGAACTTGTTA  734
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Db   264  TGTCCTAACATGCCCTGTGATTATCCGCAAACAACACCAAGGGCAGAACTTGTTA  323

Qy   735  CTTAAACACCATCCTGTTTGCTCTTTCCTCCAGGAACTGTGGCTGCACCATCTGTCTTCA  794
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Db   324  CTTAAACACCATCCTGTTTGCTCTTTCCTCCAGGAACTGTGGCTGCACCATCTGTCTTCA  383

Qy   795  TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA  854
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Db   384  TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA  443

Qy   855  ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG  914
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Db   444  ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG  503

Qy   915  GTAACTCCCAGGAGAGTGTCACAGAGGCAGGACAAGCACAGTACACCCTCAGCCTCAGCA  974
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Db   504  GTAACTCCCAGGAGAGTGTCACAGAGGCAGGACAAGCACAGTACACCCTCAGCCTCAGCA  563

Qy   975  GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA  1034
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Db   564  GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA  623

Qy  1035  CCCATCAGGGCCTCGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAGAGGG  1094
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Db   624  CCCATCAGGGCCTCGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAGAGGG  683

Qy  1095  AGAAGTGCCCCACCTGCTCCTCCCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG  1154
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Db   684  AGAAGTGCCCCACCTGCTCCTCCCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG  743

Qy  1155  ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTCAC  1214
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Db   744  ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTCAC  803

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Qy  1334  ACCAACTACTCAATTTCTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCATAAC  1393
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Qy  1394  CATTTATAAAAATCATCCTTCATTTCATTTTTACCCTATCATCCTCTGCGAAGACAGTCCTC  1453
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Qy  1454  CCTCAAACCCCACAAGCCTTCTGTGTCCTCCACAGTCCCGGGCCATGGTAGGAGAGACTTGC  1513
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Db   900  ACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGCAGCAGGACAGCAAGGACAGCA   959

Qy   421  ACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGCAGCAGGACAGCAAGGACAGCA   480
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Db   960  CCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT  1019

Qy   481  CCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT   540
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Qy  1020  ACGCCTGCGAAGTCACCCATCAGGGCCTCGCCCGTCACAAAGAGCTTCAACAGGG        1079
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Db   541  ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG     600

Qy  1080  GAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTCCTCAGTTCCAGCCCTGACCCCCTCCC   1139
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Qy  1200  CATCTTTCACCTCACCCCCTCCTCCTGGCTTAATTATGCTAATGTTGGAGGAGA       1259
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Db   781  ATGAATAAATAAAGTGAATCTTGCACCTGTGGTTTCTCTTTCCTCATTTAATAATTA      840

Qy  1320  TTATCGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATC   1379
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Search completed: July 18, 2003, 13:47:24
Job time : 5490.97 secs

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Db  1163  CGGTCATATATCCTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTCAAAAGA   1222

Qy  1634  AGAAACCTGC   1643
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Db  1223  AGAAACCTGC   1232
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RESULT 15
HSKAPPALC
LOCUS   HSKAPPALC   1075 bp   mRNA   linear   PRI 09-MAY-1996
DEFINITION H.sapiens gene encoding kappa light chain constant region.
ACCESSION   X96754
VERSION   X96754.1   GI:1237214
KEYWORDS   constant region; immunoglobulin; immunoglobulin kappa chain;
            immunoglobulin light chain; immunoglobulin superfamily.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1075)
  AUTHORS   Hilger,C., Grigioni,F. and Hentges,F.
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1075)
  AUTHORS   Hilger,C.
  TITLE   Direct Submission
  JOURNAL   Submitted (21-MAR-1996) C. Hilger, Centre Hospitalier, 4 Rue
            Barble, L-1210 Luxembourg, LUXEMBOURG
COMMENT   Related sequences V00557 and J00241.
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BASE COUNT   282 a   301 c   204 g   288 t
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Best Local Similarity   99.8%; Pred. No. 7e-244;
Matches 1073; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy   480  AAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAGAAAAGCCCTCAGAATGGCTGCAAAG   539
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Db     1  AAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAGAAAAGCCCTTAGAGTGGCTGCAAAG    60

Qy   540  AGCTCCACAAAACAATTTGAACTTTATTAAGGAAGAGGGGAAGTAGGGGAAGCTAGGAGAAACTC   599
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Db    61  AGCTCCACAAAACAATTTGAACTTTATTAAGGAAGAGGGGAAGTAGGGGAAGCTAGGAGAAACTC   120

Qy   600  AAAACATCAAGATTTTAAATAACGGTTCCTTGGTCTCCTTGCTATAAATAATTATCTGGGATAAGC   659
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Qy   660  ATGTGTTTTCTGTCGTCCTAACATGCCCTGATTATCCGCAAACACACCACCAAG   719
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Db   181  ATGTGTTTTCTGTCGTCCTAACATGCCCTGATTATCCGCAAACACACCACCCAAG   240

Qy   720  GGCAGAACTTGTACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTG   779
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Db   241  GGCAGAACTTGTACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTG   300

Qy   780  CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTG   839
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Db   301  CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTG   360

Qy   840  TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATA   899
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OM nucleic - nucleic search, using sw model

              GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.


Run on:        July 18, 2003, 04:16:54 ; Search time 3396.49 Seconds
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Title:         US-09-627-896B-21
Perfect score: 1960
Sequence:      1 tctagaccaccatggattca........cccacttctaggatcaattc 1960

Scoring table: IDENTITY_NUC
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Searched:      16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

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Post-processing: Minimum Match 0%
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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	4	521.8	26.6	557	14	BM768769	BM768769	K-EST0051
	5	521.8	26.6	610	14	BQ049622	BQ049622	AGENCOURT
	6	521.8	26.6	643	14	BQ712156	BQ712156	AGENCOURT
c	7	521.4	26.6	648	14	BM974791	BM974791	UI-CF-EC1
c	8	520.4	26.6	544	10	AW575364	AW575364	UI-HF-BL0
c	9	520.2	26.5	641	14	BQ062789	BQ062789	AGENCOURT
c	10	520.2	26.5	927	14	BQ706352	BQ706352	AGENCOURT
c	11	519.8	26.5	563	13	BM509302	BM509302	ih16b08.y
c	12	519.6	26.5	643	14	BQ573939	BQ573939	UI-H-EZ0-
c	13	519.2	26.5	618	10	AW575927	AW575927	UI-HF-BL0
c	14	518.8	26.5	731	14	BQ181514	BQ181514	UI-H-EU0-
c	15	518.4	26.4	539	10	AW575346	AW575346	UI-HF-BL0
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c	20	518.4	26.4	576	14	BM894026	BM894026	ij62c12.x
c	21	518.4	26.4	608	14	BM991141	BM991141	UI-H-DI0-
c	22	518.4	26.4	620	13	BM511892	BM511892	ij75d09.x
c	23	518.4	26.4	626	13	BM510477	BM510477	ij46b08.x
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c	27	518.4	26.4	705	14	BQ007821	BQ007821	UI-H-EI0-
c	28	518.4	26.4	737	14	BQ007971	BQ007971	UI-H-EI0-
c	29	518.4	26.4	750	14	BQ004577	BQ004577	UI-H-EI0-
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c	37	516.8	26.4	608	14	BM973577	BM973577	UI-CF-EC1
c	38	516.8	26.4	624	13	BM510468	BM510468	ij46a10.x
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c	43	516	26.3	530	13	BI711279	BI711279	i496d10.x
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ALIGNMENTS

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LOCUS       BM788938           672 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0068215 S19N665307 Homo sapiens cDNA clone S19N665307-2-D11
            5', mRNA sequence.
ACCESSION   BM788938
VERSION     BM788938.1  GI:19137170
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2  row: D  column: 11
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1..672
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Qy   1270 AAAGTGAATCTT 1281
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Db    661 AAAGTGAATCTT 672


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LOCUS       BM819800                656 bp    mRNA        linear   EST 06-MAR-2002
DEFINITION  K-EST0087997 S16N667673 Homo sapiens cDNA clone S16N667673-2-G02
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ACCESSION   BM819800
VERSION     BM819800.1  GI:1917621З
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 656)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2    row: G    column: 02
            High quality sequence stop: 656.
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                     /clone_lib="S16N667673"
                     /sex="M"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
            Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
            bacterial alkaline phosphatase (BAP) and then decapped
            with tobacco acid pyrophosphatase (TAP). The decapped
            intact mRNA was ligated with DNA-RNA linker including EcoR
            I site by treatment of T4 RNA ligase and the first strand
            cDNA was synthesized from oligo dT-selected mRNA by
            priming with dT-tailed vector. The dT-tailed vector was
            adjusted to have about 60nt. The cDNA vector was
            circularized with E. coli DNA ligase after digestion of
            EcoRI which site is also included in vector. An RNA strand
            converted to a DNA strand by Okayama-Berg method. The
            obtained cDNA vectors were used for transformation of
            competent cells E. coli Top10F' by electroporation method.
            The cDNA libraries constructed by this method are
            full-length enriched cDNA library."
BASE COUNT      182 a    166 c    148 g    160 t
ORIGIN

Query Match        28.3%;  Score 553.8;  DB 14;  Length 656;
Best Local Similarity   99.6%;  Pred No. 1.9e-103;
Matches  555;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    433 AATTCTAAACTCTGAAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTTT 492
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 AATTCTAAACTCTGAAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTTT 159

Qy    493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA 552
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCACAATGGCTGCAAAGAGCTCCAACAAA 219

Qy    553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT 612
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S19N665307-2-D11"
/clone_lib="S19N665307"
/sex="M"
/lab_host="Top10F'"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT      164 a    199 c    141 g    168 t
ORIGIN

Query Match        34.3%;  Score 672;  DB 14;  Length 672;
Best Local Similarity  100.0%;  Pred. No. 1.1e-127;
Matches  672;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    610 GATTTTAAATACGGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTT 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATTTTAAATACGGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTT 60

Qy    670 CTGTCTGTCCCTAACATGCCCTGATTATCCGCAAACAACACACCCAAGGGCAGAACTT 729
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGTCTGTCCCTAACATGCCCTGATTATCCGCAAACAACACACCCAAGGGCAGAACTT 120

Qy    730 TGTTACTTAAACACCATCCTGTTTGCTTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGT 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTTACTTAAACACCATCCTGTTTGCTTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGT 180

Qy    790 CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT 849
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Db    181 CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT 240

Qy    850 GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCA 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCA 300

Qy    910 ATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT 969
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT 360

Qy    970 CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACCAAAGTCTACGCCTGCGA 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACCAAAGTCTACGCCTGCGA 420

Qy   1030 AGTCACCCATCAGGGCCTGAGCTGCGCCGTCACCAAAGAGCTTCAACAGGGAGAGTGTTA 1089
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTCACCCATCAGGGCCTGAGCTGCGCCGTCACCAAAGAGCTTCAACAGGGAGAGTGTTA 480

Qy   1090 GAGGGAGAAGTGCCCCCACCTGCTCCTCCACCTGACCCCCTCCCCATCCTTTGGC 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GAGGGAGAAGTGCCCCCACCTGCTCCTCCACCTGACCCCCTCCCCATCCTTTGGC 540

Qy   1150 CTCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTTCTCCAGCTTCATCTTTCAC 1209
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTTCTCCAGCTTCATCTTTCAC 600

Qy   4210 CTCACCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAATGAATAAAT 1269
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTCACCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAATGAATAAAT 660
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```
Db  220  CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAGAAACTCAAAACATCAAGAT  279

Qy  613  TTTAAAATACGCTTCCTTGGTCTCCTTGCTATAATTATCTGGATAAGACATGCTGTTTTCTG  672
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  280  TTTAAAATACGCTTCCTTGGTCTCCTTGCTATAATTATCTGGATAAGACATGCTGTTTTCTG  339

Qy  673  TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCAAGGGCAGAACTTTGT  732
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  340  TCTGTCCCTAACATGCCCCGTGATTATCCGCAAACAACACACCAAGGGCAGAACTTTGT  399

Qy  733  TACTTAAACACCATCCTGTTGCTTCTTCCTCAGGAACTGTGGCTGACCATCTGTCTT  792
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Db  400  TACTTAAACACCATCCTGTTGCTTCTTCCTCAAGAACTGTGGCTGCCACCATCTGTCTT  459

Qy  793  CATCTTCCGCCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT  852
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Db  460  CATCTTCCGCCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT  519

Qy  853  GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC  912
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Db  520  GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC  579

Qy  913  GGGTAACTCCCAGGAGAGTGTCACAGAGGCAGGACAGCAGGACAGCAGCCTTCAG  972
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  973  CAGCACCCTGACGCTGA  989
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Db  640  CAGCACCCTGACGCTGA  656
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RESULT 3

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BM510472/c
LOCUS        BM510472        552 bp    mRNA    linear    EST 15-FEB-2002
DEFINITION   ij46b02.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:5633978
             3' similar to SW:KAC_HUMAN P01834 IG KAPPA CHAIN C REGION .; mRNA
             sequence.
ACCESSION    BM510472
VERSION      BM510472.1    GI:18681615
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 552)
AUTHORS      Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
             Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
             Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
             Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
             ,M., Gibbons,M., McCann,K., Cole,R., Tsagareishvili,R., Williams,T.
             , Jackson,Y. and Bowers,Y.
TITLE        Endocrine Pancreas Consortium
JOURNAL      Unpublished (2000)
COMMENT      Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
             Endocrine Pancreas Consortium
             Harvard University, Howard Hughes Medical Institute
             Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
             MA 02138
             Tel: 617-495-1812
             Fax: 617-495-8557
             Email: dmelton@biohp.harvard.edu
             Library was constructed by Dr. J. Ferrer In vivo mass-excised to
             pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
             University Genome Sequencing Center For information on obtaining a
             clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
             Seq primer: -40UP from Gibco
             High quality sequence stop: 448.
FEATURES             Location/Qualifiers
     source          1..552
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Db  118  /tissue_type="insulinoma"
              /lab_host="DH10B (phage-resistant)"
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              XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
              (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
              pBluescript SK- by Dr. H. Inoue following the Washington
              University protocol
              (http://genome.wustl.edu/est/lambda_protocol.shtml).
              Please contact Hiroshi Inoue, MD/PhD for further
              information on this library (Metabolism Division, Permutt
              Laboratory, Washington University School of Medicine, Box
              8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
              is a Washington University Pancreas EST project library. "
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BASE COUNT       118 a       162 g      154 t      118 c
ORIGIN
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Query Match           26.7%;    Score 523.4;    DB 13;    Length 552;
Best Local Similarity 99.8%;    Pred. No. 3.3e-97;
Matches 524;    Conservative 0;    Mismatches 0;    Indels 1;    Gaps 0;
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Qy  770   ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGA  829
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Db  552   ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGA  493

Qy  830   ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG  889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  492   ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG  433

Qy  890   AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGGCAGGACAGC  949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  432   AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGGCAGGACAGC  373

Qy  950   AAGGACAGCAGCCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA  1009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  372   AAGGACAGCAGCCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA  313

Qy  1010  CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCGTCGAGTCGCCCGTCACAAAGAGC  1069
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Db  312   CACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCGTCGAGTCGCCCGTCACAAAGAGC  253

Qy  1070  TTCAACAGGGGAGAGTGTTAGAGGGAGGAGAAGTGCCCCCACCTGCTTCCAGTTCCAGCCTG  1129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252   TTCAACAGGGGAGAGTGTTAGAGGGAGGAGAAGTGCCCCCACCTGCTTCCAGTTCCAGCCTG  193

Qy  1130  ACCCCCTCCATCTTTGGCCCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGG  1189
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Db  192   ACCCCCTCCATCTTTGGCCCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGG  133

Qy  1190  TCCTCCAGCTCATCTTCACCTCACCCCCCCTCCTTGGCTTTAATTATGCTAATG  1249
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Db  132   TCCTCCAGCTCATCTTCACCTCACCCCCCCTCCTCTTGGCTTTAATTATGCTAATG  73

Qy  1250  TTGGAGGAAATGAATAAATAAATAAAGTGAATCTTTGCACCTGTGGTT  1294
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Db  72    TTGGAGGAAATGAATAAATAAATAAAGTGAATCTTTGCACCTGTGGTT  28
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RESULT 4

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BM768769
LOCUS        BM768769        557 bp    mRNA    linear    EST 04-MAR-2002
DEFINITION   K-EST0051794 S14K402 Homo sapiens cDNA clone S14K402-11-A06 5',
             mRNA sequence.
ACCESSION    BM768769
VERSION      BM768769.1    GI:19098384
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 557)
AUTHORS      Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
             Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
             Kim,Y.S.
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TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 11 row: A column: 06
            clone_lib="S14K402"
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S14K402-11-A06"
                     /clone_lib="S14K402"
                     /cell_line="K402"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tobacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT    140 a    171 c    126 g    120 t
ORIGIN

Query Match          26.6%;      Score 521.8; DB 14;     Length 557;
Best Local Similarity 99.6%;      Pred. No. 7.1e-97;
Matches   523;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy    766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db     33 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 92

Qy    826 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db     93 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 152

Qy    886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
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Db    153 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 212

Qy    946 CAGCAAGGACAGCAGCACCTACAGCCTGAGCAAGCTGAGCAAAGCAGACTACGA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    213 CAGCAAGGACAGCAGCACCTACAGCCTGAGCAAGCTGAGCAAAGCAGACTACGA 272

Qy   1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Db    273 GAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 332

Qy   1066 GAGCTTCAACAGGGGAGGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCCAGTTCCAG 1125
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Db    333 GAGCTTCAACAGGGGAGGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCCAGTTCCAG 392

Qy   1126 CCTGACCCCCTCCATCTTTGGCCTTGACCCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db    393 CCTGACCCCCTCCATCTTTGGCCTTGACCCCTTTTTCCACAGGGGACCTACCCCTATT 452

Qy   1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTTGGCTTAATTATGCT 1245
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Qy   1246 AATGTTGGAGGAGAATGAATAAATAAATAAAGTGAATCTTTGCACCTGT 1290
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RESULT 5
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LOCUS       BQ049622
DEFINITION  AGENCOURT_7077241 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5787516
            5', mRNA sequence.
ACCESSION   BQ049622
VERSION     BQ049622.1  GI:19808962
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 610)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12877 row: p  column: 13
            High quality sequence stop: 595.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5787516"
                     /tissue_type="lymphoma, cell line"
                     /clone_lib="NIH_MGC_85"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.867 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT    161 a    179 c    140 g    130 t
ORIGIN

Query Match          26.6%;      Score 521.8; DB 14;     Length 610;
Best Local Similarity 99.6%;      Pred. No. 7e-97;
Matches   523;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy    766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 125

Qy    826 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 185

Qy    886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 245

Qy    946 CAGCAAGGACAGCAGCACCTACAGCCTGAGCAAGCTGAGCAAAGCAGACTACGA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CAGCAAGGACAGCAGCACCTACAGCCTGAGCAAGCTGAGCAAAGCAGACTACGA 305

Qy   1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 GAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 365
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Qy    1066  GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGGAGAGTGCCCCCACCTGCTCCTCAGTTCCAG  1125
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Db     366  GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGGAGAGTGCCCCCACCTGCTCCTCAGTTCCAG   425

Qy    1126  CCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT  1185
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Db     426  CCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT   485

Qy    1186  GCGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTCTCCTTTAATTATGCT  1245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486  GCGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTCTCCTTTAATTATGCT   545

Qy    1246  AATGTTGGAGGAGAATGAATAAATAAATGAATCTTTGCACCTGT  1290
            |||||||||||||||||||||||||||||||||||||||||
Db     546  AATGTTGGAGGAGAATGAATAAATAAATGAATCTTTGCACCTGT   590
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RESULT 6
BQ712156
BQ712156 LOCUS   BQ712156   643 bp   mRNA   linear   EST 16-JUL-2002
          DEFINITION   AGENCOURT_8349876 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280272
                       5', mRNA sequence.
          ACCESSION   BQ712156
          VERSION   BQ712156.1   GI:21851055
          KEYWORDS   EST.
          SOURCE   human.
          ORGANISM   Homo sapiens
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          REFERENCE   1 (bases 1 to 643)
          AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
          TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
          JOURNAL   Unpublished (1999)
          COMMENT   Contact: Robert Strausberg, Ph.D.
                       Email: cgapbs-r@mail.nih.gov
                       Tissue Procurement: Dr. Mark Watson
                       cDNA Library Preparation: Rubin Laboratory
                       cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                       DNA Sequencing by: Agencourt Bioscience Corporation
                       Clone distribution: MGC clone distribution information can be
                       found through the I.M.A.G.E. Consortium/LLNL at:
                       http://image.llnl.gov
                       Plate: LLCM2471 row: d column: 01
                       High quality sequence stop: 594.

FEATURES   Location/Qualifiers
     source   1..643
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6280272"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   179 a   189 c   133 g   132 t   10 others
ORIGIN

Query Match   26.6%;   Score 521.8;   DB 14;   Length 643;
Best Local Similarity   99.4%;   Pred. No. 7e-97;
Matches   523;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy     763  CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGGCCATCTGATGAGCAGTTGAA  822
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Db      69  CCCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGGCCATCTGATGAGCAGTTGAA  128

Qy     823  ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT  882
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129  ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT  188
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Qy     883  ACAGTGGAAGGTGGATAACGCCCCTCCAATCGGGTAACTCCCAGGAGAGAGTGTCACAGAGCA   942
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     189  ACAGTGGAAGGTGGATAACGCCCCTCCAATCGGGTAACTCCCAGGAGAGAGTGTCACAGAGCA   248

Qy     943  GGACAGCAAGGACAGCAGCACCTACAGCCTCAGCAGCACCCTGAGCGTGAGCAAAGCAGACTA  1002
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249  GGACAGCAAGGACAGCAGCACCTACAGCCTCAGCAGCACCCTGAGCGTGAGCAAAGCAGACTA   308

Qy    1003  CGAGAAACAAAAGTCTACGCCTGCGAAGTCACCATCAGGGGCTCGCCCGTCAC  1062
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309  CGAGAAACAAAAGTCTACGCCTGCGAAGTCACCATCAGGGGCTCGCCCGTCAC   368

Qy    1063  AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGGAGAAGTGCCCCCACCTGCTCCTCAGTTC  1122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369  AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGGAGAAGTGCCCCCACCTGCTCCTCAGTTC   428

Qy    1123  CAGCCTGACCCCCTCCCATCCTTTGGCCTTGACCCTTTTCCACAGGGGACCTACCCCTT  1182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429  CAGCCTGACCCCCTCCCATCCTTTGGCCTTCGACCCTTTTCCACAGGGGACCTACCCCT   488

Qy    1183  ATTGCGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTCTCCTTGGCTTTAATTAT  1242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     489  ATTGCGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTCTCCTTGGCTTTAATTAT   548

Qy    1243  GCTAATGTTGGAGGAGAATGAATGAATAAAGTGAATCTTTGCACCT  1288
            |||||||||||||||||||||||||||||||||||||||||||
Db     549  GCTAATGTTGGAGGAGAATGAATGAATAAAGTGAATCTTTGNCCCT   594
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RESULT 7
BM974791/c
BM974791 LOCUS   UI-CF-EC1-acd-g-18-0-UI.s1 UI-CF-EC1 Homo   648 bp   mRNA   linear   EST 21-MAR-2002
          DEFINITION   UI-CF-EC1-acd-g-18-0-UI 3', mRNA sequence.
          ACCESSION   BM974791
          VERSION   BM974791.1   GI:19592382
          KEYWORDS   EST.
          SOURCE   human.
          ORGANISM   Homo sapiens
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          REFERENCE   1 (bases 1 to 648)
          AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
          TITLE   Normalization and subtraction: two approaches to facilitate gene
                       discovery
          JOURNAL   Genome Res. 6 (9), 791-806 (1996)
          MEDLINE   97044477
          COMMENT   Contact: McCray, PB
                       McCray Lab
                       University of Iowa
                       2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
                       Tel: 319 356 4866
                       Fax: 319 356 7171
                       Email: paul-mccray@uiowa.edu
                       Tissue Procurement: Dr. M. J. Welsh, University of Iowa
                       cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
                       cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                       DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                       Clone Distribution: Researchers may obtain clones from Research
                       Genetics (www.resgen.com).
                       Seq primer: M13 FORWARD
                       POLYA=Yes.

FEATURES   Location/Qualifiers
     source   1..648
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-acd-g-18-0-UI"
                     /clone_lib="UI-CF-EC1"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a

REFERENCE   1 (bases 1 to 544)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             The sequence contained an oligo-dT track that was present in the
             oligonucleotide that was used to prime the synthesis of first
             strand cDNA and therefore this may represent a bonafide poly A
             tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward
             POLYA=Yes
FEATURES   Location/Qualifiers
     source   1..544
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3060557"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   116 a   117 c   162 g   148 t   1 others
ORIGIN

Query Match   26.6%; Score 520.4; DB 10; Length 544;
Best Local Similarity   99.6%; Pred. No. 1.4e-96;
Matches   521; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   766 AGGAACTGGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db   540 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 481

Qy   826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 421

Qy   886 GTGGAAGGTGGATAAACGCCCTCCAATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGA 945
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 GTGGAAGGTGGATAAACGCCCTCCAATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGA 361

Qy   946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 301

Qy   1006 GAAACACAAAGTCTACGGCCTGCGAAGTCACCCATCAGGGGCTGAGCTCGCCCGTCACAAA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 GAAACACAAAGTCTACGGCCTGCGAAGTCACCCATCAGGGGCTGAGCTCGCCCGTCACAAA 241

Qy   1066 GAGCTTCAACAGGGAGAGTGTTAGAGGGAGGAGAGTGCCCCACCTACCTCCTCAGTTCCAG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 GAGCTTCAACAGGGAGAGTGTTAGAGGGAGGAGAGTGCCCCACCTACCTCCTCAGTTCCAG 181

Qy   1126 CCTGACCCCTCCATCCTTGGCCTCGACCCTTTTCCACAGGGGACTACCCCTATT 1185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 CCTGACCCCTCCATCCTTTGGCCTCGACCCTTTTCCACAGGGGACTACCCCTATT 121

Qy   1186 GCGGTCCTCCAGCTCATCTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATTGCT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GCGGTCCTCCAGCTCATCTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATTGCT 61

RESULT 8
LOCUS   AW575364   544 bp   mRNA   linear   EST 15-MAR-2000
DEFINITION   UI-HF-BL0-acw-e-03-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
             IMAGE:3060557 3', mRNA sequence.
ACCESSION   AW575364
VERSION   AW575364.1   GI:7246903
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
          ||||||||||||||||||||||||||||||||||||||||||
Db   60 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 18

RESULT 9
BQ062789
LOCUS   BQ062789   641 bp   mRNA   linear   EST 02-APR-2002
DEFINITION AGENCOURT_6826785 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924314
            5', mRNA sequence.
ACCESSION   BQ062789
VERSION   BQ062789.1 GI:19889923
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 641)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished.(1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: d column: 11
            High quality sequence start: 77
            High quality sequence stop: 596.
FEATURES   Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="IMAGE:5924314"
            /clone_lib="NIH_MGC_99"
            /tissue_type="lymphoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Size-selected >500bp for average insert size
            1.8kb. Library constructed by Ling Hong in the laboratory
            of Gerald M. Rubin (University of California, Berkeley)
            using ZAP-cDNA synthesis kit (Stratagene) and Superscript
            II RT (Life Technologies). Note: this is a NIH_MGC
            Library."
BASE COUNT   181 a   182 c   140 g   138 t
ORIGIN

Query Match   26.5%;   Score 520.2; DB 14; Length 641;
Best Local Similarity   99.4%;   Pred. No. 1.5e-96;
Matches 522;   Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   766 AGGAACTGGCTGCACCATCGTCTTCATCTTCCCGCCATCTGATGAGGACAGTTGAAATC 825
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 ACGAACTGGCTGCACCATCGTCTTCATCTTCCCGCCATCTGATGAGGACAGTTGAAATC 155

Qy   826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db   156 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 215

Qy   886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAAGA 275

Qy   946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 335

Qy   1006 GAAACAAAGTTCACGGCCTGCGAAGTCACCATCAGGGCCTGAGCTCGCCCCGTCACAAA 1065
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Db   336 GAGCACAAAGTCACGGCCTGCGAAGTCACCATCAACAAGGCCTGAGCTCGCCCCGTCACAAA 395

Qy   1066 GAGCTTCACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCTCAGTTCCAG 1125
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   396 GAGCTTCACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCTCAGTTCCAG 455

Qy   1126 CCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCACAGGGGACTACCCCTATT 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   456 CCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCACAGGGGACTACCCCTATT 515

Qy   1186 GCGGTCCTCCAGCTCATCTTCACCTCACCCCTCCTCCTCCTTGGCTTAATTATGCT 1245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   516 GCGGTCCTCCAGCTCATCTTCACCTCACCCCTCCTCCTCCTTGGCTTAATTATGCT 575

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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Db   576 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 620

RESULT 10
BQ706352/c
LOCUS   BQ706352   927 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8355349 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279733
            5', mRNA sequence.
ACCESSION   BQ706352
VERSION   BQ706352.1 GI:21845251
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 927)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: m column: 14
            High quality sequence start: 658.
            High quality sequence stop: 658.
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:6279733"
            /clone_lib="NIH_MGC_113"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
BASE COUNT   247 a   202 c   278 g   200 t
ORIGIN

Query Match   26.5%;   Score 520.2; DB 14; Length 927;
Best Local Similarity   98.5%;   Pred. No. 1.5e-96;
Matches 525;   Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy   753 TGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG 812
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Db   550 TGCTTCTGGATCCCTGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG 491

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Qy    813  AGCAGTTGAAATCTGGAACTGCCCTCGTTGTGCCTGCTGAATAACTTCTATCCCAGAG  872
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Db    490  AGCAGTTGAAATCTGGAACTGCCCTCGTTGTGCCTGCTGAATAACTTCTATCCCAGAG  431

Qy    873  AGGCCAAAGTACAGTCAGTGGAAGGTGGATAACGCCCTCCAATCGGTAACTCCCAGGAGAGTG  932
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Db    430  AGGCCAAAGTACAGTCAGTGGAAGGTGGATAACGCCCTCCAATCGGTAACTCCCAGGAGAGTG  371

Qy    933  TCACAGCAGCAGGACAGCAGCAAGGACAGACACCTACAGCCTCAGCAGCAGCACCCTGACGGCTGAGCA  992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370  TCACAGCAGCAGGACAGCAGCAAGGACAGACACCTACAGCCTCAGCAGCAGCACCCTGACGCTGAGCA  311

Qy    993  AAGGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCT  1052
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310  AAGGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCT  251

Qy    1053 CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGC  1112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250  CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGC  191

Qy    1113 TCCTCAGTTCCAGCCTGACCCCCTCCCATCTTCTTTGGCCTCTGACCCTTTTCCACAGGGG  1172
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Db    190  TCCTCAGTTCCAGCCTGACCCCCTCCCATCTTCTTTGGCCTCTGACCCTTTTCCACAGGGG  131

Qy    1173 ACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTCCTTGG  1232
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Db    130  ACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTCCTTGG  71

Qy    1233 CTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA  1285
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Db    70   CTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA  18
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RESULT 11
BM509302/c
LOCUS   BM509302   563 bp   mRNA   linear   EST 15-FEB-2002
DEFINITION   ih16b08.y1 Human insulinoma Homo sapiens cDNA 5' similar to
              SW:KAC_HUMAN P01834 IG KAPPA CHAIN C REGION. ; mRNA sequence.
ACCESSION   BM509302
VERSION   BM509302.1 GI:18680445
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 563)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
              Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
              Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
              Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
              ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
              , Jackson,Y. and Bowers,Y.
TITLE   Endocrine Pancreas Consortium
JOURNAL   Unpublished (2000)
COMMENT   Other ESTs: ih16b08.x1
              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
              Endocrine Pancreas Consortium
              Harvard University, Howard Hughes Medical Institute
              Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
              MA 02138
              Tel: 617-495-1812
              Fax: 617-495-8557
              Email: dmelton@biohp.harvard.edu
              Library was constructed by Dr. J. Ferrer In vivo mass-excised to
              pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
              University Genome Sequencing Center For information on obtaining a
              clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
              Possible reversed clone: similarity on wrong straid
              Seq primer: -40RP from Gibco
              High quality sequence stop: 428.
FEATURES   Location/Qualifiers
     source   1..563

              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_lib="Human insulinoma"
              /tissue_type="insulinoma"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
              XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
              (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
              pBluescript SK- by Dr. H. Inoue following the Washington
              University protocol
              (http://genome.wustl.edu/est/lambda_protocol.shtml)
              Please contact Hiroshi Inoue, MD/PhD for further
              information on this library (Metabolism Division, Permutt
              Laboratory, Washington University School of Medicine, Box
              8127, 660 S Euclid Ave. St. Louis, MO 63110). Note: this
              is a Washington University Pancreas EST project library. "

BASE COUNT   119 a   128 c   169 g   146 t   1 others
ORIGIN

Query Match   26.5%;   Score 519.8; DB 13;   Length 563;
Best Local Similarity 99.4%;   Pred. No. 1.8e-96;
Matches   521; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy    766  AGGAACTGTGGCTGCCACCATCTGTCTTCCCGCCATCTGATGAGCAGTTGAAATC  825
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ACGANCTGTGGCTGCCACCATCTGTCTTCCCGCCATCTGATGAGCAGTTGAAATC  482

Qy    826  TGGAACTGCCCTCGTTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA  885
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TGGAACTGCCCTCGTTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA  422

Qy    886  GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCGGAGAGTGTCACAGAGCAGGA  945
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCGGAGAGTGTCACAGAGCAGGA  362

Qy    946  CAGCAAGGACAGCACCTACAGCCTCAGCAGCAGCACCCTGACGCTGAGCAAAGCAAGCAGACTACGA  1005
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CAGCAAGGACAGCACCTACAGCCTCAGCAGCAGCACCCTGACGCTGAGCAAAGCAAGCAGACTACGA  302

Qy    1006 GAAACACAAAGTCTACGCTGCGAAGTCACCAGGGCCTGAGCTCGCCCGTCACAAA  1065
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GAAACACAAACTCTACGCTGCGAAGTCACCAGGGCCTGAGCTCGCCCGTCACAAA  242

Qy    1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG  1125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG  182

Qy    1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT  1185
           |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    181  CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT  122

Qy    1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCT  1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCT  62

Qy    1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTG  1289
           |||||||||||||||||||||||||||||||||||||||||||
Db    61   AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTG  18
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RESULT 12
BQ573939/c
LOCUS   BQ573939   643 bp   mRNA   linear   EST 19-JUN-2002
DEFINITION   UI-H-EZ0-bax-d-24-0-UI.s1 NCI_CGAP_Chi Homo sapiens cDNA clone
              UI-H-EZ0-bax-d-24-0-UI 3', mRNA sequence.
ACCESSION   BQ573939
VERSION   BQ573939.1 GI:21477256
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 643)

```
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
           Orthoapedics
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Clone distribution information can be obtained
           from Dr. M. Bento Soares, bento-soares@uiowa.edu
           Seq primer: M13 FORWARD
           POLYA=Yes.
FEATURES        Location/Qualifiers
   source       1..643
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="UI-H-EZ0-bax-d-24-0-UI"
                /clone_lib="NCI_CGAP_Ch1"
                /tissue_type="Chondrosarcoma Grade II"
                /dev_stage="Adult"
                /lab_host="DH10B (Life Technologies)"
                /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                NCI_CGAP_Ch1 is a cDNA library containing the following
                tissue(s): Chondrosarcoma Grade II. The library was
                constructed according to Bonaldo, Lennon and Soares,
                Genome Research, 6:791-806, 1996. First strand cDNA
                synthesis was primed with an oligo-dT primer containing a
                Not I site. Double stranded cDNA was ligated to an EcoR I
                adaptor, digested with Not I, and cloned directionally
                into pT7T3-Pac vector. The oligonucleotide used to prime
                the synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (dT)18 tail. The sequence tag for this library is
                TGATCACGCT.
                TAG_LIB=UI-H-EZ0
                TAG_TISSU=grade-2-chondrosarcoma
                TAG_SEQ=ATCTAATATG"
BASE COUNT   142 a    182 g    142 c    176 t    1 others
ORIGIN

Query Match       26.5%;    Score 519.6;  DB 14;  Length 643;
Best Local Similarity 99.2%;  Pred. No. 2e-96;
Matches 522;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

Qy    766 AGGAACTGGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db    544 AAGAACTGGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 485

Qy    826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 425

Qy    886 GTGGAAGGTGGATAACGGCCCTCCAATCGGTAACTCCGGTAACTCCGGTGTCACAGAGCAGGA 945
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Db    424 GTGGAAGGTGGATAACGGCCCTCCAATCGGTAACTCCGGTAACTCCGGTGTCACAGAGCAGGA 365

Qy    946 CAGCAAGGACAGCAGCCACCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 CAGCAAGGACAGCAGCCACCTACAGCCTCAGCAGCACCCTGACGTTGAGCAAAGCAGACTACGA 305

Qy   1006 GAAACACAAAGTCACGGCCTGCGAAGTCACCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GAAACACAAAGTTACGGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 245

Qy   1066 GAGCTTCACAGGGAGAGTGTTAGAGGAGGAGAGTGCCCCACCTGCTCCTCAGTTCCAG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 GAGCTTCACAGGGAGAGTGTTAGAGGAGGAGAGTGCCCCACCTGCTCCTCAGTTCCAG 185

Qy   1126 CCTGACCCCCTCCCATCCTTGGCCTCAGCTCTGACCCTTTTCCACAGGGAGACCTACCCCTATT 1185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 CCTGACCCCCTCCCATCCTTGGCCTCAGCTCACCTCACCCCACCCCCTCCTCTCCTCTTGGCTTAATTATGCT 125
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Qy   1186 GCGGTCCTCCAGCTCCATCTTCACCTCACCCCACCCCCTCCTCTCCTCTTGGCTTAATTATGCT 1245
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Db    124 GCGGTCCTCCAGCTCATTTTCACCTCACCCCTCCTCCTCTCCTCTTGGCTTAATTATGCT 65

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 1291
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Db     64 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 19
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```
RESULT 13
AW575927/c
LOCUS       AW575927                618 bp    mRNA    linear    EST 15-MAR-2000
DEFINITION  UI-HF-BL0-acl-e-02-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3059426 3', mRNA sequence.
ACCESSION   AW575927
VERSION     AW575927.1  GI:7247382
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES        Location/Qualifiers
   source       1..618
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:3059426"
                /clone_lib="NIH_MGC_37"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LTI)"
                /note="Vector: pT7T3-Pac; Site_1: NotI; Site 2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   136 a    180 g    136 c    165 t    1 others
ORIGIN

Query Match       26.5%;    Score 519.2;  DB 10;  Length 618;
Best Local Similarity 98.5%;  Pred. No. 2.4e-96;
Matches 524;  Conservative 0;  Mismatches 8;  Indels 0;  Gaps 0;

Qy    754 GCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA 813
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 GCTGGAGTCCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA 489

Qy    814 GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGA 873
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGA 429

Qy    874 GGCCAAAGTACAGTGGAAGGTGGAGGTGGATAACGGCCCTCCAATCGGTAACTCCGGTAACTCCCAGGAGAGTGT 933
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```
Db    428 GGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT 369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934 CACAGAGCAGGACAGCAGGACAGGACAGCAGGACACCTACAGCCTCAGCAGCCTGACGCTGAGCAA 993
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    368 CACAGAGCAGCAGGACAGGACAGCAGGACAGCAGCACCTACAGCCTCAGCAGCCTGACGCTGAGCAA 309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994 AGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCATCAGGGCCTGAGCTC 1053
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    308 AGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTCACCATCAGGGCCTGAGCTC 249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054 GCCCGTCACAAAGAGCTTCAACACAGGGAGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCT 1113
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Db    248 GCCCGTCACAAAGAGCTTCAACACAGGGAGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCT 189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1114 CCTCAGTTCCAGCCTGACCCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTTCCACAGGGGA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 CCTCAGTTCCAGCCTGACCCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTTCCACAGGGGA 129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1174 CCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGC 1233
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 CCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGC 69
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1234 TTTAATTATGCTAATGTTGGAGGAGGAATAAAGTGAATCTTTGCA 1285
          ||||||||||||||||||||||||||||||||||||||||||||||
Db     68 TTTAATTATGCTAATGTTGGAGGAGGAATAAAGTGAATCTTTGCA 17
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RESULT 14
BQ181514
BQ181514/c
LOCUS   BQ181514   731 bp   mRNA   linear   EST 30-APR-2002
DEFINITION   UI-H-EU0-azu-i-21-0-UI.s1 NCI_CGAP_Carl Homo sapiens cDNA clone
             IMAGE: 5853788 3', mRNA sequence.
ACCESSION   BQ181514
VERSION   BQ181514.1 GI:20357006
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 731)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Jose Mercuende
             cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Seq primer: M13 FORWARD
             POLYA=Yes.
FEATURES   Location/Qualifiers
     source   1..731
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5853788"
                     /clone_lib="NCI_CGAP_Carl"
                     /tissue_type="Osteoarthritic Cartilage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP Carl is a cDNA library containing the following
                     tissue(s): Osteoarthritic Cartilage The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_LIB=UI-H-EU0
                     TAG_TISSUE=osteoarthritic cartilage
                     TAG_SEQ=TGATCACGCT"

BASE COUNT   158 a   165 c   214 g   194 t
ORIGIN

Query Match   26.5%; Score 518.8; DB 14; Length 731;
Best Local Similarity 99.6%; Pred. No. 2.9e-96;
Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATC 825
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    540 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATC 481
Qy    826 TGGAACTGCCTCTGTTGTGTGTCCTGCTGGAATAACTTCTATCCAGAGAGGCCAAAGTACA 885
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 TGGAACTGCCTCTGTTGTGTGTCCTGCTGGAATAACTTCTATCCAGAGAGGCCAAAGTACA 421
Qy    886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 361
Qy    946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 301
Qy   1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 GAAACACAAAGTCTACGCCTGCGAAGTCACCATCAGGGCCTGAGCTCGCCCGTCACAAA 241
Qy   1066 GAGCTTCAACAGGGAGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GAGCTTCAACAGGGAGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 181
Qy   1126 CCTGACCCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGACCTACCCCTATT 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CCTGACCCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGACCTACCCCTATT 121
Qy   1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCT 1245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCT 61
Qy   1246 AATGTTGGAGGAGAATGAATAAAGTGAATCTTTGCACC 1287
          |||||||||||||||||||||||||||||||||| ||
Db     60 AATGTTGGAGGAGAATGAATAAAGTGAATCTTTGCCCC 19
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RESULT 15
AW575346/c
LOCUS   AW575346   539 bp   mRNA   linear   EST 15-MAR-2000
DEFINITION   UI-HF-BL0-acv-b-06-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
             IMAGE:3060418 3', mRNA sequence.
ACCESSION   AW575346
VERSION   AW575346.1 GI:7246885
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 539)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             The sequence contained an oligo-dT track that was present in the
             oligonucleotide that was used to prime the synthesis of first
             strand cDNA and therefore this may represent a bonafide poly A

```
           tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: M.B. Soares Lab
           cDNA Library Arrayed by: M.B. Soares Lab
           DNA Sequencing by: M.B. Soares Lab
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Seq_primer: M13 Forward
           POLYA=Yes.
FEATURES          Location/Qualifiers
     source       1..539
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3060418"
                  /clone_lib="NIH_MGC_37"
                  /tissue_type="lymph"
                  /cell_type="germinal center B cells"
                  /cell_line="MGC85"
                  /lab_host="DH10B (LTI)"
                  /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                  Constructed from size fractionated cytoplasmic mRNA
                  (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                  M. Staudt, Ph.D. Library preparation by Maria de Fatima
                  Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      114 a     117 c     161 g     147 t
ORIGIN

Query Match           26.4%;   Score 518.4;  DB 10;  Length 539;
Best Local Similarity 99.8%;   Pred. No. 3.5e-96;
Matches  519;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC  825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    536 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC  477

Qy    826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA  885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    476 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA  417

Qy    886 GTGGAAGTGGATAACGGCCTCCAATCGGGTAACTCCCAGGACGAGTGTCACAGAGCAGGA  945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    416 GTGGAAGTGGATAACGGCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA   357

Qy    946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAGCAAAGCAGACTACGA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAGCAAAGCAGACTACGA  297

Qy   1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    296 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA  237

Qy   1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCCTCCTCAGTTCCAG 1125
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Db    236 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCCTCCTCAGTTCCAG  177

Qy   1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCCTATT 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCCTATT  117

Qy   1186 GCGGTCCTCCAGCTCATCTTCACCTCACCCCCCCCTCCTCCTTGGCTTTAATTATGCT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 GCGGTCCTCCAGCTCATCTTCACCTCACCCCCCCCTCCTCCTTGGCTTTAATTATGCT   57

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db     56 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA   17
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Search completed: July 18, 2003, 09:25:54
Job time : 3400.49 secs

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               Copyright  GenCore version 5.1.6
                          (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        July 18, 2003, 04:14:58 ; Search time 508.109 Seconds
                          (without alignments)
                          8686.944 Million cell updates/sec

Title:         US-09-627-896B-21
Perfect score: 1960
Sequence:      1 tctagaccaccatggattca.........cccacttctaggatcaattc 1960
Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0
Searched:      2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:        4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
               Listing first 45 summaries

Database :     N Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1682.8	85.9	1950	22	AAS11981	DNA encoding Human
2	1635.4	83.4	8897	19	AAV18692	Plasmid pTWD-cJVK.
3	1625.8	82.9	8897	19	AAV18693	Plasmid pD16hJ1.L1
4	1611.8	82.2	8858	20	AAZ10202	Expression vector
5	1611.8	82.2	8858	24	AAH43777	Chi220 light chain
6	1429.4	72.9	1701	13	AAQ30919	pMDR1006 insert.
7	1427.8	72.8	1701	13	AAQ30920	Vector pMDR1007.
8	1184.2	60.4	13999	14	AAQ43845	Plasmid pAH4611.
9	1181.4	60.3	1276	13	AAQ30918	pMDR986 insert. S

```
10  1181.2  60.3  1241  13  AAQ30916    pSAB153 insert.  S
11  1044    53.3  3880  19  AAV39242    Plasmid pCK7-96 nu
12  1044    53.3  3881  18  AAT78801    Kappa light chain
13  1044    53.3  3881  20  AAZ21996    Nucleotide sequenc
14  1044    53.3  3881  24  ABK85575    Human IgGkappa lig
15  1040.4  53.1  7059  15  AAQ5004     Humanised anti-CD1
16  1040.4  53.1  8400  15  AAQ62611    Humanised anti-CD1
17   776.4  39.6  1721  22  AAS22530    Human cDNA encodin
18   776.4  39.6  1736  22  AAS22532    Human cDNA encodin
19   776.4  39.6  1741  22  AAS22531    Human cDNA encodin
20   758.4  38.7  1178  22  AAF57572    Humanised anti-car
21   736    37.6  1552  22  AAF57571    Light chain constr
22   709.4  36.2  3819  18  AAT78825    Kappa light chain
23   709.4  36.2  3819  19  AAV39266    Nucleotide sequenc
24   709.4  36.2  3819  20  AAZ22020    Plasmid pLC6G5 nuc
25   698    35.6  8068  20  AAZ32781    pKN100 F19 chimeri
26   694.2  35.4  8068  20  AAS22533    Human cDNA encodin
27   667.6  34.1  8068  20  AAZ32784    pKN100 human resha
28   595.8  30.4  1244  24  ABK64543    Human benign prost
29   595.8  30.4  1244  24  ABL65461    Human breast cance
30   593.8  30.3  1242  12  AAQ11878    1B1 IgG aberrant 1
31   590.6  30.1  1517  22  AAH98191    Human EST-derived
32   523.4  26.7   948  24  AAS99475    Anti-human AILIM m
33   523    26.7   941  22  AAF97954    Human secreted pro
34   522.8  26.7   913  24  AAS62744    cDNA sequence #531
35   522.4  26.7  1404  22  AAS22861    Human cDNA encodin
36   520.2  26.5   944  22  AAF44892    Human breast cance
37   518.4  26.4   851  22  AAH98251    Human EST-derived
38   518.4  26.4   931  22  AAC66524    Human immune syste
39   518.4  26.4   936  21  AAA27390    Human IGFAM-10 imm
40   518.4  26.4   958  22  AAC66520    Human immune syste
41   518.4  26.4   962  21  AAA09154    Human BMDSP-1 codi
42   518.4  26.4   970  24  AAS99477    Anti-human AILIM m
43   518.4  26.4   974  24  AAS99473    Anti-human AILIM m
44   518.4  26.4   990  22  AAF97952    Human secreted pro
45   518.4  26.4  1003  22  AAS00145    Human cDNA clone H
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ALIGNMENTS

```
RESULT 1
AAS11981
ID   AAS11981 standard; DNA; 1950 BP.
XX
AC   AAS11981;
XX
DT   04-DEC-2001  (first entry)
XX
DE   DNA encoding Humanised monoclonal antibody Hu266, light chain.
XX
KW   Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW   Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW   light chain; ds; gene therapy.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             12..1084
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FT   sig_peptide     12..68
FT                   /*tag= b
FT   mat_peptide     69..1081
FT                   /*tag= c
FT                   /label= "Mature_Hu266_light_chain"
FT   exon            1..406
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FT                   /number= 1
FT   intron          407..763
FT                   /*tag= e
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FT                   /number=1
FT                   /note= "The figure indicates that the intron
FT                   finishes at nucleotide 762 but this would alter the
FT                   reading frame of the second exon and is possibly a
FT   exon            mistake by the authors"
FT                   /*tag= f
FT                   /number=2
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PN   WO20016 2801-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US06191.
XX
PR   24-FEB-2000; 2000US-0184601.
PR   08-DEC-2000; 2000US-0254465.
PR   08-DEC-2000; 2000US-0254498.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI   Vasquez M;
XX
DR   WPI; 2001-550087/61.
DR   P-PSDB; AAU07744.
XX
PT   New humanised antibody for the treatment of Alzheimer's comprises the
PT   inhibition and reduction of the formation of amyloid plaques -
XX
PS   Example 13; Fig 4; 63pp; English.
XX
CC   The invention relates a humanised antibody that specifically binds
CC   an epitope contained within positions 13-28 of amyloid beta peptide,
CC   Abeta. The antibody is useful to inhibit and reduce the formation of
CC   amyloid plaques or the effects of toxic soluble Abeta species in humans
CC   their fragments are used for the manufacture of a medicant. This includes
CC   the prolonged expression of recombinant sequences of them in human
CC   tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC   Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC   Specifically, the antibody is used to sequester Abeta into plasma, brain
CC   or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC   peptide within the brain thereby improving cognition. The present
CC   sequence encodes the light chain of a humanised monoclonal antibody,
CC   Hu266, based on the mouse antibody 266.
XX
SQ   Sequence 1950 BP; 547 A; 488 C; 383 G; 532 T; 0 other;
```

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Query Match             85.9%;  Score 1682.8;  DB 22;  Length 1950;
Best Local Similarity   93.2%;  Pred. No. 0;
Matches 1795;  Conservative  0;  Mismatches 122;  Indels  9;  Gaps  3;
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Qy   333  GACGTGGCAGTTTATTACTGCGGCCAA---TCTTATAAATCTTTACACGTTCGGACAGGGG  389
          ||| ||| |||||||||||||| ||||||   || ||||| || ||||| |||| |||| |
Db   327  GATGTGGGAGTTTATTACTGTTCTCAAAGTACACATGTTCCGTGGAGTTCGTCAAGC      386

Qy   390  ACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTGAGAAATTCTAAACTCTCGAGG  449
          |||||||||||||| ||||||| ||||        | ||| ||||| |||||||||||||||
Db   387  ACCAAGGTGGAAATCAAACGTGAGTAGTAGAATT---TAATCTAGAAATTCTAAACTCTGAGG 443

Qy   450  GGGTCGGATGAGTGGCCATTCTTTGCCTAAAGCATTGAGTTACTGCAAGTCAGAAAA    509
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   444  GGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTACTGCAAGTCAGAAAA   503

Qy   510  GCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCAACAAAACAATTAGAACTTTATT   569
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Db   504  GCATGCAAAGCCCTCAGAATGCTGCAAAGAGCTCCAACAAAACAATTAGAACTTTATT   563

Qy   570  AAGGAATAGGGGGAAGCTAGGAAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTG  629
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Db   564  AAGGAATAGGGGGAAGCTAGGAAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTG 623

Qy   630  GTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTCTGTCTGTCTGTCCCTAACATGCC  689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624  GTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTCTGTCTGTCTGTCCCTAACATGCC 683

Qy   690  CTGTGATTATCCGCAAACAACACACCCAAGGCAGAACTTTGTTACTTAAACACCATCCT     749
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Db   684  CTGTGATTATCCGCAAACAACACACCCAAGGCAGAACTTTGTTACTTAAACACCATCCT    743

Qy   750  GTTTGCTTCTTCCTCAGGAACTGGAACTGCCTCCTGTTGTGCTGCTCCATCTTCCGCCATCTG  809
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744  GTTTGCTTCTTCCTCAGGAACTGGAACTGCCTCCTGTTGTGCTGCTCCATCTTCCGCCATCTG 803

Qy   810  ATGAGCAGTTGAAATCTGGAACTGCCTCCTGTTGTGCTGATAACTTCTATCCCA          869
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   804  ATGAGCAGTTGAAATCTGGAACTGCCTCCTGTTGTGCTGATAACTTCTATCCCA         863

Qy   870  GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGAGA     929
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864  GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGAGA    923

Qy   930  GTGTCACAGAGCAGGACAGCAAGGACAGCACTACAGCCTCAGCGACCTCAGCAGCCTGACGGTGA  989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924  GTGTCACAGAGCAGGACAGCAAGGACAGCACTACAGCCTCAGCGACCTCAGCAGCCTGACGGTGA 983

Qy   990  GCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA     1049
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Db   984  GCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA    1043

Qy  1050  GCTCGCCCGTCACACAGAGCTTCAACAGGGGAGAGTGTTAGAGGAGAAGTGCCCCCACC    1109
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Db  1044  GCTCGCCCGTCACACAGAGCTTCAACAGGGGAGAGTGTTAGAGGAGAAGTGCCCCCACC   1103

Qy  1110  TGCTCCTCAGTTCCAGCCTGACCCCCCCATCCTTTGGCCTTCGACCCTTTTCCACAG     1169
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Qy  1170  GGGACCTACCCCTATTGCGGTCCTCCAGCTATTAGCTGCAAATCCAGTCAG          1229
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Db  1164  GGGACCTACCCCTATTGCGGTCCTCCAGCTATTAGCTGCAAATCCAGTCAG          1223

Qy  1230  TGGCTTTAATTATGCTAATGTTGAGGAGAGAGAATGAATAAATAAGTGAATCTTGCACCTG  1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224  TGGCTTTAATTATGCTAATGTTGAGGAGAGAGAATGAATAAATAAGTGAATCTTGCACCTG 1283

Qy  1290  TGGTTTCTCTCTTTCCTCATTTAATAATTATCTGTTGTTTTACCAACTACTCAATTT     1349
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Db  1284  TGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTT  1343

Qy  1350  CTCTTATAAGGACTAAAATATGTAGTCATCCTAAGGCGCATAAACCATTTATAAAAATCAT  1409
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Db  1344  CTCTTATAAGGACTAAAATATGTAGTCATCCTAAGGCGCATAAACCATTTATAAAAATCAT 1403

Qy  1410  CCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCCCCTCAAACCCACAAGC  1469
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Qy    33  CTTATATTGCTGCTGCTATGGGTATCTGGGACATTGTGGGGACACAGTGCTGCTGACACAGTCT   92
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Db    30  CTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGGTGTGATGTTGTGATGACCCAGAGC       89

Qy    93  CCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGAGGCCACTATTAGCTGCAAATCCAGTCAG     152
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Db    90  CCACTCTCCCTGCCTGTCACCCTGGACAACCGCTCACCATCTCCATCTGCAGATCTAGTCAG    149

Qy   153  AGTGTGCTCAACAGTAGAACCGCAGAGAACTACTGGCTTGGTACCAGCAGAAACCAGGG     212
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Db   150  AGCCTTATA---TAGTGATGGAAACCGCCTATTTACATTGGTTTCTGCAGAAGCCAGGC    206

Qy   213  CAGCCTCCAAAGCTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGC    272
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Db   207  CAGTCTCCAAAGCTCCTGATCTCACTACAAAGTTTCACACTCGGGGTCCCAGACAGG      266

Qy  *273  TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAA   332
          ||||||||||||||||| ||||||||||||||| |||| ||||||||| ||| || ||
Db   267  TTCAGTGGCAGTGGATCGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCCGAG    326
```

PT   immunotherapy - by administration of immunoglobulin fusion protein
PT   modified prior to administration by inactivation of part of
PT   the constant region
XX
PS   Disclosure; Pages 58-60; 140pp; English.
XX
CC   The sequence is that of a plasmid expressing a structurally
CC   altered BR96 antibody, having the variable region of BR96 and
CC   a modified variable region. It can be used in the production of the
CC   structurally altered antibodies which are useful for the
CC   treatment of cancer and carcinomas in vivo, especially when
CC   conjugated to cytotoxic agents. Structurally altered BR96 Ab is
CC   used, especially conjugated to doxorubicin, to treat proliferative
CC   type diseases where a cell has a BR96 antigen on the cell surface.
CC   The chimeric and humanised BR96 Ab are also used in the methods to
CC   inhibit and prevent BR96-induced toxicity resulting from immunotherapy
CC   for cancer.
XX
SQ   Sequence 8897 BP; 2410 A; 2112 C; 1967 G; 2407 T; 1 other;

Query Match   83.4%; Score 1635.4; DB 19; Length 8897;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1780; Conservative 0; Mismatches 131; Indels 26; Gaps 4;

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Qy     93 CCAGATTCCCTGGCTGTGAAGCTTAGGAGGAGGGCCACTATTAGCTGCAAATCCAGTCAG  152
          | ||||||| ||||| ||||| ||| || |||||| || || ||  ||| |||| ||||||
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Qy    153 AGTCTGCTCAACAGTAGACCCAGAGAGACTACTGGCTTGGTACCAGCAGAAACCAGGG  212
          || ||| |||||  ||||||  |||||||||||  |||||||||||| |||||||| |||
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Qy    213 CAGCCTCCTAAACTGCTGATCTACTGGCATCCACTAGGGAATCTGGGGTCCCTGATCGC  272
          |||| ||||  |||||||||||||| ||||||||  ||||| ||||| |||||||| ||
Db    237 CAGTCTCCACAGCTCCTGATCTACACAAAGTTCCACACCGATTTTCTGGGGTCCCAGACAGG  296

Qy    273 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAA  332
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Db    297 TTCAGCGGCAGTGGATCAGGGACAGACAGATTTCACACTCAAGATCAGCAGTGTGGAGGCTGAG  356

Qy    333 GACGTGGCAGTTTATTACTGCCAGCCAA---TCTTATATATCTTTACACGTTCGGACAGGGG  389
          ||| |||||||||||||||||||| ||  | ||| | |  |||| |||||| ||| |||||
Db    357 GATCTGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCACATGTTCACATGTTCCATTCACATGTTCCATTCGCTCGGGG  416

Qy    390 ACCAAGGTGGAAATAAAACCTAAG----------------TAGTCTTCTCAACTCTAGAAA  434
          |||||||||||||||||||||||                ||  || |  ||||  | |||
Db    417 ACAAAGGTTGGAAATAAAAACGTAGTCTCTGAGTCTCGAGTAACCGGTCAATCCGGTCAATCGATTGGAA  476

Qy    435 TTCTAAACTCTGAGGGGTCGATGACGTGGCCATTCTTGCCTAAGCATTGAGTTTAC  494
          ||||||||||||||||||||| |||| |||| ||||||| ||||||||||||||||||
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Qy    495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGGCTCCAACAAACA  554
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    537 TGCAAGGTCAGAAAATGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGGCTCCAACAAAACA  596

Qy    555 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGGAGAAACTCAAAACATCAAGATTT  614
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Db    597 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGGAGAAGAAACTCAAAACATCAAGATTT  656

Qy    615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAAGCATGCTGTTTTCTGTC  674
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Db    657 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAAGCATGCTGTTTTCTGTC  716

Qy    675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCAAGGGCAGAGAACTTTGTTA  734
          |||||||||||||       ||||| |||||||||||||||||||||||||||||||||
Db    717 TGTCCCTAACATGCCC----TTATCCCAAACAACAACACCCAAGGGCAGAGAACTTTGTTA  771

Qy    735 CTTAAACACCATCCGTGTTGCTTCTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA  794
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Db

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Db   1404 CCTTCATTCTATTTTACCCTATCATCATCCTGCGAAGACAGTCCTCCTCCAAACCCACAGC  1463

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Qy   1530 CCTCAGCAAGCCCCATAGTCCTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTT  1589
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1524 CCTCAGCAAGCCCCATAGTCCTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTT  1583

Qy   1590 GATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTCAAAGAGAAACCTGCTATAAA  1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1584 GATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAGAGAAACCTGCTATAAA  1643

Qy   1650 GAGAATCATTCATTGCAACATGATATAAAATAACAACAACAATAAAAGCAATAAAATAAAC  1709
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1644 GAGAATCATTCATTGCAACATGATATAAAATAACAACAACAATAAAAGCAATAAAATAAAC  1703

Qy   1710 AAACAATAAGGGAAATGTTTAAGTTCATCATGTACTTAGACTTAGAAGTGAATGTCATGCCT  1769
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1704 AAACAATAAGGGAAATGTTTAAGTTCATCATGTACTTAGACTTAGAAGTGAATGTCATGCCT  1763

Qy   1770 TATTTACATTTTTAAACAGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTAC  1829
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1764 TATTTACATTTTTAAACAGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTAC  1823

Qy   1830 TTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGT  1889
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1824 TTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGT  1883

Qy   1890 TGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTATTCTATAACTCAGCAATCCCACTTCT  1949
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1884 TGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTATTCTATAACTCAGCAATCCCACTTCT  1943

Qy   1950 AGGATC  1955
          ||||||
Db   1944 AGGATC  1949
```

RESULT 2
AAV18692
ID   AAV18692 standard; cDNA; 8897 BP.
XX
AC   AAV18692;
XX
DT   03-AUG-1998 (first entry)
XX
DE   Plasmid pTWD-cJVK.L1 expressing cBR96-light chain.
XX
KW   plasmid; BR96; antibody; chimeric; humanised; immunotherapy;
KW   immunoglobulin-induced toxicity; cancer; inhibition; BR-96-induced;
KW   ss.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Simian virus 40.
XX
PN   WO9805787-A1.
XX
PD   12-FEB-1998.
XX
PF   01-AUG-1997; 97WO-US13562.
XX
PR   02-AUG-1996; 96US-0023033.
XX
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI   Rosok MJ, Yelton DE;
XX
DR   WPI; 1998-145622/13.
XX
PT   Inhibiting immunoglobulin-induced toxicity resulting from

```
Db   1852  GGCGTATTGAGTACTTCCACAACCTAATTAATCCACTATACTGTGAGATTAAAAA  1911
                  ||||||||||||||||||||| ||||||| ||||||||||||||| ||||||||||
Qy   1875  CATTCATTAAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATTCTATAAACTC  1934
                  ||||||||||||||||||||| ||||||| |||||||||||||| ||||||||||
Db   1912  CATTCATTAAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAACTC  1971

Qy   1935  AGCAATCCCACTTCTAG  1951
                  ||||||  |||||||||
Db   1972  AGCAATCCCACTTCTAG  1988


RESULT 3
AAV18693
ID   AAV18693  standard; cDNA; 8897 BP.
XX
AC   AAV18693;
XX
DT   03-AUG-1998  (first entry)
XX
DE   Plasmid pD16hJ1.L1 expressing hBR96-light chain.
XX
KW   plasmid; BR96; antibody; chimeric; humanised; immunotherapy;
KW   immunoglobulin-induced toxicity; cancer; inhibition; BR-96-induced;
KW   ss.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Simian virus 40.
XX
PN   WO9805787-A1.
XX
PD   12-FEB-1998.
XX
PF   01-AUG-1997;  97WO-US13562.
XX
PR   02-AUG-1996;  96US-0023033.
XX
PA   (BRIM )  BRISTOL-MYERS SQUIBB CO.
XX
PI   Rosok MJ,  Yelton DE;
XX
DR   WPI; 1998-145622/13.
XX
PT   Inhibiting immunoglobulin-induced toxicity resulting from
PT   immunotherapy - by administration of immunoglobulin fusion protein
PT   modified prior to administration by inactivation of part of
PT   the constant region
XX
PS   Disclosure; Pages 63-66; 140pp; English.
XX
CC   The sequence is that of a plasmid expressing a structurally
CC   altered BR96 antibody, having the variable region of BR96 and
CC   a modified variable region. It can be used in the production of the
CC   structurally altered antibodies which are useful for the
CC   treatment of cancer and carcinomas in vivo, especially when
CC   conjugated to cytotoxic agents. Structurally altered BR96 Ab is
CC   used, especially conjugated to doxorubicin, to treat proliferative
CC   type diseases where a cell has a BR96 antigen on the cell surface.
CC   The chimeric and humanised BR96 Ab are also used in the methods to
CC   inhibit and prevent BR96-induced toxicity resulting from immunotherapy
CC   for cancer.
XX
SQ   Sequence 8897 BP;  2407 A;  2119 C;  1972 G;  2398 T; 1 other;

Query Match        82.9%;  Score 1625.8;  DB 19;  Length 8897;
Best Local Similarity  91.6%;  Pred. No. 0;
Matches 1774;  Conservative  0;  Mismatches 137;  Indels  26;  Gaps  4;

Qy    33  CTTATATTGCTCGTCGCTCATGGGTATCGGCACCTGTGGGACATTGTGCTGACACAGTCT   92
                 ||||| |||||| ||||| |||||| |||||||||||||||||||||||||||||||||
Db  1058  CTGTTGGGCTGATGTCTCGGATTCGTCGGATTCCTGCTTCCAGCAGTGACCCAAAACC  1117

Qy    93  CCAGATTCCCTGGCTGTAAGCTTAGGAGAGGGCCACTATTAGCTGCAAATCCAGTCAG  152
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Db   772  CTTAAACACCATCCTGTTTGCTTCTTTCCTCCAGGAACTGTGGCTGCACCATCTGTCTTCA  831
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   795  TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCGTGTGTGCCTGCTGA  854
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   832  TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCGTGTGTGCCTGCTGA  891

Qy   855  ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG  914
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   892  ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG  951

Qy   915  GTAACTCCCAGGAGAGTGTCACAGAGCAGGACACCAGCAGCCTCAGCA  974
                |||||||||||||||||||||||||||||||||||||||||||||||
Db   952  GTAACTCCCAGGAGAGTGTCACAGAGCAGGACACCAGCAGCCTCAGCA  1011

Qy   975  GCACCCTGACGCTGAGCAAAGACAGAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA  1034
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1012  GCACCCTGACGCTGAGCAAAGACAGAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA  1071

Qy  1035  CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG  1094
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1072  CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG  1131

Qy  1095  AGAAGTGCCCCCACCTGTCCTCAGTTCCAGCCTGACCCCCCATCCTTTGGCCTCTG  1154
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1132  AGAAGTGCCCCCACCTGTCCTCAGTTCCAGCCTGACCCCCCATCCTTTGGCCTCTG  1191

Qy  1155  ACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACTTCAC  1214
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1192  ACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACTTCAC  1251

Qy  1215  CCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT  1274
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1252  CCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT  1311

Qy  1275  GAATCTTTGCACCTGTGGTTTCTCTCTTTTCCTCATTTAATTATTATTCGTTGTTTTA  1334
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1312  GAATCTTTGCACCTGTGGTTTCTCTCTTTTCCTCATTTAATTATTATTCGTTGTTTTA  1371

Qy  1335  CCAACTACTCAATTTCTCAATTTCTCTATAAGGACTAAATATGTAGTCATCCTAAGGCGCCATAACC  1394
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1372  CCAACTACTCAATTTCTCAATTTCTCTATAAGGACTAAATATGTAGTCATCCTAAGGCACGTAACC  1431

Qy  1395  ATTTATAAAAATCATCCTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCC  1454
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1432  ATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCC  1491

Qy  1455  CTCAAACCCACAAGCCTTCTGTCTCCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGCT  1514
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1492  CTCAAACCCACAAGCCTTCTGTCGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGCT  1551

Qy  1515  TCCTTGTTTTCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGTCTTAC  1574
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1552  TCCTTGTTTTTCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGTCTTAC  1611

Qy  1575  AGTCATATATCCTTGATTCAATTCCTGGAATCAACCAAAGCAAATTTTTCAAAAGAA  1634
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1612  AGTCATATATCCTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGAA  1671

Qy  1635  GAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACAATAAA  1694
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1672  GAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACAATAAA  1731

Qy  1695  AGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTTAA  1754
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1732  AGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTTAA  1791

Qy  1755  TGGAATGTCATGCCTTATTTACATTTTAAACAGGTACTGAGGGACTTCCTGTCTGCCAAG  1814
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1792  TGGAATGTCATGCCTTATTTACATTTTAAACAGGTACTGAGGGACTTCCTGTCTGCCAAG  1851

Qy  1815  GGCCGTATTTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAA  1874
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 4
AAZ10202
ID   AAZ10202 standard; DNA; 8858 BP.
XX
AC   AAZ10202;
XX.
DT   01-NOV-1999 (first entry)
XX
DE   Expression vector of light chain of chimeric anti-CD40 antibody chi22.
XX
KW   Light chain variable region; chimeric antibody; anti-CD40 antibody;
KW   chi220; humoral immune response; T cell dependent antigen;
KW   collagen induced arthritis; transplant induced rejection;
KW   T cell mediated disorder; autoimmune disease; inflammatory disease;
KW   transplantation; ss.
XX
OS   Synthetic.
XX

```
FH   Key            Location/Qualifiers
FT   CDS            1065..1388
FT                  /*tag= a
FT                  /note= "no termination sequence"
XX
PN   WO9942075-A2.
XX
PD   26-AUG-1999.
XX
PF   10-FEB-1999;   99WO-US02949.
XX
PR   19-FEB-1998;   98US-0026291.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;
PI   Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;
XX
DR   WPI; 1999-527408/44.
XX
PT   Antibody that binds human CD40, for treating T cell mediated
PT   disorders
XX
PS   Claim 18; Fig 14A-C; 77pp; English.
XX
CC   The present sequence represents an expression vector for expressing
CC   the light chain of a chimeric anti-CD40 antibody designated chi220.
CC   The antibodies are effective in modulating humoral immune response
CC   against T cell dependent antigens, collagen induced arthritis and
CC   transplant induced rejection. They are also useful for their
CC   anti-inflammatory properties. The antibodies have wide therapeutic
CC   applications, including autoimmune and inflammatory diseases and
CC   transplantation. The antibody can be used in a pharmaceutical composition
CC   for treating a patient suffering from a T cell mediated disorder. They
CC   can also be used to treat autoimmune diseases, inflammatory diseases,
CC   and transplantation.
XX
SQ   Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;
```

Query Match 82.2%;   Score 1611.8;   DB 20;   Length 8858;
Best Local Similarity 90.6%;   Pred. No. 0;
Matches 1783;   Conservative 0;   Mismatches 137;   Indels 49;   Gaps 4;

```
Qy      9 ACCATGGATTCACAGGGCCAGGTTCTATATTGCTCGTGCTATGGGTATCTGGCACCTGT  68
          |||||||  || ||||||||  ||||||   |  | |||  ||||  || ||||||||
Db   1002 ACCATGGAAGCCCAGCTCAGCTTCTTCTTCCTGCTACTCTGGCTCCAGGATACCACC 1061

Qy     69 GGGGACATTGTGTGACACAGTCTCCAGATTCCCTGGCTGTGTCTCTGGCTGTAAGCTTAGGAGAGAGGGC 128
          ||| ||||||| | ||| |||||||||        |||||||| |  |  |  |||
Db   1062 GGAGACATTGTTCTGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGAGAGATAGAGTC 1121

Qy    129 ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTGACGTCAACAGTAGAACCCGGAGAACTACTTG 188
          ||| || |||| || ||||||||||||  |                    ||||||||
Db   1122 TCTCTTTCCTGCAGGGCCAGTCAGAGTGTTAGC------------GACTACTTA 1163

Qy    189 GCTTGGTACCAGCAGAAACACAGGGGCCAGCCTCCCAAACTGCTCATCTACTGGGCATCCACT 248
          |||||||| || ||||| |   ||| ||||| ||| |||  ||||||| |   |||||||||
Db   1164 CACTGGTATCAACAAAAATCAACATGATGCTTCCAAGGCTTCCATCAATATGCTTCCCAT 1223

Qy    249 AGGGAATCTGGGGTCCCTGATCGCTTCAGTGCAGTGGATCTGGACAGATTTCACTCTC 308
          || |||||||| ||||| | ||| |||||||| ||||||||||| ||||||||||||
Db   1224 TCCATCTCTGGGATCCCTGCCAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTC 1283

Qy    309 ACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA-- 366
          |||||||| ||| || ||| ||||||| || |||||||||||||  |||| | || |
Db   1284 AGTATCAACAGTGTGGAACCTGAAGATGTTGGAATTTATTACTGTCAACATGGTCAACAGC 1343

Qy    367 -ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGT--------- 414
           |||   | | ||||||  | |||||||||  || ||||| |||||||||
Db   1344 TTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGTAAGTGAGTCTCGAGT 1403

Qy    415 ---------AGTCTTCTCAACTCTAGAAATTCTAAA 462
              |   ||  | | |   |  ||||
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Db   1404 AGATAACCGGTCAATCGGTCAATCGATTGGAATCTAAACTCTGAGGGGGTCGGATGACG 1463
Qy    463 TGGCCATTCTTGCCTAAAGCATTGAGTTTACTGCAAGGTTCAGAAAAGCATGCAAAGCCC 522
          |||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||
Db   1464 TGGCCATTCTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAAGCATGCAAAGCCC 1523

Qy    523 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGG 582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1524 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGG 1583

Qy    583 AAGCTAGGAGAAACTCAAAACATCAAGATTTAAATACGCTTCTTGGTCTCCTTGCTAT 642
          ||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db   1584 AAGCTAGGAGAAGAAACTCAAAACATCAAGATTTAAATACGCTTCTTGGTCTCCTTGCTAT 1643

Qy    643 AATTATCTGGATAAGCATGCTGTTTCTGTCTGTCCCTAACATGCCCTGATTATCCG 702
          ||||||||||||||||||||||||||||||||||||||||||||||||     |||||
Db   1644 AATTATCTGGATAAGCATGCTGTTTCTGTCTGTCCCTAACATGCCC-----TTATCCG 1698

Qy    703 CAAACAACACACCCAAGGGCAGAACTTGTTACTTAAACACCATCCTGTTTGCTTCTTC 762
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1699 CAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTC 1758

Qy    763 CTCAGGAACTGTGGCTGCCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTGAA 822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 CTCAGGAACTGTGGCTGCCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTGAA 1818

Qy    823 ATCTGAACTGCCTCTGTGTGCCGTGAATAACTTCTATCCCAGAGAGGCCAAAGT 882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 ATCTGAACTGCCTCTGTGTGCCGTGAATAACTTCTATCCCAGAGAGGCCAAAGT 1878

Qy    883 ACAGTTGGAAGTGGATAACGCCCTCAATGGGTAACTCCAGGAGAGTGTCACAGAGCA 942
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1879 ACAGTTGGAAGTGGATAACGCCCCAATGGGTAACTCCAGGAGAGTGTCACAGAGCA 1938

Qy    943 GGACAGCAAGGACAGCAGCACCACCACCCTGAGCGCTGAGCAGCGCTGAGCAAAGCAGACTA 1002
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 GGACAGCAAGGACAGCAGCACCACCACCCTGAGCGCTGAGCAGCGCTGAGCAAAGCAGACTA 1998

Qy   1003 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATGAGGGCCTGAGCTCGCCGTCAC 1062
          |||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||
Db   1999 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGGCTGAGCTCGCCGTCAC 2058

Qy   1063 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTCCTCCAGTTC 1122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTCCTCCAGTTC 2118

Qy   1123 CAGCCTGACCCCTCCATCTTTGGCCTCTGAAGCTTAGGAGAGAGGGCCTACCCCT 1182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 CAGCCTGACCCCTCCATCTTTGGCCTCTGAAGCTTAGGAGAGAGGGCCTACCCCT 2178

Qy   1183 ATTGGGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTTGGCTTTAATTAT 1242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 ATTGGGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTTGGCTTTAATTAT 2238

Qy   1243 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTTCTCTCTT 1302
          |||   | ||||||||| ||| |||| || ||||||||| |||||| ||| | ||
Db   2239 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTTCTCTCTT 2298

Qy   1303 TCCTCATTTAATAATTAATTATTATCGTGTTGTTTACCAACTACTCAATTTCACTCTC 1362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TCCTCATTTAATAATTAATTATTATCGTGTTGTTTACCAACTACTCAATTTCACTCTC 2358

Qy   1363 CTAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATT 1422
          |||||||||||||||||||||| | | |||||||||||||||||||||||||||||||||
Db   2359 CTAAATATGTAGTCATCCTAAGGCACGTAACCATTTATAAAAATCATCCTTCATTCTATT 2418

Qy   1423 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCCAAACCCACAAGCCTTCGTCTCCAC 1482
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCCAAACCCACAAGCCTTCGTCTCCAC 2478

Qy   1483 AGTCCCCTGGGCCATGGTAGGAGGACGACTTCGCTTCCCTGTTTCCCCTCGTTCCCCTCCTCCAGCAAGCCC 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 AGTCCCCTGGGCCATGGTAGGAGGACGACTTCGCTTCCCTGTTTCCCCTCGTTCCCCTCCTCCAGCAAGCCC 2538
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Qy   1543  TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT  1602
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539  TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT  2598

Qy   1603  GGGAATCAACCAAAGCAAATTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCAT   1662
               | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599  GAGAATCAACCAAAGCAAATTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCAT   2658

Qy   1663  TGCAACATGATATAAATAACACACAACAATTAAAATAACAATGCAATTAAATAAACAATAAACAATAGGGAA  1722
               ||||||||||||| ||||||||||||||||||||| ||||||||||||| |||||||||||||||||
Db   2659  TGCAACATGATATAAATAACACACAACAATTAAAATAACAATGCAATTAAATAAACAATAAACAATAGGGAA  2718

Qy   1723  ATGTTTAAGTTCATCATGGTACTTAGACTTAGAATGGAATGCCTTATTTACATTTTT  1782
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2719  ATGTTTAAGTTCATCATGGTACTTAGACTTAGAATGGAATGCCTTATTTACATTTTT  2778

Qy   1783  AAACAGGTACTGAGGGACTCCTGTCGCAAGGGCCGTATTGAGTACTTTCCACAACCTA  1842
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2779  AAACAGGTACTGAGGGACTCCTGTCGCAAGGGCCGTATTGAGTACTTTCCACAACCTA  2838

Qy   1843  ATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAAATGTTGCAAAGGTTCTA  1902
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839  ATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAAATGTTGCAAAGGTTCTA  2898

Qy   1903  TAAAGCTGAGAGAGACAAAATATATTCTATAACTCAGCAATCCCACTTCTAG  1951
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2899  TAAAGCTGAGAGAGACAAAATATATTCTATAACTCAGCAATCCCACTTCTAG  2947


RESULT 5
AAH43777
ID   AAH43777  standard; DNA; 8858 BP.
XX
AC   AAH43777;
XX
DT   30-JAN-2002  (first entry)
XX
DE   Chi220 light chain expression vector.
XX
KW   complementarity determining region; humanised; chimerised; light;
KW   heavy; chain; F4; chi220; L3.17; human; CD40; monoclonal antibody;
KW   gp39; variable; region: murine; CDR; humoral immune response;
KW   kidney; transplant rejection; anti-inflammatory; autoimmune disease;
KW   type I diabetes; psoriasis; multiple sclerosis; rheumatoid arthritis;
KW   systemic lupus erythematosus; myasthenia gravis; inflammatory disease;
KW   T cell-dependent antigen; collagen induced arthritis; skin; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   CDS            1005..1007
FT                  /*tag= a
FT                  /function= "Start codon of inserted signal sequence"
FT   CDS            1065..1388
FT                  /*tag= b
FT                  /product= "Variable light chain"
FT                  /note= "No stop codon"
XX
PN   US6312693-B1.
XX
PD   06-NOV-2001.
XX
PF   10-FEB-1999;  99US-0247352.
XX
PR   19-FEB-1998;  98US-0026291.
XX
PA   (ARUF/)  ARUFFO A A.
PA   (HOLL/)  HOLLENBAUGH D.
PA   (SIAD/)  SIADAK A W.
PA   (BERR/)  BERRY K K.
PA   (HARR/)  HARRIS L.
```

```
PA   (THOR/)  THORNE B A.
PA   (BAJO/)  BAJORATH J.
PA   (HUSE/)  HUSE W D.
PA   (WUHH/)  WU H.
PA   (WATK/)  WATKINS J D.
XX
PI   Aruffo AA,  Hollenbaugh D,  Siadak AW,  Berry KK,  Harris L;
PI   Thorne BA,  Bajorath J,  Huse WD,  Wu H,  Watkins JD;
XX
DR   WPI; 2002-024899/03.
XX
PT   New humanized anti-human CD40 antibodies which block interaction
PT   between gp39 and CD40 for modulating humoral immune responses against T
PT   cell-dependent antigens, collagen induced arthritis, and transplant
PT   rejection -
XX
PS   Example 2; Fig 14; 54pp; English.
XX
CC   This sequence shows the expression vector encoding the light chain of
CC   the chimerised anti-human monoclonal antibody (mAb), Chi220. Chi220
CC   binds to human CD40 (or its active portion). It comprises murine
CC   variable and human kappa and gamma 1 constant regions. It binds to
CC   CD40 and effectively blocks humoral immune responses to T cell-dependent
CC   antigens in a dose dependant fashion. The antibodies of the invention
CC   are useful for modulating humoral immune responses against T cell-
CC   dependent antigens, collagen induced arthritis, and skin and kidney
CC   transplant rejection and are also useful for their anti-inflammatory
CC   properties. They are useful for treating autoimmune disease such as
CC   type I diabetes, psoriasis, multiple sclerosis, rheumatoid arthritis,
CC   systemic lupus erythematosus and myasthenia gravis, inflammatory
CC   diseases and transplantation.
XX
SQ   Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;

Query Match             82.2%;  Score 1611.8;  DB 24;  Length 8858;
Best Local Similarity   90.6%;  Pred. No. 0;
Matches 1783;  Conservative   0;  Mismatches 137;  Indels  49;  Gaps   4;

Qy      9  ACCATGGATTCAACAGGCCCAGGTCTTCTTATATTGCTGCGCTGCGCTATGGTATCTGCACCTGT   68
               |||||||||||||||||||||||||||||||||||  | |||||| | ||||||  |||
Db   1002  ACCATGGAAGCCCCAGTCAGTTCGTTCTCTTTCCTCCTGGCTCCCAGATACCACC  1061

Qy     69  GGGGACATTGTGCTGACACAGTCTCCAGATTCCTGGCGTGTAAGCTTAGGAGAGAGGGCC   128
               | ||||||||||||||||| | | | |||||||||||||||||||||||||||||||
Db   1062  GGAGACATTGTTCTGACCTGTCCAGTCTCCAGCCACCCTGTCTGTGTGACTCCAGGAGATAGAGTC  1121

Qy    129  ACTATTAGCTGCAAATCCAGTCAGAGTCTTGCTCAACAGTAGAACCCGAGAGAACTACTTG  188
               ||||||||||||||||||||||||||||||||||||||||            |||||||
Db   1122  TCTCTTTCCTGCAGGGCCCAGCAGGTCCAGAGTATTAGC-------------GACTACTTA  1163

Qy    189  GCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACT  248
               ||||||||| |||| ||||||||| |||||||||||||||||| | |||||| |||||
Db   1164  CACTGGTATCAACAGAAAATCACATGAGTCTTCCAAGGCTTCTCATCAAATATGCTTCCAT  1223

Qy    249  AGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTC  308
               ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224  TCCATCTCTGGGATCCCCTCCAGGTTCAGTGGCAGTGGATCAGGGTCAGATTCACTCTC  1283

Qy    309  ACCATCAGCAGTCTGCAGGTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA--  366
               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1284  AGTATCAACAGTGTGGAACCTGGAGATGTTGGAGATGTTGGAATTTATTACTGTCAACATGTCAACAGC  1343

Qy    367  -ATCTTTACACGTTCGGACAGGGGACCAAGCTGGAGCTGAAA  414
                |||||  |||||||||||||||||||
Db   1344  TTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGTAAGTCTGAGTCTCT  1403

Qy    415  --------AGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGGGGTCGGATGACG  462
                       |||||||| || | ||||||||||||||||||||||||||||
Db   1404  AGATAACCGGTCAATCGGTCAATCGATTCGATTGGAATTCTAAACTCTGAGGGGTCGGATGACG  1463

Qy    463  TGGCCATTCTTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAAGGTCATGCAAGCCC  522
               ||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1464  TGGCCATTCTTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAAGGTCATGCAAAAGCCC  1523
```

```
Qy  1603  GGGAATCAACCAAAGCAAATTTTCAAAAGAAGAAGAAACCTGCTATAAAGAGAATCATTCAT  1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2599  GAGAATCAACCAAAGCAAATTTTCAAAAGAAGAAGAAACCTGCTATAAAGAGAATCATTCAT  2658

Qy  1663  TGCAACATGATATAAAATAACACACAATTAAATAAACAATTAAATAAACAAACAATAGGGAA  1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2659  TGCAACATGATATAAAATAACACACAATTAAATAAACAATTAAATAAACAAACAATAGGGAA  2718

Qy  1723  ATGTTTAAGTTCATCATGGTACTTAGACTTAATGAATGTCATGCCTTATTTACATTTTT  1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2719  ATGTTTAAGTTCATCATGGTACTTAGACTTAATGAATGTCATGCCTTATTTACATTTTT  2778

Qy  1783  AAACAGGTACTGAGGGACTCCTGCTCGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA  1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2779  AAACAGGTACTGAGGGACTCCTGCTCGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA  2838

Qy  1843  ATTTAATCCACCACTATACTGTGAGATTAAAAACATTCATTAAAATGTGCAAAGGTTCTA  1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2839  ATTTAATCCACCACTATACTGTGAGATTAAAAACATTCATTAAAATGTGCAAAGGTTCTA  2898

Qy  1903  TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG  1951
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2899  TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG  2947
```

RESULT 6

```
AAQ30919
ID  AAQ30919  standard; DNA; 1701 BP.
XX
AC  AAQ30919;
XX
DT  02-APR-1993  (first entry)
XX
DE  pMDR1006 insert.
XX
KW  Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
KW  pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;
KW  NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
KW  melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
KW  humanised; 5A8; light chain; variable region; LV; genomic; constant
KW  antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
KW  lymphocyte; helper; inducer; HIV; syncytia; formation; ss.
XX
OS  Synthetic.
XX
PN  WO9209305-A.
XX
PD  11-JUN-1992.
XX
PF  27-NOV-1991;    91WO-US08843.
XX
PR  27-NOV-1990;    90US-0618542.
XX
PA  (BIOJ ) BIOGEN INC.
XX
PI  Burkly LC,   Chisholm PL,   Rosa JJ,   Rosa MD,   Thomas DW;
XX
DR  WPI; 1992-398399/48.
XX
PT  New anti-CD4 antibody homolognes - which bind CD4, do not block
PT  binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT  formation between CD4+ cells
XX
PS  Disclosure; Page 162-3; 205pp; English.
XX
CC  The sequence given is the insert of the intermediate plasmid pMDR1006.
CC  This plasmid and pSAB132 (see AAQ30906) were used in the construction of
CC  the vector pMDR1007 (see AAQ30920). Three fragments were ligated
CC  together to generate pMDR1006; a 572 bp fragment of pMDR985 (see
CC  AAQ30913), a 3442bp AatII/EcoRV fragment of pMDR986 (see AAQ30918) and a
CC  326 bp EcoRV/BglII fragment of pMDR1003 (see AAQ30900). The ligation
CC  mixture was used to transform E. coli JA221(Iq) to ampicillin
CC  resistance. pMDR1006 was cleaved with NotI and the 1693 bp fragment
```

```
Qy   523  TCAGAATGGCTGCCAAAGAGCTCCAACAAAACAATTTATTAAGGAATAGGGG  582
          |||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db  1524  TCAGAATGGCTGCCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGG  1583

Qy   583  AAGCTAGGAAGAAACTCAAAACATCAAGATTTAAATACGCTTCTTGGTCTCCTTGCTAT  642
          |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db  1584  AAGCTAGGAAGAAACTCAAAACATCAAGATTTTCGTCTTCTTGGTCTCCTTGCTAT  1643

Qy   643  AATTATCTGGATAAGCATGCTGTTTCGTCTGTCCCTAACATGCCCTGTGATTATCCG  702
          |||||||||||||||||||||||  ||||  |||||||           ||||||||
Db  1644  AATTATCTGGGATAAGCATGCTGTTTCGTCTGTCCCTAACATGCCC-----TTATCCG  1698

Qy   703  CAAACAACAACACCCAAGGCAGAACTTTGTTACTTAAAACACCATCCGTTTGCTTCTTC  762
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1699  CAAACAACAACACCCAAGGCAGAACTTTGTTACTTAAAACACCATCCGTTTGCTTCTTTC  1758

Qy   763  CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAA  822
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1759  CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAA  1818

Qy   823  ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT  882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1819  ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT  1878

Qy   883  ACAGTGGAAGGTGGATAACGCCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA  942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1879  ACAGTGGAAGGTGGATAACGCCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA  1938

Qy   943  GGACAGCAAGGACAGCAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA  1002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1939  GGACAGCAAGGACAGCAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA  1998

Qy  1003  CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC  1062
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1999  CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC  2058

Qy  1063  AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC  1122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2059  AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC  2118

Qy  1123  CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACTACCCCT  1182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2119  CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACTACCCCT  2178

Qy  1183  ATTGCGGGTCCTCCAGCTCATCTTCACCTCACCCCCCTCCTGGCTTAATTAT  1242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2179  ATTGCGGGTCCTCCAGCTCATCTTCACCTCACCCCCCTCCTGGCTTAATTAT  2238

Qy  1243  GCTAATGTTGGAGGAGAATGAATAAAGTGAATCTTGCACCTGTGGTTTCTCTCTT  1302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2239  GCTAATGTTGGAGGAGAATGAATAAAGTGAATCTTGCACCTGTGGTTTCTCTCTT  2298

Qy  1303  TCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAGGGA  1362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2299  TCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAGGGA  2358

Qy  1363  CTAAATATGTAGTCATCCTAAGGCGCATAACCATTATAAAAAATCATCCTTCATTCTATT  1422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2359  CTAAATATGTAGTCATCCTAAGGCACCTAACCATTATAAAAAATCATCCTTCATTCTATT  2418

Qy  1423  TTACCCCATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCGTCCTCAC  1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2419  TTACCCCATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCGTCCTCAC  2478

Qy  1483  AGTCCCCTGGGCCATGGTAGGAGGAGACTTGTCTTCCTTGTTTCCCCCTCCTCAGCAAGCCC  1542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2479  AGTCCCCTGGGCCATGGTAGGAGGAGACTTGCTTCCTTGTTTCCCCCTCCTCAGCAAGCCC  2538

Qy  1543  TCATAGTCCTTTTAAGGGTGACCAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT  1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2539  TCATAGTCCTTTTTAAGGGTGACCAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT  2598
```

CC isolated was ligated into NotI linearised pSAB132 which had been
CC dephosphorylated by calf alkaline phosphatase. This generates the
CC plasmid pMDR1007. The dephosphorylated mixture was fractionated
CC through low temperature melting agarose and used to transform E. coli
CC JA221(Iq) to ampicillin resistance. The pMDR1007 insert comprises
CC DNA encoding, in a 5' to 3' order, the immunoglobulin kappa chain
CC signal peptide, amino acid (AA) 1-AA112 of the humanised 5A8 light
CC chain variable region (LV) followed by genomic DNA encoding AA108-
CC AA214 of the human kappa light chain, ie. the light chain constant
CC region (LC).   The polypeptide encoded by pMDR1007 is an antibody
CC homolog which was shown to bind to CD4 but did not block the binding
CC of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
CC lymphocytes (helper/inducer cells).   The homolog blocked HIV-induced
CC syncytia formation. This homolog can be used in the detection,
CC prophylaxis and treatment of diseases caused by infective agents whose
CC primary targets are CD4+ cells.
XX
SQ Sequence 1701 BP; 435 A; 468 C; 361 G; 437 T; 0 other;

Query Match   72.9%; Score 1429.4; DB 13; Length 1701;
Best Local Similarity   93.1%; Pred. No. 0;
Matches 1534; Conservative   0; Mismatches 96; Indels 17; Gaps 3;

Qy   11 CATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATATGGTATGGTATCTGCACCTGTGG 70
Db   40 CATGAGGGTCCCCGCTCCAGCTCCTGCGGCTCTGCTGCTCTGCCAGGTGCCAGAGG 99

Qy   71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTAGGAGAGAGGGCCAC 130
Db   100 TGATATCGTAATGACCCCAGTCTCCAGACTCCCCAGCTGTGTCACTTGGAGAGAGGGCTAC 159

Qy   131 TATTAGTTGCAAATCCAGTCAGAGTCTGTCTCACAATCAGTAGAACCCGAGAGAACTACTTGGC 190
Db   160 TATAAACTGCAGTCCAGTCCAGTGGGAGCCTTTATATAGTACCAATCAAAGAACTACTTGGC 219

Qy   191 TTGGTACCAGCAGAAACCAGGGCAGCCCTCCTAAACTGCTGATCTACTGGCATCCACTAG 250
Db   220 CTGGTACCAGCAGCAGAAACCAGGGCAGCCCTCCTAAACTGCTGATTTACTGGCATCCACTAG 279

Qy   251 GGAATCGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC 310
Db   280 GGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC 339

Qy   311 CATCAGCAGTCTGCGGGTCTGAGACGTGGCAGTTGATTACTGGACTGGCCAATCTTATAATCT 370
Db   340 CATCAGCAGTTTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAATATTATAGCTA 399

Qy   371 TTACACGTTCGGACAGGGGACCAAGGTGAAAATAAAACGTAAGTAGTCTTCTCAAACTCTA-------- 448
Db   400 TCGGACGTTCGGTTCGGAGGGACCAAGGCTGGAGATCAAACTGAGATCAAACGTAAGTAAGTGCACT 448

Qy   431 GAAATTTCAAACTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGT 490
Db   449 ----TTCTAAACTCGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 504

Qy   491 TTACTGCAAGGTCAGAAAGCATGCAAGAGCCCTCAGATAGTGGCTGCAAAGAGTTCCAACAA 550
Db   505 TTACTGCAAGGTCAGAAAGCATGCAAGAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 564

Qy   551 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAG 610
Db   565 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAG 624

Qy   611 ATTTTAAATACGCTTCTTGGTTCCTTGCTATAATTATCTGGAATAAGCATGCTGTTTTC 670
Db   625 ATTTTAAATACGCTTCTTGGTTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTTC 684

Qy   671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAAACACACACCCAAGGCAGAACTTT 730
Db   685 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAAACAACAACACCCAAGGCAGAACTTT 744

Qy   731 GTTACTTAAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTGCACCATCTGTC 790
Db   745 GTTACTTAAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTGCACCATCTGTC 804

Qy   791 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 850
Db   805 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 864

Qy   851 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 910
Db   865 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 924

Qy   911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 970
Db   925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 984

Qy   971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1030
Db   985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1044

Qy   1031 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1090
Db   1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1104

Qy   1091 AGGGAGAAGTGCCCCACCACCTGCTCCTGACCGTCCTCAGTTCAGCCCCTCCCATCCTTGGCC 1150
Db   1105 AGGGAGAAGTGCCCCACCACCTGCTCCTGACCGTCCTCAGTTCAGCCCCTCCCATCCTTGGGCC 1164

Qy   1151 TCTGACCCTTTTCCACAGGGGACCACCCCTATTGCGGTCCTCCAGCTTCATCTTTCACC 1210
Db   1165 TCTGACCCTTTTTCCACAGGGGACCACCCCTATTGCGGTCCTCCAGCTTCATCTTTCACC 1224

Qy   1211 TCACCCCCCTCCTCCTTGGCTTTATTATGTCTAATGTTGGAGGAATGAATAAAATA 1270
Db   1225 TCACCCCCCTCCTCCTTGGCTTTATTATGTCTAATGTTGGAGGAATGAATAAAATA 1284

Qy   1271 AAGTGAATCTTTGCACCTGTGTTCTCCTTCCTC-ATTTAATAATTATTATTCTGTTG 1329
Db   1285 AAGTGAATCTTTGCACCTGTGTTCTCCTTCCTCCTCAATTTAATAATTATTATTCTGTTG 1344

Qy   1330 TTTTACCACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAACTCTGCAAGACAGT 1389
Db   1345 -TTTTACCACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAACTCTGCAAGACAGT 1403

Qy   1390 TAACCATTTATAAAAATCATCCTCATTTCATTCATTTACCCTATCTTTACCCTGCAAGACAGT 1449
Db   1404 TAACCATTTATAAAAATCATCCTCATTTCATTTATTTACCCTATCTTTACCCTGCAAGACAGT 1463

Qy   1450 CCTCCCTCAAACCCACCAGCCTTCTGTCCTCCAGTCCCCATGGTGCCAGTCCCATGGTAGGAGAGAC 1509
Db   1464 CCTCCCTCAAACCCACCAGCCTTCTGTCCTCCAGTCCCCAGTCCCCGTGGTGAGGAGAGAC 1523

Qy   1510 TTGCTTCCTGTTTCCCCTCCTCAGCCCTCCTTTTTAAGGGTGACAGT 1569
Db   1524 TTGCTTCCTGTTTCCCCTCCTCAGCCCTCCTTTTTAAGGGTGACAGT 1583

Qy   1570 CTTACAGTCTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGCAAATTTTCAA 1629
Db   1584 CTTACGGTCTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGCAAATTTTTCAA 1643

Qy   1630 AAGAAGAAACCTGCTATAAAGAGAATC 1656
Db   1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670

RESULT 7
AAQ30920
ID   AAQ30920 standard; DNA; 1701 BP.
XX
AC   AAQ30920;
XX
DT   02-APR-1993 (first entry)
XX
DE   Vector pMDR1007.
XX

```
KW  Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
KW  pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;
KW  NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
KW  melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
KW  humanised; 5A8; light chain; variable region; LV; genomic; constant
KW  antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
KW  lymphocyte; helper; inducer; HIV; syncytia; formation; ss.
XX
OS  Synthetic.
XX
FH  Key             Location/Qualifiers
FT  sig_peptide     35..100
FT                  /*tag= a
FT                  /note= "Immunoglobulin kappa chain signal sequence"
FT  mat_peptide     101..1101
FT                  /*tag= b
FT  exon            35..436
FT                  /*tag= c
FT                  /number= 1
FT                  /note= "AA1-AA112 of humanised 5A8 LV"
FT  intron          438..781
FT                  /*tag= d
FT                  /number= 1
FT  exon            782..1101
FT                  /*tag= e
FT                  /number= 2
FT                  /note= "AA108-AA214 of human kappa LC"
FT  CDS             35..1104
FT                  /*tag= f
XX
PN  WO9209305-A.
XX
PD  11-JUN-1992.
XX
PF  27-NOV-1991;   91WO-US08843.
XX
PR  27-NOV-1990;   90US-0618542.
XX
PA  (BIOJ ) BIOGEN INC.
XX
PI  Burkly LC,  Chisholm PL,  Rosa JJ,  Rosa MD,  Thomas DW;
XX
DR  WPI; 1992-398399/48.
DR  P-PSDB; AAR28809.
XX
PT  New anti-CD4 antibody homolognes - which bind CD4, do not block
PT  binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT  formation between CD4+ cells
XX
PS  Claim 27; Page 164-5; Page 27, 205pp; English.
XX
CC  The sequence given is the insert of the vector pMDR1006. pMDR1007
CC  (see AAQ30919) and pSAB132 (see AAQ30906) were used in the construction
CC  of this vector. Three fragments were ligated together to generate
CC  pMDR1006; a 572 bp fragment of pMDR985 (see AAQ30913), a 3442bp AatII/
CC  EcoRV fragment of pMDR986 (see AAQ30918) and a 326 bp EcoRV/BglII
CC  fragment of pMDR1003 (see AAQ30900). The ligation mixture was used to
CC  transform E. coli JA221(Iq) to ampicillin resistance. pMDR1006 was
CC  cleaved with NotI and the 1693 bp fragment isolated was ligated into
CC  NotI linearised pSAB132 which had been dephosphorylated by calf
CC  alkaline phosphatase. This generates the plasmid pMDR1007. The
CC  dephosphorylated mixture was fractionated through low temperature
CC  melting agarose and used to transform E. coli JA221(Iq) to ampicillin
CC  resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
CC  order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
CC  1-AA112 of the humanised 5A8 light chain variable region (LV) followed
CC  by genomic DNA encoding AA108-AA214 of the human kappa light chain,
CC  ie. the light chain constant region (LC). The polypeptide encoded by
CC  pMDR1007 is an antibody homolog which was shown to bind to CD4 but did
CC  not block the binding of gp120 to CD4. CD4 is a cell surface
CC  glycoprotein of CD4+ lymphocytes (helper/inducer cells). The homolog
CC  blocked HIV-induced syncytia formation. This homolog can be used in
CC  the detection, prophylaxis and treatment of diseases caused by
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CC  infective agents whose primary targets are CD4+ cells.
XX
SQ  Sequence 1701 BP; 435 A; 469 C; 361 G; 436 T; 0 other;

    Query Match            72.8%;   Score 1427.8;   DB 13;   Length 1701;
    Best Local Similarity  93.1%;   Pred. No. 0;
    Matches 1533;  Conservative  0;  Mismatches  0;  Indels  17;  Gaps  3;

Qy   11  CATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTCATGGGTATCTGCACCTGTGG   70
         ||||                   |  |||  ||       || |  ||| || |  ||
Db   40  CATGAGGGTCCCCGTCAGCTCCTGGGGCTTCCTGCTCGTCTGCTGCCAGGTGCCAGAGG   99

Qy   71  GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGCCAC  130
         || ||| |||  |||||||||||||||| |||||| ||||| ||||||||||||| |||
Db  100  TGATATCGTAATGACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGCTAC  159

Qy  131  TATTAGCTGCAAATCCAGTCAGAGTGTGCTCAACAGTAGAACCCGAGAGAACTACTTGGC  190
         ||| | ||||||| |||||||||||  |    ||  | | |||| | |||||||||||||
Db  160  TATAAACTGCAAGTCCAGTCAGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGC  219

Qy  191  TTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAG  250
         ||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db  220  CTGGTACCAGCAGAAACCAGGGCAGCGTCCTAAACTGCTGATTTACTGGGCATCCACTAG  279

Qy  251  GGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGACAGATTTCACTCTCAC  310
         ||||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Db  280  GGAATCTGGGGTCCCTGATCGCTTCTCAGCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC  339

Qy  311  CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGACAGCAATCTTATAATCT  370
         ||||||||| | |||||||||||||||||||||||||||||  |||||||| |||| |
Db  340  CATCAGCAGTTTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGCTA  399

Qy  371  TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTTCTTCTCAACTCTA  430
         | |||||||||| ||||| ||||||| |||||| |||||||||| | |
Db  400  TCGGACGTTCGGTCGGAGGGACCAAGGACCAAGGATCAAACGTAAGTGCACT------  448

Qy  431  GAAATTCTAAACTCTGAGGGGTCGATGACGTGCCATTCTTCTTGCCTAAAGCATTGAGT  490
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  449  ----TTCTAAACTCTGAGGGGTCGATGACGTGCCATTCTTCTTGCCTAAAGCATTGAGT  504

Qy  491  TTACTGCAAGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA  550
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  505  TTACTGCAAGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA  564

Qy  551  AACAATTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAGAAACTCAAAACATCAAG  610
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565  AACAATTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAGAAACTCAAAACATCAAG  624

Qy  611  ATTTTAAATACGCCTTCTTGGGTCTTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC  670
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625  ATTTTAAATACGCCTTCTTGGGTCTTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC  684

Qy  671  TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAAACAACACACCCAGGCAGAACTTT  730
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  685  TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAAACAACACACCCAGGCAGAACTTT  744

Qy  731  GTTACTTAAACACCATCCTGTTGCTCTTCCTCCAGGAACTGTGGCTGCACCATCTGTC  790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  745  GTTACTTAAACACCATCCTGTTGCTCTTCCTCCAGGAACTGTGGCTGCACCATCTGTC  804

Qy  791  TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG  850
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  805  TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG  864

Qy  851  CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA  910
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  865  CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA  924

Qy  911  TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCACCTACAGCCTC  970
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  925  TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCACCTACAGCCTC  984

Qy  971  AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAA  1030
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Db        985  AGCAGCACCCTGAGCGCTGAGCTGAGTCTGCCCGTCACAAAGAGCTTCAACAGGGAGAAACACAAAGTCTACGCGCCTGCGAA  1044
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy       1031  GTCACCCATCAGGGACCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAG  1090
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045  GTCACCCATCAGGGGCCTGAGCTCCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAG  1104

Qy       1091  AGGGAGAAGTGCCCCACCTGCTTCCTCAGTTCCACCCCTCCCATCCTTTGGCC  1150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105  AGGGAGAAGTGCCCCACCTGCTTCCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCC  1164

Qy       1151  TCTGACCCTTTTCCACAGGGGACCTACCCTATTGCGTCCTCCAGCTCATCTTCACC  1210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165  TCTGACCCTTTTCCACAGGGGACCTACCCTATTGCGTCCTCCAGCTCATCTTCACC  1224

Qy       1211  TCACCCCCTCCTCCTCCTTGGCTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA  1270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225  TCACCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA  1284

Qy       1271  AAGTGAAATCTTTGCACCTGGTTCTCCTTTTCTCTTTCCTC-ATTTAATTAATAATTATTATTATCTGTTG  1329
               |||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db       1285  AAGTGAAATCTTTGCACCTGTGGTTCTCCTTTTCTCTTTCCTCAATTTAATTAATTAATAATTATTATTATCTGTTG  1344

Qy       1330  TTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTTAAGGCGCA  1389
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345  -TTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTTAAGGCGCCA  1403

Qy       1390  TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT  1449
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404  TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT  1463

Qy       1450  CCTTCCCTCAAACCCACCAAGAGCCTTCGTCCTCCACAGTCCCCTGGGCCATTGGCTAGGAGAGAC  1509
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464  CCTTCCCTCAAACCCACCAAGAGCCTTCGTCCTCCACAGTCCCCTGGGCCGTGGTAGGAGAGAC  1523

Qy       1510  TTGCTTCCTTGTTTTCCCCTCCTCCAGCAAGCCCTCATAGTCCTTTTAAGGGGTGACAGT  1569
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524  TTGCTTCCTTGTTTTCCCCTCCTCCAGCAAGCCCTCATAGTCCTTTTAAGGGGTGACAGT  1583

Qy       1570  CTTACAGTCTCATATATCCTTTGATTCAAATCCCTGGGAATCAACCAAAGCAAATTTTTCAA  1629
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584  CTTACGGTCTCATATATCCTTTGATTCAAATCCCTGGGAATCAACCAAGGCAAATTTTTCAA  1643

Qy       1630  AAGAAGAAAACCTGCTATAAAGAGAATC  1656
               ||||||||||||||||||||||||||||
Db       1644  AAGAAGAAAACCTGCGGCCGATCGATTC  1670
```

RESULT 8

AAQ43845

ID   AAQ43845 standard; DNA; 13999 BP.

XX

AC   AAQ43845;

XX

DT   20-OCT-1993 (first entry)

XX

DE   Plasmid pAH4611.

XX

KW   Polymerase chain reaction; primer; PCR; amplify; murine;
KW   heavy;light; chain; variable; constant; region; anti-human;
KW   transferrin; receptor; antibody; brain; capillary;
KW   endothelial cell; conjugate; tumour; AIDS; neuropharmaceutical;
KW   diagnostic; agent; tumour; AIDS; stroke; epilepsy;
KW   Parkinsons disease; Alzheimers disease; ss.

XX

OS   Synthetic.

XX

FH   Key   Location/Qualifiers
FH
FT   unsure   3396..5095
FT   /*tag= a
FT   CDS   5233..5616
FT   /*tag= b
FT   /note= "128.1 VL region"

FT   unsure   6920..7218
FT   /*tag= c
FT   CDS   8424..8741
FT   /*tag= d
FT   /note= "Undefined ORF"
FT   unsure   9300..12092
FT   /*tag= e

XX

PN   WO9310819-A.
XX
PD   10-JUN-1993.
XX
PF   24-NOV-1992;   92WO-US10206.
XX
PR   26-NOV-1991;   91US-0800458.
XX
PA   (ALKE-) ALKERMES INC.
XX
PI   Friden PM;
XX
DR   WPI; 1993-196742/24.
DR   P-PSDB; AAR41686-87.
XX
PT   Antibody conjugates specific for transferrin receptor - used
PT   for diagnosis and treatment of cancer, AIDS and neurological
PT   disorders
XX
PS   Disclosure; Fig 13A-F; 151pp; English.
XX
CC   This sequence represents the expression vector pAH4611.
CC   This vector was produced from the plasmid pAG4270. pAG4270
CC   is the expression vector for the light chain variable region
CC   (VL) of the antibody 128.1 which was obtained by PCR with
CC   leader/J region priming (see also AAQ43842).   The vector also
CC   contains an ampicillin resistance gene, a gpt (mycophenolic
CC   acid resistance) selected marker, an immunoglobulin H
CC   enhancer and an intron for V-constant region splicing.
CC   Transcription of the CH gene is from the VH promoter of the
CC   murine 27.44 gene.   The cloning of the 128.1 VL region was
CC   accomplished in two stages with the production of plasmid
CC   pSV4271 as an intermediate vector which lacks the promoter
CC   region.   This plasmid was used in conjunction with pAH4602
CC   in the production of the chimeric antibody 128.1.   128.1 is
CC   an anti-human transferrin receptor antibody which binds to
CC   the transferrin receptor on brain capillary endothelial
CC   cells.   This antibody may be used in a conjugate in which it
CC   is linked to a neuropharmaceutical or diagnostic agent. The
CC   conjugate may be used to treat or prevent neurological
CC   disorders eg brain tumours, AIDS, stroke, epilepsy,
CC   Parkinsons and Alzheimers disease.   It may also be used for
CC   diagnostic methods.
XX
SQ   Sequence 13999 BP; 2534 A; 2085 C; 2104 G; 2472 T; 4804 other;

Query Match   60.4%; Score 1184.2; DB 14; Length 13999;
Best Local Similarity   99.5%; Pred. No. 4e-268;
Matches 1208; Conservative   0; Mismatches   4; Indels   2; Gaps   2;

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Qy   433  AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTT  492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8087  AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTT  8146

Qy   493  ACTGCAAGTCAGAAAAGCATGCAAAGCCCTCGCAAATGGCTGCAAAGAGCTCCAACAAA  552
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8147  ACTGCAAGTCAGAAAAGCATGCAAAGCCCTCGCAAATGGCTGCAAAGAGCTCCAACAAA  8206

Qy   553  CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAAACTCAAAACATCAAGAT  612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8207  CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAAACTCAAAACATCAAGAT  8266

Qy   613  TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG  672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8267  TTTAAATACGCTTCCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG  8326
```

XX
AC   AAQ30918;
XX
DT   02-APR-1993 (first entry)
XX
DE   pMDR986 insert.
XX
KW   primer; polymerase chain reaction; PCR; amplify; intermediate;
KW   plasmid; pMDR986; genomic; DNA; human; kappa; light; chain; constant;
KW   region; LC; placenta; EcoRI; pUC8; pAB8; EcoRV; pNNO3; pSAB153;
KW   dephosphorylated; calf; alkaline phosphatase; E. coli; JA221(Iq);
KW   EcoO109 I; E. coli; GM2929; methylate; cloning artifact; NotI; PvuI;
KW   CD4; CD4+; HIV; gp120; syncytia; formation; ss.
XX
OS   Synthetic.
XX
PN   WO9209305-A.
XX
PD   11-JUN-1992.
XX
PF   27-NOV-1991;   91WO-US08843.
XX
PR   27-NOV-1990;   90US-0618542.
XX
PA   (BIOJ) BIOGEN INC.
XX
PI   Burkly LC,   Chisholm PL,   Rosa JJ,   Rosa MD,   Thomas DW;
XX
DR   WPI; 1992-398399/48.
XX
PT   New anti-CD4 antibody homolognes - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Disclosure; Page 161-2; 205pp; English.
XX
CC   The sequence given is the insert of the intermediate plasmid pMDR986.
CC   pMDR986 was constructed to carry genomic DNA encoding amino acid (AA)
CC   108-AA214 of a human kappa light chain ie. the light chain constant
CC   region (LC). Human placental genomic DNA was prepared and cleaved
CC   with EcoRI to give a 2.5 kb fragment. This fragment comprising the
CC   kappa chain constant region was cloned into the EcoRI site of pUC8 to
CC   give pAB8. The DNA encoding LC was amplified from pAB8 using the
CC   primer sequences given in AAQ30914-15. The 1240 bp reaction product
CC   was ligated into EcoRV linearised pNNO3 (see AAQ30566) that had been
CC   dephosphorylated. This generated plasmid pSAB153 (see AAQ30916). LC
CC   was amplified from pSAB153 using the primers given in AAQ30915 and
CC   AAQ30917 to generate an approx. 1276 bp fragment. This fragment was
CC   ligated to EcoRV linearised pNNO3 that had been dephosphorylated by
CC   calf alkaline phosphatase. The ligation mixture was used to transform
CC   E. coli JA221(Iq) to ampicillin resistance. Plasmid pMDR986 was
CC   identified by the presence of a 1122 bp EcoO109 I restriction fragment.
CC   pMDR986 was used to transform E. coli GM2929, which does not methylate
CC   its own DNA. Sequence analysis of pMDR986 showed that a cloning
CC   artifact caused a NotI site 3' of the constant region to be been
CC   replaced with a PvuI site.
XX
SQ   Sequence 1276 BP; 340 A; 352 C; 244 G; 340 T; 0 other;

Query Match   60.3%; Score 1181.4; DB 13; Length 1276;
Best Local Similarity   98.9%; Pred. No. 7.6e-268;
Matches 1210; Conservative   0; Mismatches 11; Indels 2; Gaps   2;

Qy   673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGAGAACTTTGT 732
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8327 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGAGAACTTTGT 8386

Qy   733 TACTTAAACACCATCCTCCTGTTTCTTCTTTGCTCTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8387 TACTTAAACACCATCCTCCTGTTTCTTCTTTGCTCTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 8446

Qy   793 CATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8447 CATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 8506

Qy   853 GAATAACTTCATCCCAGAGAGAGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8507 GAATAACTTCATCCCAGAGAGAGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 8566

Qy   913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACACCTACAGCCTCAG 972
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8567 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACACCTACAGCCTCAG 8626

Qy   973 CAGCACCCTGACCCTGCGAGCAAGCAGACTACAGAAGACACAAAGTCTACGGCCTGCGAAGT 1032
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8627 CAGCACCCTGACCCTGCGAGCAAGCAGACTACAGAAGACACAAAGTCTACGGCCTGCGAAGT 8686

Qy   1033 CACCCATCAGGGGCCTGAGCTCCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8687 CACCCATCAGGGGCCTGAGCTCCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 8746

Qy   1093 GGAGAAGTGCCCCCACCTGCTCCTCCAGTTCCAGCCTGACCCCCTCCCATCCTTGGCCTC 1152
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8747 GGAGAAGTGCCCCCACCTGCTCCTCCAGTTCCAGCCTGACCCCCTCCCATCCTTGGCCTC 8806

Qy   1153 TGACCCTTTTCCACAGGGGACCTACCCCCATTGCGGTCCTCCAGTCATCTTCACCTC 1212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8807 TGACCCTTTTCCACAGGGGACCTACCCCCATTGCGGTCCTCCAGTCATCTTCACCTC 8866

Qy   1213 ACCCCCCCTCCTCCCTCCTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
               ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   8867 ACCCCCCCTCCTCCCTCCTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 8926

Qy   1273 GTGAATCTTGCACCTGTGGTTTCTCTTCCTC-ATTTAATAATTATTATCTCGTTGTT 1331
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   8927 GTGAATCTTTGCACCTGTGGTTTCTCTTCCTCAATTTAATAATTATTATCTCGTTG-T 8985

Qy   1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8986 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 9045

Qy   1392 ACCATTTATAAAAATCATCCTTCATTCTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9046 ACCATTTATAAAAATCATCCTTCATTCTTTACCCTATCATCCTCTGCAAGACAGTCC 9105

Qy   1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCCACAGTCCCTGGGCCATGGTAGGAGGACTT 1511
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9106 TCCCTCAAACCCACAAGCCTTCTGTCCTCCACAGTCCCTGGGCCGTGGTAGGAGGACTT 9165

Qy   1512 GCTTCCTTGTTTTCCCCCTCCTCCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 1571
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9166 GCTTCCTTGTTTTCCCCCTCCTCCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 9225

Qy   1572 TACAGTCATATATCCTTTGATTCAATTCCCTGGAATCAACCAAAGCAAATTTTTCAAAA 1631
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9226 TACGGTCATATATCCTTTGATTCAATTCCCTGGAATCAACCAAAGCAAATTTTTTCAAAA 9285

Qy   1632 GAAGAAACCTGCTA 1645
               ||||||||||||||
Db   9286 GAAGAAACCTGCNA 9299

RESULT 9
AAQ30918
ID   AAQ30918 standard; DNA; 1276 BP.

Qy   435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGGAGTTTAC 494
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGGAGTTTAC 83

Qy   495 TGCAAGGTCAGAAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCACAAAACA 554
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 TGCAAGGTCAGAAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCACAAAACA 143

Qy   555 ATTTAGAACTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAAACATCAAGATTT 614
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
AAQ30916
ID   AAQ30916 standard; DNA; 1241 BP.
XX
AC   AAQ30916;
XX
DT   02-APR-1993 (first entry)
XX
DE   pSAB153 insert.
XX
KW   Primer; polymerase chain reaction; PCR; amplify; intermediate;
KW   plasmid; pMDR986; genomic; DNA; human; kappa; light; chain; constant;
KW   region; LC; placenta; EcoRI; pUC8; pAB8; EcoRV; pNN03; pSAB153;
KW   dephosphorylated; calf; alkaline phosphatase; E. coli; JA221(Iq);
KW   Eco0109 I; E. coli; GM2929; methylate; cloning artifact; NotI; PvuI;
KW   CD4; CD4+; HIV; gp120; syncytia; formation; ss.
XX
OS   Synthetic.
XX
PN   WO9209305-A.
XX
PD   11-JUN-1992.
XX
PF   27-NOV-1991;   91WO-US08843.
XX
PR   27-NOV-1990;   90US-0618542.
XX
PA   (BIOJ) BIOGEN INC.
XX
PI   Burkly LC,   Chisholm PL,   Rosa JJ,   Rosa MD,   Thomas DW;
XX
DR   WPI; 1992-398399/48.
XX
PT   New anti-CD4 antibody homologues - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Disclosure; Page 159-60; 205pp; English.
XX
CC   The sequence given is the insert from the intermediate plasmid pSAB153.
CC   This plasmid was used in the construction of the intermediate plasmid
CC   pMDR986 (see AAQ30918).   pMDR986 was constructed to carry genomic DNA
CC   encoding amino acid (AA) 108-AA214 of a human kappa light chain ie.
CC   the light chain constant region (LC).   Human placental genomic DNA was
CC   prepared and cleaved with EcoRI to give a 2.5 kb fragment. This
CC   fragment comprising the kappa chain constant region was cloned into
CC   the EcoRI site of pUC8 to give pAB8.   The DNA encoding LC was amplified
CC   from pAB8 using the primer sequences given in AAQ30914-15.   The 1240 bp
CC   reaction product was ligated into EcoRV linearised pNN03 (see AAQ30566)
CC   that had been dephosphorylated.   This generated plasmid pSAB153. LC
CC   was amplified from pSAB153 using the primers given in AAQ30915 and
CC   AAQ30917 to generate an approx. 1276 bp fragment.   This fragment was
CC   ligated to EcoRV linearised pNN03 (see AAQ30566) that had been
CC   dephosphorylated by calf alkaline phosphatase.   The ligation mixture
CC   was used to transform E. coli JA221(Iq) to ampicillin resistance.
CC   Plasmid pMDR986 was identified by the presence of a 1122 bp Eco0109 I
CC   restriction fragment.   pMDR986 was used to transform E. coli GM2929,
CC   which does not methylate its own DNA.   Sequence analysis of pMDR986
CC   showed that a cloning artifact caused a NotI site 3' of the constant
CC   region to be been replaced with a PvuI site.
XX
SQ   Sequence 1241 BP; 329 A; 340 C; 242 G; 330 T; 0 other;

Query Match   60.3%;   Score 1181.2;   DB 13;   Length 1241;
Best Local Similarity   99.6%;   Pred. No. 8.4e-268;
Matches 1205;   Conservative   0;   Mismatches   3;   Indels   2;   Gaps   2;

Qy   435 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83

Db   144 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAGATTT 203

Qy   615 TAAATACGGCTTCTTGGTCTCCTTGCTATATAATTATCTGGGATAAGCATGCTGTTTCTGTC 674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 TAAATACGGCTTCTTGGTCTCCTTGCTATATAATTATCTGGGATAAGCATGCTGTTTCTGTC 263

Qy   675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACACACCCAAGGGCAGAACTTTGTTA 734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACACACCCAAGGGCAGAACTTTGTTA 323

Qy   735 CTTAAACAACCATCCTGTTTTGCTTCTTCTTCCTCAGGAACTGTGGCTGCACCATCTGCTTCA 794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 CTTAAACAACCATCCTGTTTTGCTTCTTCTTCCTCAGGAACTGTGGCTGCACCATCTGCTTCA 383

Qy   795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443

Qy   855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy   915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGAGCAAGCAGGACAGGAGAGTGTTAGAGGG 974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGAGCAAGCAGGACAGGAGAGTGTTAGAGGG 563

Qy   975 GCACCCTGACGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 GCACCCTGACGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy   1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAGAGGAGTGTTAGAGGG 1094
          |||||||||||||||||||||||||||||||||||||||||||||
Db   624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGTGTTAGAGGG 683

Qy   1095 AGAAGTGCCCCCACCTGCTCCTGACCCCTCCATCCTTTGGCTCTG 1154
          |||||||||||||||||||||||||||||||||||||||||||||
Db   684 AGAAGTGCCCCCACCTGCTCCTGACCCCTCCATCCTTTGGCTCTG 743

Qy   1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCGTCCTCCTCCAGCTCATCTTCACCTCAC 1214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCGTCCTCCTCCAGCTCATCTTCACCTCAC 803

Qy   1215 CCCCTCCTCCTCCTGGCTTTAATTATGCTAATGTTGGAGGAGGAATGAATAAATAAAGT 1274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 CCCCTCCTCCTCCTGGCTTTAATTATGCTAATGTTGGAGGAGGAATGAATAAATAAAGT 863

Qy   1275 GAATCTTTGCACCTGTGGTTTCTCTCTTCCTC-ATTTAATAATTATTATCTGTTGTTT 1333
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   864 GAATCTTTGCACCTGTGGTTTCTCTCTTCCTCAATTTAATAATTATTATCTGTTGTTT 923

Qy   1334 ACCAACTACTCAATTTCTTATTAGGGACTAAAATATGTAGTCATCCTAAGGGCATAAC 1393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 ACCAACTACTCAATTTCTTATTAGGGACTAAAATATGTAGTCACTCCTAAGGGC-ATAAC 982

Qy   1394 CATTTATAAAAATCATCCTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   983 CATTTATAAAAATCATCCTTGATTCAATTCCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy   1454 CCTCAAACCCACAAGCCTTCGTCTCCTCACAGTCCCTGGGCCATGTGGGGCAGACTTGC 1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 CCTCAAACCCACAAGCCTTCGTCTCCTCACAGTCCCTGGGCCATGTGGGGCAGACTTGC 1102

Qy   1514 TTCCTTGTTTCCCCTCCTCAGCAGCCCTCCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1103 TTCCTTGTTTCCCCTCCTCAGCAGCCCTCCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162

Qy   1574 CAGTCATATATCCTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAGA 1633
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1163 CAGTCATATATCCTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAGA 1222

Qy   1634 AGAAACCTGCTATAAAGAGAATC 1656
          |||||||||||||||||||||||
Db   1223 AGAAACCTGCGGCCGATCGATTC 1245

Db   1163 CGTTCATATATCCTTTGATTCAATTCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1222
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1634 AGAAACCTGC 1643
              ||||||||||
Db   1223 AGAAACCTGC 1232

RESULT 11
AAV39242
ID   AAV39242 standard; DNA; 3880 BP.
XX
AC   AAV39242;
XX
DT   18-DEC-1998 (first entry)
XX
DE   Plasmid pCK7-96 nucleotide sequence.
XX
KW   Transgenic animal; human heterologous antibody; transgene;
KW   isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW   autoimmune reaction; inflammatory response; transplant rejection;
KW   acid induced lung injury; acute adult respiratory distress syndrome;
KW   ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW   cystic fibrosis; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9824884-A1.
XX
PD   11-JUN-1998.
XX
PF   01-DEC-1997;   97WO-US21803.
XX
PR   02-DEC-1996;   96US-0758417.
XX
PA   (GENP-) GENPHARM INT.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1998-333306/29.
XX
PT   Hybridoma producing antibody specific for interleukin-8 - used to
PT   prevent efflux of neutrophils from vasculature, and treat
PT   reperfusion injury
XX
PS   Example 42; Pages 310-312; 452pp; English.
XX
CC   The present sequence represents the kappa light chain plasmid, pCK7-96,
CC   which includes the kappa constant region and polyadenylation site. The
CC   plasmid is used in the construction of minigenes for expression of
CC   IgGkappa anti-CD4 antibodies, in the transgenic mouse of the invention.
CC   The specification describes transgenic non-human animals, especially a
CC   mouse which are capable of producing a human heterologous antibodies of
CC   multiple isotypes by undergoing isotype switching. The transgenic animals
CC   have human heavy and light chain transgenes. The transgenes are capable
CC   of functionally rearranging a heterologous diversity (D) gene in a
CC   variable-diversity-junction (V-D-J) recombination. The transgenes include
CC   a heavy chain transgene comprising at least one V, D and J gene segment,
CC   and one constant region gene segment. The immunoglobulin (Ig) light chain
CC   transgene comprises at least one V and J gene segment and one constant
CC   region gene segment. The gene segments are heterologous to the transgenic
CC   animal. The antibody can be used to prevent efflux of neutrophils from
CC   vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC   antibodies are used to reduce undesirable autoimmune reactions,
CC   inflammatory responses and rejection of transplanted organs. The
CC   anti-IL-8 antibodies can reduce tissue damage and prolong survival in
CC   animal models of acute adult respiratory distress syndrome (ARDS) and
CC   acid induced lung injury. The anti-IL-8 antibodies can also be used for
CC   the treatment of vasculitis, septic shock, allergic reactions
CC   (e.g. asthma) and cystic fibrosis.
XX
SQ   Sequence 3880 BP; 981 A; 1013 C; 921 G; 965 T; 0 other;

Qy   495 TGCAAGGTCAGAAAAGCATGCAAAGCCTCCAGAAGTGGCTCCAACAAAACA 554
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 TGCAAGGTCAGAAAAGCATGCAAAGCCTCCAGAAGTGGCTCCAACAAAACA 143

Qy   555 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAGAAACTCAAAACATCAAGATTT 614
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAGAAACTCAAAACATCAAGATTT 203

Qy   615 TAAATACGGCTTCTTGGTCTCCTGCTATAATTATCTGGGATAAGCATGCGTGTTTTCTGTC 674
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 TAAATACGGCTTCTTGGTCTCCTGCTATAATTATCTGGGATAAGCATGCGTGTTTTCTGTC 263

Qy   675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy   735 CTTAAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGTGGCTCGCACCATCTGTCTTCA 794
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 CTTAAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGTGGCTCGCACCATCTGTCTTCA 383

Qy   795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCGTTGTGTGCCTCTGA 854
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCGTTGTGTGCCTCTGA 443

Qy   855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGATAACGCCCTCCAATCGG 914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGATAACGCCCTCCAATCGG 503

Qy   915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAGCA 974
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAGCA 563

Qy   975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAAACACAAAGTCTTACGCCTGCGAAGTCA 1034
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAAACACAAAGTCTTACGCCTGCGAAGTCA 623

Qy   1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAGAGGAGAGTGTTAGAGGG 1094
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   624 CCCATCAGGGCCTGAGCTCGCCCGTCACAGAGGAGAGTGTTAGAGGG 683

Qy   1095 AGAAGTGCCCCCACCTGCTCTCCAGTTCCAGCCTGACCCCCTCCATCCTTTGGCCTCTG 1154
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684 AGAAGTGCCCCCACCTGCTCTCCAGTTCCAGCCTGACCCCCTCCATCCTTTGGCCTCTG 743

Qy   1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTCAC 1214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTCAC 803

Qy   1215 CCCCTCCTCCTCCTGGCTTAATATGCTAATGTTGGAGGAGGAGATGAATAAATAAAGT 1274
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 CCCCTCCTCCTCCTGGCTTAATATGCTAATGTTGGAGGAGGAGATGAATAAATAAAGT 863

Qy   1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTAATAATTATTATTATCTGTTGTTTT 1333
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATTATCTGTTG-TTT 922

Qy   1334 ACCAACTACTCAATTCTTCTTATAAGGGACTAAAATATGTAGTCATCCTAAGGCGGCCATAAC 1393
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   923 ACCAACTACTCAATTCTTCTTATAAGGGACTAAAATATGTAGTCATCCTAAGGCGGCCATAAC 982

Qy   1394 CATTTATAAAAATCATCCTTCATTCATTTACCCTCTGCCAAGACAGTCCTC 1453
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   983 CATTTATAAAAATCATCCTTCATTCATTTACCCTCTGCCAAGACAGTCCTC 1042

Qy   1454 CCTCAAACCCACACAAGCCTTCTGTCCTCCACAGTCCCCTGGCCATGGTAGGAGACTTGC 1513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 CCTCAAACCCACACAAGCCTTCTGTCCTCCACAGTCCCCTGGCCATGGTAGGAGACTTGC 1102

Qy   1514 TTCCTTGTGTTTCCCCTCCTCCAGCCAAGCCCTCCATAGTCCTTTTAAGGGTGACAGTCTTA 1573
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1103 TTCCTTGTGTTTCCCCTCCTCCAGCCAAGCCCTCCATAGTCCTTTTAAGGGTGACAGTCTTA 1162

Qy   1574 CAGTCATATATCCTTTGATTCAATTCCTGGGAATCAACCAAGCAAATTTTTCAAAAGA 1633

Qy   1452 TCCCTCAAACCCACCAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3573 TCCCTCAAACCCACCAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3620

RESULT 12
AAT78801
ID   AAT78801 standard; DNA; 3881 BP.
XX
AC   AAT78801;
XX
DT   23-JAN-1998 (first entry)
XX
DE   Kappa light chain plasmid pCK7-96.
XX
KW   Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW   transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW   transplant rejection; immunoglobulin; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9713852-A1.
XX
PD   17-APR-1997.
XX
PF   10-OCT-1996; 96WO-US16433.
XX
PR   10-OCT-1995; 95US-0544404.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1997-235888/21.
XX
PT   Novel anti-CD4 antibody produced by transgenic mice - used in the
PT   treatment of auto-immune disease etc.
XX
PS   Example 42; Page 260-262; 396pp; English.
XX
CC   A novel composition has been developed which comprises an immunoglobulin
CC   (Ig) having an affinity constant (Ka) of at least 2 multiply
CC   1000000000 M-1 for binding to a predetermined human antigen. The
CC   present sequence represents the kappa light chain plasmid pCK7-96
CC   which includes the kappa constant region and polyadenylation site. Anti-
CC   CD4 antibodies may be used in therapeutic and diagnostic applications,
CC   especially for the treatment of human diseases. These antibodies reduce
CC   activity of CD4 cells and reduce undesirable autoimmune reactions,
CC   inflammatory response and transplant rejection. Transgenic animals are
CC   capable of producing heterologous antibodies of multiple isotypes by
CC   undergoing isotype switching. These animals produce a first Ig type
CC   that is necessary for antigen-stimulated B-cell maturation and can
CC   switch to encode and produce one or more subsequent heterologous
CC   isotypes.
XX
SQ   Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;

Query Match   53.3%; Score 1044; DB 18; Length 3881;
Best Local Similarity   99.8%; Pred. No. 2.3e-235;
Matches 1066; Conservative   0; Mismatches   0; Indels   2; Gaps   2;

Qy   433 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT   492
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2555 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy   493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA   552
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA 2674

Qy   553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGTAGGAGAAGAAACTCAAAACATCAAGAT   612
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2675 CAATTTAGAACTTTATTAAGGAATAGGGGAAGTAGGAGAAGAAACTCAAAACATCAAGAT 2734

Qy   613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATTAAGCATGCTGTTTTCTG   672
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2734 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATTAAGCATGCTGTTTTCTG 2793

Qy   673 TCTGTCCCTAAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT   732
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2794 TCTGTCCCTAAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2853

Qy   733 TACTTAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT   792
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2854 TACTTAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2913

Qy   793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTCTGTGTGTGCCTGCT   852
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2914 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTCTGTGTGTGCCTGCT 2973

Qy   853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC   912
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2974 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3033

Qy   913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAGCAAGGACAGCAGGACACCTACAGCCTCAG   972
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3034 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAGCAAGGACAGCAGGACACCTACAGCCTCAG 3093

Qy   973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3094 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3153

Qy   1033 CACCCATCAGGGGCCTGAGCTCGCCCGTCACAGGGGAGAGTTGTTAGAG 1092
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3154 CACCCATCAGGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTTGTTAGAG 3213

Qy   1093 GGAGAAGTGCCCCCACCTGCCCACTGCTCCAGTTCCAGCCTGACCCCCCATCCTTTGGCCTC 1152
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3214 GGAGAAGTGCCCCCACCTGCCCACTGCTCCAGTTCCAGCCTGACCCCCCATCCTTTGGCCTC 3273

Qy   1153 TGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTGGTCCTCCAGCTCATCTTCACCTC 1212
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3274 TGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTGGTCCTCCAGCTCATCTTCACCTC 3333

Qy   1213 ACCCCCTCCTCCTCCTTGGCTTTAATTATGTGGAGGAATGAATAAATAAA 1272
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3334 ACCCCCTCCTCCTCCTTGGCTTTAATTATGTAATGTGGAGGAATGAATAAATAAA 3393

Qy   1273 GTGAATCTTTGCACCTGTCGTTTCTCTTTCTCCTC-ATTTAATAATTATTATTCTGTTGT   1331
            ||||||||||||||||||||||||||||||||||| |||||||||||||||| |||| |
Db   3394 GTGAATCTTTGCACCTGTCGTTTCTCTTTCTCCTTCTCCAATTTAATTATTATTATTCTGTTG-T 3452

Qy   1332 TTACCAACTACTCAATTTCCTTATAGGGACTAAAATATGTAGTCATCCTAAGGCGCATA 1391
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3453 TTACCAACTACTCAATTTCCTTATAGGGACTAAAATATGTAGTCATCCTAAGGCGCATA 3512

Qy   1392 ACCATTTATAAAAATCATCCTCATTTTACCCTATCATTCTTCCGCAAGACAGTCC 1451
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3513 ACCATTTATAAAAATCATCCTCATTTTACCCTATCATTCTTCCGCAAGACAGTCC 3572

```
KW   transgenic mouse; human heavy chain transgene; digoxin;
KW   human light chain transgene; immortalized cell; immunoglobulin;
KW   Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Synthetic.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;    99WO-US05535.
XX
PR   13-MAR-1998;    98US-0042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Fishwild DM,  Ball WJ;
XX
DR   WPI; 1999-551219/46.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies
XX
PS   Example 42; Page 311-313; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable
CC   amount of an immunoglobulin that specifically binds digoxin or
CC   Shinga-like toxin. B cells from transgenic animals can be used to
CC   generate hybridomas expressing monoclonal high affinity human sequence
CC   antibodies. Antibodies produced from the transgenic animals of the
CC   invention can be used to treat human diseases, e.g. autoimmune
CC   diseases, cancer, infectious disease, transplant rejection, blood
CC   disorders such as coagulation disorders and other diseases. The
CC   present sequence is used in the course of the invention.
XX
SQ   Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;
```

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Query Match             53.3%;  Score 1044;  DB 20;  Length 3881;
Best Local Similarity   99.8%;  Pred. No. 2.3e-235;
Matches 1066;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;
```

```
Qy      433 AATTCTAAACTCTGAGGGGTCGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2555 AATTCTAAACTCTGAGGGGTCGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy      493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy      553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGGGGAAGAGAAACATCAAGAT 612
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2675 CAATTTAGAACTTTATTAAGGAATAGGGGAAGGGGAAGAGAAACATCAAGAT 2734

Qy      613 TTTAAATACGCTTCTTGGTCTCCTTGTCCTTGTCTATAATTATTCCGCAAACAACACCCAGAACTTTG 672
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2735 TTTAAATACGCTTCTTGGTCTCCTTGTCCTTGTCTATAATTATTCCGCAAACAACACCCAGAACTTTGT 2794

Qy      673 TCTGTCCCTAACATGCCCTGATTATCCGCAAAGCTCTTTGCTCTTTCCTCAGGAACTGTGGCCATCTGTCTT 732
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2795 TCTGTCCCTAACATGCCCTGATTATCCGCAAAGCTCTTTGCTCTTTCCTCAGGAACTGTGGCCATCTGTCTT 2854

Qy      733 TACTTAAACACCATCCATCCTGTTTGCTCGTTGTCTTTCCTCAGGAACTCGGCCACCATCTGTCTT 792
            ||||||||||||||||||||||||||||||||||
Db     2855 TACTTAAACACCATCCATCCTGTTTGCTCGTTGTCTTTCCTCAGGAACTCGGCCACCATCTGTCTT 2914

Qy      793 CATCTTCCCGCCATCTGAAGAGCAGTTGAAATCTGAAATCTGAACTGAACTCGAACTGCCTGCT 852
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Qy      613 TTTAAATACGCTTCTTGGTCTCCTTGTCTATAATTATTCCGGATAAGCATGCTGTTTTCTG 672
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2735 TTTAAATACGCTTCTTGGTCTCCTTGTCTATAATTATTCCGGATAAGCATGCTGTTTTCTG 2794

Qy      673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACACACCCAAGGGCAGAACTTTGT 732
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACACCCAAGGGCAGAACTTTGT 2854

Qy      733 TACTTAAACACCATCCATCCTGTTTGCTCGTTGTCTTTCCTCAGGAACTCGGCCACCATCTGTCTT 792
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2855 TACTTAAACACCATCCATCCTGTTTGCTCGTTGTCTTTCCTCAGGAACTCGGCCACCATCTGTCTT 2914

Qy      793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAAATCTGAACTGCCTGTTGTCCTGCT 852
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAAATCTGAACTGCCTGTTGTGTGCCTGCT 2974

Qy      853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy      913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAG 972
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAG 3094

Qy      973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy     1033 CACCCATCAGGGCCTGAGCTCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3155 CACCCATCAGGGCCTGAGCTCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy     1093 GGAGAAGTGCCCCACCAACTGCTCCAGCCTGACCCCCTCCATCCTTTGGCCTC 1152
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3215 GGAGAAGTGCCCCACCAACTGCTCCAGCCTGACCCCCTCCATCCTTTGGCCTC 3274

Qy     1153 TGACCCTTTTCCACAGGGACCTACCCCATTGCGGTCCTCCCAGCTCATCTTTCACCTC 1212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3275 TGACCCTTTTCCACAGGGACCTACCCCATTGCGGTCCTCCCAGCTCATCTTTCACCTC 3334

Qy     1213 ACCCCCCTCCTCCTCGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3335 ACCCCCCTCCTCCTCGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy     1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTCCCTC-ATTTAATAATTATTATCTGTTGTT 1331
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTCCCTCTAATTTAATAATTATTATCTGTTG-T 3453

Qy     1332 TTACCAACTACTCAATTTCTATTTTCTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3454 TTACCAACTACTCAATTTCTATTTTCTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy     1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy     1452 TCCCTCAAACCCACCACCAAGCCTTCTGTCCTCCACAGTCCCCTGGGCCATGG 1499
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3574 TCCCTCAAACCCACCACCAAGCCTTCTGTCCTCCACAGTCCCCTGGGCCATGG 3621
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```
RESULT 13
AA221996
ID   AA221996 standard; DNA; 3881 BP.
XX
AC   AA221996;
XX
DT   24-NOV-1999  (first entry)
XX
DE   Nucleotide sequence of plasmid pCK7-96.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
```

PA (MEDA-) MEDAREX INC.
PA (KIRI) KIRIN BEER KK.
XX
PI Tomizuka K, Ishida I, Lonberg N, Halk E;
XX
DR WPI; 2002-500300/53.
XX
PT New transgenic nonhuman mammal, useful for generating B-cells expressing human antibody sequences and generating antigen-specific hybridomas secreting human sequence antibody, comprises two human immunoglobulin loci -
XX
PS Disclosure; Page 46-47; 110pp; English.
XX
CC The present invention relates to novel transgenic nonhuman mammals, particularly rodents, comprising two human immunoglobulin (Ig) loci, where one of two the human immunoglobulin loci is a human heavy chain locus and the other locus is a human light chain locus, and where only one of the loci is of a transchromosome. The transgenic animals are useful for generating a number of B-cell expressing human antibody sequences. They are also useful for producing rearranged immunoglobulin sequences, producing human antibody display libraries, and generating a human sequence antibody that binds to a predetermined antigen. The produced antibodies are useful for treating immune-related disorders. The present sequence represents a plasmid used in the construction of expression vectors for human IgG.
XX
SQ Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;

Query Match   53.3%;   Score 1044; DB 24; Length 3881;
Best Local Similarity 99.8%;   Pred. No. 2.3e-235;
Matches 1066; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy  433 AATTCTAAACTCTGAGGGGTCGGATGACGTCGCCATTCTTGCCTAAAGCATTGAGTTT  492
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2555 AATTCTAAACTCTGAGGGGTCGGATGACGTCGCCATTCTTGCCTAAAGCATTGAGTTT 2614

Qy  493 ACTGCAAGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTAGGGGAAGAGCTCCAACAAAA  552
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2615 ACTGCAAGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTAGGGGAAGAGCTCCAACAAAA 2674

Qy  553 CAATTAGAACTTTATTAAGGAATAGGGGAAGTAGGGGAAGTAGGAAGAAACTCAAAACATCAAGAT  612
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2675 CAATTAGAACTTTATTAAGGAATAGGGGAAGTAGGGGAAGTAGGAAGAAACTCAAAACATCAAGAT 2734

Qy  613 TTTAAATACGCTTCTCTGGTCTCCTTGCTCTATAATTATCTGGATAAGCATGCTGTGTTTTCTG  672
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2735 TTTAAATACGCTTCTCTGGTCTCCTTGCTCTATAATTATCTGGATAAGCATGCTGTGTTTTCTG 2794

Qy  673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCAAGGCAGAACTTTGT  732
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCAAGGCAGAACTTTGT 2854

Qy  733 TACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGTGCTGCACCATCGTGTCTT  792
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2855 TACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGTGCTGCACCATCGTGTCTT 2914

Qy  793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT  852
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy  853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC  912
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy  913 GGGTAACTCCCAGGAGAGTGTCACAGGCCTGAGCAAAGCAGACTACGAGAAACACAAAGT  972
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3035 GGGTAACTCCCAGGAGAGTGTCACAGGCCTGAGCAAAGCAGACTACGAGAAACACAAAGT 3094

Qy  973 CAGCACCCTGACGCTGAGCAGCACCCTGACGCTGAGCAAAGTCTACGCCTGCGAAGT 1032
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3095 CAGCACCCTGACGCTGAGCAGCACCCTGACGCTGAGCAAAGTCTACGCCTGCGAAGT 3154
```

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Qy 1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAGAG 1092
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAGAG 3214

Qy 1093 GGGAAGTGCCCCACCTGCTCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCCCTC 1152
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3215 GGGAAGTGCCCCACCTGCTCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCCCTC 3274

Qy 1153 TGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCTCCTCCAGTCATCTTCACCTC 1212
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3275 TGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCTCCTCCAGTCATCTTCACCTC 3334

Qy 1213 ACCCCCTCCTCCTCCTTGCTTTAATTATGCTAATGTTGGAGAGAATGAATAAATAAA 1272
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3335 ACCCCCTCCTCCTCCTTGCTTTAATTATGCTAATGTTGGAGAGAATGAATAAATAAA 3394

Qy 1273 GTGAATCTTTGCACCTGTGGTTCTCTCTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
        ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||| |
Db 3395 GTGAATCTTTGCACCTGTGGTTCTCTCTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy 1332 TTACCAACTACTCAATTTCTCTTATATAAGGGACTAAAATATGTAGTCATCCTAAGGCGCATA 1391
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3454 TTACCAACTACTCAATTTCTCTTATATAAGGGACTAAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy 1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy 1452 TCCCTCAAACCCACCAAGCCTTCTGTCCTCCACAGTCCCCTGGGGCCATGG 1499
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3574 TCCCTCAAACCCACCAAGCCTTCTGTCCTCCACAGTCCCCTGGGGCCATGG 3621
```

RESULT 14
ABK85575
ID ABK85575 standard; DNA; 3881 BP.
XX
AC ABK85575;
XX
DT 03-SEP-2002 (first entry)
XX
DE Human IgGkappa light chain plasmid pCK7-96.
XX
KW Transgenic; rodent; immunoglobulin; Ig; transchromosome; B-cell;
KW human antibody display library; immune-related disorder; mutant;
KW immunomodulatory; IgGkappa light chain; pCK7-96; cyclic;
KW circular; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO20243478-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US45293.
XX
PR 30-NOV-2000; 2000US-250340P.
XX

CC   These two sequences are not identical; AAQ55004 comprising 7059 bases
CC   and AAQ62611 comprising 8400 bases. Fig 10 should consist of
CC   4 pages (1/4, 2/4, 3/4 and 4/4), however, page 2/4 is duplicated
CC   and page 4/4 is missing. The sequence found in AAQ62611 represents
CC   pages 1/4 - 3/4.
CC   A humanised monoclonal antibody corresponding to the murine anti-CD18
CC   antibody 60.3 was prepared. The variable (V) region sequences from
CC   both the heavy (H) and light (L) chains were determined from cDNA
CC   (amplified by PCR), and spliced onto human constant (C) regions,
CC   resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC   expressed in tissue culture (Ag8.653 mouse myeloma cells, detected
CC   by ELISA), and examined in binding assays. The results from
CC   competition and inhibition assays showed that the chimeric Ab was
CC   as effective as the murine 60.3 MAb. The deduced murine VH and VL
CC   protein sequences were compared to the protein sequence data base,
CC   and two human Ig protein sequences were selected to be used as
CC   templates. A murine 60.3 Fv was modeled according to the deduced
CC   VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC   human template sequences selected from the protein data base, a
CC   humanised Fv was modeled. Construction of the humanised 60.3 was
CC   done by piecing 5 pairs of complementary oligonucleotides together
CC   (spanning the entire V region) to form the VH and VL. These were
CC   then attached onto vectors containing genes for appropriate C regions
CC   to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC   expressed in Ag8.653 cells and binding assays were done. FACS analyses
CC   indicated that the humanised Ab recognised cells expressing CD18.
CC   About a dozen of the humanised 60.3 Ab master wells were transferred
CC   and assayed for Ig.
XX
SQ   Sequence 7059 BP; 1938 A; 1576 C; 1659 G; 1886 T; 0 other;

```
Query Match             53.1%;  Score 1040.4;  DB 15;  Length 7059;
Best Local Similarity   98.1%;  Pred. No. 2e-234;
Matches 1065;  Conservative    0;  Mismatches   16;  Indels   16;  Gaps    1;

Qy    410 TAAGTAGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGGGGTCGGATGACGTGGCCAT 469
              |||||||| ||||||| || || |||||||||||||||||||||||||||||||||||
Db   5450 TATCTAGGATCTAGATATCGATGAATTCTAAACTCTGAGGGGTCGGATGACGTGGCCAT 5391

Qy    470 TCTTTGCCTAAAGCATTGAGTTTACTGCAAGTCAGAAACGATGCAAAGCCCTCAGAAT 529
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5390 TCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCAAAGCCCCTCAGAAT 5331

Qy    530 GGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAAGTAGGGGAAGCTAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5330 GGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAAGTAGGGGAAGCTAG 5271

Qy    590 GAAGAAACTCAAAACATCAAGATTTAAATAACGGTTCTTGGTCTCCTTGCTATAATTATC 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5270 GAAGAAACTCAAAACATCAAGATTTAAATAACGGTTCTTGGTCTCCTTGCTATAATTATC 5211

Qy    650 TGGGATAAGCATGCTGTTTTCTGTCGTCGTCCTCAACATGCCCTGATTATCCGCAAACAA 709
              ||||||||||||||||||||||||||    ||||||||||||    ||||||||||||||
Db   5210 TGGGATAAGCATGCTGTTTTCTGTCGTCGTCCTCAACATGCCC----TTATCCGCAAACAA 5156

Qy    710 CACACCCAAGGGCAGAACTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGA 769
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5155 CACACCCAAGGGCAGAACTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGA 5096

Qy    770 ACTGTGGCTGCACCATCGTCTTCATCTCCCGCCATCTGATGAGCAGCAGTTGAAATCTGA 829
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5095 ACTGTGGCTGCACCATCGTCTTCATCTCCCGCCATCTGATGAGCAGCAGTTGAAATCTGA 5036

Qy    830 ACTGCCTCGTTGTGTGCCCTGGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTCG 889
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   5035 ACTGCCTCGTTGTGTGCCCTGGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG 4976

Qy    890 AAGGTGGATAACGGCCCTCCAATCGGGTAACTCGGCAGGAGTGTCACAGGACAGC 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4975 AAGGTGGATAACGGCCCTCCAATCGGGTAACTCGGCAGGAGTGTCACAGGACAGAGC 4916

Qy    950 AAGGACAGCACCTACAGCGCCCTCAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGCTACGAGAAA 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy   1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy   1093 GGAGAAGTGCCCCCACCTGCTCCTCCAGTTCCAGCCTGACCCCCTCCCATCCTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3215 GGAGAAGTGCCCCCACCTGCTCCTCCAGTTCCAGCCTGACCCCCTCCCATCCTTGGCCTC 3274

Qy   1153 TGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACCTC 1212
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3275 TGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACCTC 3334

Qy   1213 ACCCCCCTCCTCCTCCTTGGCTTAATGATGTTGAGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||  || |||||||||||||||||||||||
Db   3335 ACCCCCCTCCTCCTCCTTGGCTTAATTATGCTAATGTGGAGGAGAATGAATAAATAAA 3394

Qy   1273 GTGAATCTTGCACCTGGTGTTTCTCTCTTCCTC-ATTTAATAATTATTATTATCTGTTGTT 1331
              |||||||||||||||| |||||||||||||||| |||||||||||||||||||||||| |
Db   3395 GTGAATCTTGCACCTGTGGTTTCTCTCTTCCTCAATTTAATAATTATTATTATCTGTTG-T 3453

Qy   1332 TTACCAACTACTCAATTTCTTCTTATAGGGACTAAATATGTAGTCATCCTAAGGGCGCATA 1391
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   3454 TTACCAACTACTCAATTTCTTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGGCGCATA 3513

Qy   1392 ACCATTTATAAAAAATCATCCTTCTCATTCTATTTTACCCTATCATCTCCTGCAAGACAGTCC 1451
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   3514 ACCATTTATAAAAATCATCCTTCTCATTCTATTTTACCCTATCATCTCCTGCAAGACAGTCC 3573

Qy   1452 TCCCTCAAACCCACAAGCCTTCGTCCTCCACAGTCCCCTGGGCCATGG 1499
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   3574 TCCCTCAAACCCACAAGCCTTCGTCCTCCACAGTCCCCTGGGCCATGG 3621
```

RESULT 15
AAQ55004/c
ID   AAQ55004 standard; DNA; 7059 BP.
XX
AC   AAQ55004;
XX
DT   06-JUL-1994 (first entry)
XX
DE   Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11).
XX
KW   Monoclonal antibody; MAb; heavy chain; light chain;
KW   constant region; variable region; amplification; primer;
KW   polymerase chain reaction; PCR; chimera; Ig;
KW   immunoglobulin; humanised antibody; leucocyte; integrin; ss.
XX
OS   Chimeric: Homo sapiens.
OS   Chimeric: Mus sp.
XX
PN   EP578515-A.
XX
PD   12-JAN-1994.
XX
PF   24-MAY-1993; 93EP-0401328.
XX
PR   26-MAY-1992; 92US-0888233.
XX
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI   Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
XX
DR   WPI; 1994-010334/02.
XX
PT   Humanised monoclonal antibodies prepn. - using comparative model
PT   building, by computer database searching
XX
PS   Disclosure; Page 27-31; 68pp; English.
XX
NB: Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11)
CC   sequences are given in Fig 10 and Sequence ID 10 of the
CC   specification; corresp. to AAQ62611 and AAQ55004 respectively.

```
Db   4915 AAGGACAGCACCTACAGCCTCAGCGACACCCTGACGCTGAGCAAAGCAGACTACGAGAAA 4856

Qy   1010 CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTCGCCCGTCACAAAGAGC 1069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4855 CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTCGCCCGTCACAAAGAGC 4796

Qy   1070 TTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAGCCTG 1129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4795 TTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAGCCTG 4736

Qy   1130 ACCCCCTCCCATCCTTTGGCCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGG 1189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4735 ACCCCCTCCCATCCTTTGGCCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGG 4676

Qy   1190 TCCTCCAGTCATCTTTCACCTCACCCCCCCTCCTCCTGGCTTTAATTATGCTAATG 1249
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Search completed: July 18, 2003, 06:43:57
Job time : 513.109 secs

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OM nucleic - nucleic search, using sw model

Copyright GenCore version 5.1.6
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Run on: July 18, 2003, 06:19:39 ; Search time 473.815 Seconds
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	595.8	30.4	1244	11		US-09-954-456-771	Sequence 771, App
5	523.4	26.7	948	11		US-09-859-053-33	Sequence 33, Appl
6	523.4	26.7	1045	15		US-10-198-846-13629	Sequence 13629, A
7	523	26.7	941	10		US-09-800-729-81	Sequence 81, Appl
8	523	26.7	968	12		US-09-992-600A-7	Sequence 7, Appli
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17	518.4	26.4	1230	15		US-10-158-646-59	Sequence 59, Appl
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ALIGNMENTS

RESULT 1
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; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 21
; LENGTH: 1960
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(408)
; FEATURE:
; NAME/KEY: CDS
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US-09-249-011A-21

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Best Local Similarity   100.0%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          COUNTRY: USA
          ZIP: 02109-1875
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          COMPUTER: IBM PC compatible
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          SOFTWARE: PatentIn Release #1.0, Version #1.25
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          FILING DATE: 20-Dec-2001
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 09/227,595
          FILING DATE: <Unknown>
     ATTORNEY/AGENT INFORMATION:
          NAME: Amy E. Mandragouras
          REGISTRATION NUMBER: 36,207
          REFERENCE/DOCKET NUMBER: <Unknown>
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (617)227-7400
          TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 31:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 1708 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
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US-10-027-075-31

Query Match      55.7%;  Score 1091.2;  DB 15;  Length 1708;
Best Local Similarity   99.6%;  Pred. No. 2.1e-267;
Matches 1115;  Conservative  0;  Mismatches  0;  Indels  3;  Gaps  2;

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Db   1010 ACAGCAAGGACAGCACCTACAGCCTCAGCGAGCACCTGACGCTGAGCAAAGCAGACTACG 1069

Qy   1005 AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA 1064
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA 1129

Qy   1065 AGAGCTTCAACAGAGGGGAGAGTGTTAGAGGGAGGAGAGTGCCCCACCTGCTCCTCAGTTCCA 1124
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 AGAGCTTCAACAGAGGGGAGAGTGTTAGAGGGAGGAGAGTGCCCCACCTGCTCCTCAGTTCCA 1189

Qy   1125 GCCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGACCTACCCCTAT 1184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 GCCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGACCTACCCCTAT 1249

Qy   1185 TGGGTCCTCCAGCTCATCTTCACTCACCTCCTCCTCCTCCTTGGCTTTAATTATGC 1244
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TGGGTCCTCCAGCTCATCTTCACTCACCTCCTCCTCCTCCTTGGCTTTAATTATGC 1309

Qy   1245 TAATGTTGGAGGAGAATGAATAAATAAATAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1304
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TAATGTTGGAGGAGAATGAATAAATAAATAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1369

Qy   1305 CTC-ATTTAATAATTATTATCGTTGTTTACCAACTACTCAATTTCTCTTATAAGGGAC 1363
          ||| ||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1370 CTCAATTTAATAATTATTATCGTTG-TTTACCAACTACTCAATTTCTCTTATAAGGGAC 1428

Qy   1364 TAAATATGTAGTCATCCTCAAGGCGCATAAAATCATTTATAAAAATCATCCTTCATTCTATTT 1423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 TAAATATGTAGTCATCCTCAAGGCGCATAAAATCATTTATAAAAATCATCCTTCATTCTATTT 1488

Qy   1424 TACCCTATCATCCTCTGCAAGACAGTCCCCTCCAAACCCACAGAGCCTTCGTCTCTCACA 1483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 TACCCTATCATCCTCTGCAAGACAGTCCCCTCCAAACCCACAGAGCCTTCGTCTCTCACA 1548

Qy   1484 GTCCCCTCGGCCATGGTAGGAGAGACTTGCTTCCTCCTTGTTTCCCCTCTGTTTCCCCTCAGCAAGCCCT 1543
          |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 GTCCCCTCGGCCGGTGGTAGGAGAGACTTGCTTCCTCCTTGTTTCCCCTCTGTTTCCCCTCAGCAAGCCCT 1608

Qy   1544 CATAGTCCTTTTTAAGGGTGACAGGTCTTCACAGTCATATATCCTTTGATTCAATTCCCTG 1603
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   1609 CATAGTCCTTTTTAAGGGTGACAGGTCTTCACGGTCTCATATATCCTTTGATTCAATTCCCTG 1668

Qy   1604 GGAATCAACCAAAGCAAATTTTCAAAAGAAGAAACCTGC 1643
          |||||||||||| |||||||||| ||||||||||||||||
Db   1669 GGAATCAACCAAGGCAAATTTTTCAAAAGAAGAAACCTGC 1708


RESULT 3
US-10-000-433-1
; Sequence 1, Application US/10000433
; Publication No. US2002019921A1
; GENERAL INFORMATION:
     APPLICANT: Tomizuka, Kazuma
     APPLICANT: Ishida, Isao
     APPLICANT: Lonberg, Nils
     APPLICANT: Halk, Ed
     TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN
     TITLE OF INVENTION: ANTIBODIES
     FILE REFERENCE: 014643-012110US
     CURRENT APPLICATION NUMBER: US/10/000,433
     CURRENT FILING DATE: 2001-11-30
     PRIOR APPLICATION NUMBER: US 60/250,340
     PRIOR FILING DATE: 2000-11-30
     NUMBER OF SEQ ID NOS: 10
     SOFTWARE: PatentIn Ver. 2.1
     SEQ ID NO 1
     LENGTH: 3881
     TYPE: DNA
     ORGANISM: Artificial Sequence
     FEATURE:
     OTHER INFORMATION: Description of Artificial Sequence: Kappa light
     OTHER INFORMATION: chain plasmid
     OTHER INFORMATION: pCK7-96
US-10-000-433-1

Query Match      53.3%;  Score 1044;  DB 15;  Length 3881;
Best Local Similarity   99.8%;  Pred. No. 3.7e-255;
Matches 1066;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    433 AATTCTAAACTGAGGGGGTCGATGACGTGGCCATTCTTGCTAAAGCATTGAGTTT 492
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US-09-954-456-771
; Sequence 771, Application US/09954456
; Patent No. US2002011505 7A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca...
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 771
; LENGTH: 1244
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-771

Query Match   30.4%;   Score 595.8;   DB 11;   Length 1244;
Best Local Similarity 69.3%;   Pred. No. 2.8e-141;
Matches 882;   Conservative 0;   Mismatches 362;   Indels 29;   Gaps 4;

Qy   12 ATGGATTCACAGGCCCAGGTTCTTATATTGTGCTGCTATGGTATCTGGCACCTGTGGG   71
           | |||| | |||||||||||||| || |||| ||| || || |||| ||| ||||||
Db   1 ATGGAAGCCCCAGCTCAGCTTCTTCTCTGCTCCTGCTACTCTGGCTCCCAGATACCACCGGA 60

Qy   72 GACATTGTCTGACACAGTCTCCAGATTCCCGGCTGTAAGCTTAGAGAGAGGGGCCACT 131
           | |||||||| ||||||||||||||| |||| ||||| |||||| ||| ||||
Db   61 GAAATTGTGTTGACACAGTCTCCAGCCACCCCTGTCTTTGTCCCAGGGGAAAGAGCCACC 120

Qy   132 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 191
           ||| | | |||||| |||| | ||| |||||||||||| || | | ||
Db   121 CTCTCCTGCAGGGCCAGTCAGAGTGT------------------TGGCAGCTACTTAGCC 162

Qy   192 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 251
           |||||||| ||| | |||| |||||| ||| || |||| |||| || | ||||||||
Db   163 TGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCATCCAACAGG 222

Qy   252 GAATCTGGGGTCCCTGATGCTGCTTCAGTGGCCAGTGGATCTGGGACAGATTTCACTCTCACC 311
           | |||||| ||| || ||||| |||| ||||| ||| |||| |||| ||| |||||||||
Db   223 GCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC 282

Qy   312 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAATCTTATAATCTT 371
           ||||| | | ||| | |||||| || ||| | | | || | | || ||
Db   283 ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACCCGTGACAA--TT 340

Qy   372 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTAG 431
           | | ||||| || | | || |||| || || || | | | | |||||||
Db   341 GGCCTCCGGGGACCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACATACCACCGGAG 400

Qy   432 AAATTCTAAACTCTGAGGGGGTCGGATGAGCGGCCATTCTTTGCTAAAGCATTGAGTT 491
           |||| | | | || ||||| | | |||||||||
Db   401 AAATTGTGT-----TGACACAGTCTCCAGCCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCC 456

Db   2555 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   493 ACTGCAAGGTCAGAAAAGCATGCAAAAGCCCTCAGAATGGCTGCAAATGACGTCCAACAAAA 552
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2615 ACTGCAAGGTCAGAAAAGCATGCAAAAGCCCTCAGAATGGCTGCAAATGACGTCCAACAAAA 2674

Qy   553 CAATTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAGAAACTCAAAACATCAAGAT 612
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2675 CAATTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAGAAACTCAAAACATCAAGAT 2734

Qy   613 TTTAAATACGCTTCTTGGTCTCTATAATTAATTATCTGGGATAAGCATGCTGTTTTCTG 672
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2735 TTTAAATACGCTTCTTGGTCTCTATAATTAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy   673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGCAGAAACTTTGT 732
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGCAGAAACTTTGT 2854

Qy   733 TACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGCTGCACCATCTGTCTT 792
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2855 TACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGCTGCACCATCTGTCTT 2914

Qy   793 CATCTTCCCGCCATCGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGCCTGCT 852
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2915 CATCTTCCCGCCATCGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGCCTGCT 2974

Qy   853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCCTCCAATC 912
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCCTCCAATC 3034

Qy   913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAG 972
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAG 3094

Qy   973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTTCACGCCTGCGAAGT 1032
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTTCACGCCTGCGAAGT 3154

Qy   1033 CACCCATCAGGGGCCTGAGCTGCCCGTCACACAGGGGAGAGTGTTAGAG 1092
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3155 CACCCATCAGGGGCCTGAGCTGCCCGTCACACAGGGGAGAGTGTTAGAG 3214

Qy   1093 GGAGAAGTGCCCCCACCTGCTCTCCAGTTCCAGCCTGACCCCCCATCCTTGGCCTC 1152
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3215 GGAGAAGTGCCCCCACCTGCTCTCCAGTTCCAGCCTGACCCCCCATCCTTGGCCTC 3274

Qy   1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTC 1212
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCCAGCTCATCTTTCACCTC 3334

Qy   1213 ACCCCCCTCCTCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAA 1272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3335 ACCCCCCTCCTCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAAA 3394

Qy   1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTCCTC-ATTTAATTAATTATTATCTGTTGTT 1331
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3395 TGGTAATCTTTGCACCTGTGGTTTCTCTCTTCCTCAATTTAATTAATTATTATCTGTTG-T 3453

Qy   1332 TTACCAACTACTCCAATTTCTCTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3454 TTACCAACTACTCCAATTTCTCTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy   1392 ACCATTATAAAAATCATCCTCTTCCATTCCCCTGGGCCATGG 1499
            ||||||||||||||||||||||||||||||||||||||||||
Db   3514 ATCAGAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACACCGTGACAA--TT 3573

Qy   1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCTGGGCCATGG 1499
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCTGGGCCATGG 3621

RESULT 4

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;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 33
;  LENGTH: 948
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: 5'UTR
;  LOCATION: (1)...(27)
;  NAME/KEY: CDS
;  LOCATION: (28)...(735)
;  NAME/KEY: 3'UTR
;  LOCATION: (739)...(948)
;  NAME/KEY: sig_peptide
;  LOCATION: (28)...(87)
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(948)
;  OTHER INFORMATION: n = A,T,C or G
US-09-859-053-33

  Query Match             26.7%;  Score 523.4;  DB 11;  Length 948;
  Best Local Similarity   99.6%;  Pred. No. 6.7e-123;
  Matches  524;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    766 AGGAACTGTGGCTGCACCATCTCTTCATCTTCCGCCATCTGATGAGCAGTGAAATC 825
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 ACGAACTGTGGCTGCACCATCTCTTCATCTTCCGCCATCTGATGAGCAGTGAAATC 473

Qy    826 TGGAACTGCCTCTGTGTGTCGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 TGGAACTGCCTCTGTGTGTCGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 533

Qy    886 GTGGAAGGTGGATAACGCCCTCCAATCGGTAACTCCCAGGAGTGTCACAGAGCAGGA 945
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 GTGGAAGGTGGATAACGCCCTCCAATCGGTAACTCCCAGGAGTGTCACAGAGCAGGA 593

Qy    946 CAGCAAGGACAGCACCTACAGCCTCAGCGCTCAGCGACGCTGAGCGAGCAAAGCAGACTACGA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 CAGCAAGGACAGCACCTACAGCCTCAGCGCTCAGCGACGCTGAGCGAGCAAAGCAGACTACGA 653

Qy   1006 GAAACACAAAGTCTACGGCCTGGAAGTCTCACGGCCTGGAAGTCTCCCGTCACAAA 1065
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    654 GAAACACAAAGTCTACGGCCTGGAAGTCTCACGGCCTGGAAGTCTCCCGTCACAAA 713

Qy   1066 GAGCTTCAACAGGGAGGAGAGTGTTAGAGGAGAGTGTTAGAGGAGAGTGTCCCCCACCTGCTCCTCAGTTCCAG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    714 GAGCTTCAACAGGGAGGAGAGTGTTAGAGGAGAGTGTTAGAGGAGAGTGAANTGCCCCCCACCTGCTCCTCAGTTCCAG 773

Qy   1126 CCTGACCCCTCCCATCCTTGGCCTCTGACCCCTCCCATCCTTTTCCACAGGGGACCTACCCCTATT 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    774 CCTGACCCCTCCCATCCTTGGCCTCTGACCCCTCCCATCCTTTTCCACAGGGGACCTACCCCTATT 833

Qy   1186 GCGGTCCTCCAGCTCATCTTTCACCCCACCCCCCTCCTCCTTGGCTTTAATTATGCT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    834 GCGGTCCTCCAGCTCATCTTTCACCCCACCCCCCTCCTCCTTGGCTTTAATTATGCT 893

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCCTGTG 1291
          |||||||||||||||||||||||||||||||||||||||
Db    894 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCCTGTG 939
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Qy    492 TACTGCAAGGTCAGAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGAGCTCCAACAAA 551
          |||
Db    457 ACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCTACTTAGCCTGGTACCAACAGAAA 516

Qy    552 ACAATTAGAACTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAGA 611
                                  |||         |||
Db    517 CCTGGCCCAGGCTCCCAGGCCCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCA 576

Qy    612 TTTTAAATACGGCTTCTTGGTCTCCTTGCTGTATAATTATCTGGGATAAGCATGCTGTTTTCT 671
                                  |||
Db    577 GCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGACTTCACTTCTCCACCATCAGCAGCCTA-- 633

Qy    672 GTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACACACAACACCCAAGGGCAGAACTTTG 731
                             |||                     |||
Db    634 --GAGCCTGAAGATTTTGCAGTTTATTACTGTCAACACCGTGACAATTGGCCTTCCGGGGG 691

Qy    732 TTACTTAAACACCATCCTGTTTGTGCTTCTTCCTCAGGAACGTGGCTGCACCATCTGTCT 791
          |||                                           |||||||||||||||
Db    692 CCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCT 751

Qy    792 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAAATCTGTGTGTGTGCCTGC 851
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAAATCTGTGTGTGTGCCTGC 811

Qy    852 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAT 911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    812 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAT 871

Qy    912 CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGCAGGACAGCAGCACCTACAGCCTCA 971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    872 CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGCAGGACAGCAGCACCTACAGCCTCA 931

Qy    972 GCAGCACCCTGACGCTGAGCGAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG 1031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 GCAGCACCCTGACGCTGAGCGAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG 991

Qy   1032 TCACCCATCAGGGCCTGCGAGCTCGCCGTCGTCAGTTCCAGCTTCAACAGGGGGAGTTGTTAGA 1091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 TCACCCATCAGGGCCTGCGAGCTCGCCGTCGTCAGTTCCAGCTTCAACAGGGGGAGTTGTTAGA 1051

Qy   1092 GGGAGAAGTGCCCCCCATCCTCCTCCAGTTCCAGCCTGACCCCCATCCTTTTGGGCCT 1151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 GGGAGAAGTGCCCCCCATCCTCCTCCAGTTCCAGCCTGACCCCCATCCTTTTGGGCCT 1111

Qy   1152 CTGACCCCTTTTCCACAGGGGACCTACCCCTATGCGGTCCTCCAGCTCATCTTTCACCT 1211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1112 CTGACCCCTTTTCCACAGGGGACCTACCCCTATGCGGTCCTCCAGCTCATCTTTCACCT 1171

Qy   1212 CACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAATGAATAAATAA 1271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1172 CACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAATGAATAAATAA 1231

Qy   1272 AGTGAATCTTTGC 1284
          |||||||||||||
Db   1232 AGTGAATCTTTGC 1244
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RESULT 5
US-09-859-053-33
; Sequence 33, Application US/09859053
; Patent No. US2002010265BA1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Hori, Katsunari
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508

RESULT 6
US-10-198-846-13629
; Sequence 13629, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13629
; LENGTH: 1045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13629

Query Match   26.7%;   Score 523.4; DB 15; Length 1045;
Best Local Similarity   99.8%;   Pred. No. 7.1e-123;
Matches   524; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

Qy   766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 552

Qy   826 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 612

Qy   886 GTGGAAGTGGATAAACGCCCTCCAATCGGGTAACTCCAGAGAGTGTCACAGCAGGA 945
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 GTGGAAGTGGATAAACGCCCTCCAATCGGGTAACTCCAGAGAGTGTCACAGCAGGA 672

Qy   946 CAGCAAGGACAGCAGCACCTACAGCCTCAGCGACACCCTGACGCTGAGCAAAGCAGACTACGA 1005
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   673 CAGCAAGGACAGCAGCACCTACAGCCTCAGCGACACCCTGACGCTGAGCAAAGCAGACTACGA 732

Qy   1006 GAAACACAAAGTCTACGCCTGCGAAGTCGCTGCGAAGTCGCCGTCGCCGTCACAAA 1065
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   733 GAAACACAAAGTCTACGCCTGCGAAGTCGCTGCGAAGTCGCCGTCGCCGTCACAAA 792

Qy   1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGTCTCCTCAGTTCCAG 1125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   793 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGTCTCCTCAGTTCCAG 852

Qy   1126 CCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT 1185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   853 CCTGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCCTATT 912

Qy   1186 GCGGTCCTCCAGTCATCTTCACCTCACCTCCCTCCCCCCCTCCTCCCTTGGCTTTAATTATGCT 1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   913 GCGGTCCTCCAGTCATCTTCACCTCACCTCCCTCCCCCCCTCCTCCCTTGGCTTTAATTATGCT 972

Qy   1246 AATGTTGAGGAGAATGAATAAATAAATAAAGTGAATCTTTGCACCTGT 1290
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   973 AATGTTGAGGAGAATGAATAAATAAATAAAGTGAATCTTTGCACCTGT 1017

RESULT 7
US-09-800-729-81
; Sequence 81, Application US/09800729
; Patent No. US2002006831JAl
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 81
; LENGTH: 941
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-81

Query Match   26.7%;   Score 523;   DB 10; Length 941;
Best Local Similarity 100.0%;   Pred. No. 8.4e-123;
Matches   523; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 460

Qy   828 GAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 GAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 520

Qy   888 GGAAGGTGGATAAACGCCCTCCAATCGGGTAACTCCAGAGAGTGTCACAGCAGGACA 947
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 GGAAGGTGGATAAACGCCCTCCAATCGGGTAACTCCAGAGAGTGTCACAGCAGGACA 580

Qy   948 GCAAGGACAGCAGCACCTACAGCCTCAGCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA 1007
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 GCAAGGACAGCAGCACCTACAGCCTCAGCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA 640

Qy   1008 AACACAAAGTCTACGCCTGCGAAGTCGCTGCGAAGTCGCCGTCGCCGTCACAAAGA 1067
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641 AACACAAAGTCTACGCCTGCGAAGTCGCTGCGAAGTCGCCGTCGCCGTCACAAAGA 700

Qy   1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTTCCTCCAGCC 1127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   701 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTTCCTCCAGCC 760

Qy   1128 TGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCTATTGC 1187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   761 TGACCCCCTCCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGACCTACCCTATTGC 820

Qy   1188 GGTCCTCCAGTCATCTTCACCTCACCTCCCTCCCCCCCTCCTCCCTTGGCTTTAATTATGCTAA 1247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   821 GGTCCTCCAGTCATCTTCACCTCACCTCCCTCCCCCCCTCCTCCCTTGGCTTTAATTATGCTAA 880

Qy   1248 TGTTGGAGGAGAATGAATAAATAAATAAAGTGAATCTTTGCACCTGT 1290
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   881 TGTTGGAGGAGAATGAATAAATAAATAAAGTGAATCTTTGCACCTGT 923

RESULT 8
US-09-992-600A-7
; Sequence 7, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 7

; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..748
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 953..968
US-09-924-340-7

Query Match 26.7%; Score 523; DB 12; Length 968;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG  827
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG  488

Qy  828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT  887
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT  548

Qy  888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGACA  947
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  549 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGACA  608

Qy  948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA 1007
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  609 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA  668

Qy 1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCGGAGAAGTCGCCCGTCACAAAGA 1067
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  669 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCGGAGAAGTCGCCCGTCACAAAGA  728

Qy 1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCCTCCTCAGTTCCAGCC 1127
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  729 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCCTCCTCAGTTCCAGCC  788

Qy 1128 TGACCCCTCCATCCTTTGGCCTCTGACCCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  789 TGACCCCTCCATCCTTTGGCCTCTGACCCCTTTTTCCACAGGGGACCTACCCCTATTGC  848

Qy 1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCCCTCCTCCCTTGGCTTTAATTATGCTAA 1247
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCCCTCCTCCCTTGGCTTTAATTATGCTAA  908

Qy 1248 TGTTGGAGAGAATGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  909 TGTTGGAGAGAATGAATGAATAAATAAAGTGAATCTTTGCACCTGT  951
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RESULT 10
US-10-000-489-7
; Sequence 7, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane

; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..748
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 953..968
US-09-992-600A-7

Query Match 26.7%; Score 523; DB 12; Length 968;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG  827
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG  488

Qy  828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT  887
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT  548

Qy  888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGAGAGTGTCACAGAGCAGGACA  947
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  549 GGAAGGACAGCACCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA  608

Qy  948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA 1007
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  609 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGAGA  668

Qy 1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCGGAGAAGTCGCCCGTCACAAAGA 1067
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  669 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCGGAGAAGTCGCCCGTCACAAAGA  728

Qy 1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCCTCCTCAGTTCCAGCC 1127
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  729 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCCTCCTCAGTTCCAGCC  788

Qy 1128 TGACCCCTCCATCCTTTGGCCTCTGACCCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
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Db  789 TGACCCCTCCATCCTTTGGCCTCTGACCCCTTTTTCCACAGGGGACCTACCCCTATTGC  848

Qy 1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCCCTCCTCCCTTGGCTTTAATTATGCTAA 1247
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Db  849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCCCTCCTCCCTTGGCTTTAATTATGCTAA  908

Qy 1248 TGTTGGAGAGAATGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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Db  909 TGTTGGAGAGAATGAATGAATAAATAAAGTGAATCTTTGCACCTGT  951
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RESULT 9
US-09-924-340-7
; Sequence 7, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91_US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456

APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 7
LENGTH: 968
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..31
NAME/KEY: CDS
LOCATION: 32..748
NAME/KEY: 3'UTR
LOCATION: 749..968
NAME/KEY: polyA_signal
LOCATION: 928..933
NAME/KEY: polyA_site
LOCATION: 953..968
US-10-000-489-7

Query Match   26.7%; Score 523; DB 15; Length 968;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 488

Qy   828 GAACTGCCTCTGTTGTGTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 GAACTGCCTCTGTTGTGTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 548

Qy   888 GGAAGGTGGATAACGGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   549 GGAAGGTGGATAACGGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 608

Qy   948 GCAAGGACAGCAGCCTACAGCCTCAGCGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   609 GCAAGGACAGCAGCCTACAGCCTCAGCGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 668

Qy   1008 AACACAAAGTCTACGGCTGGAAGTCACCCATCAGGGGCTGAGCTCGCCCGTCACAAAGA 1067
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   669 AACACAAAGTCTACGGCTGGAAGTCACCCATCAGGGGCTGAGCTCGCCCGTCACAAAGA 728

Qy   1068 GCTTCAACAGGGAGGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   729 GCTTCAACAGGGAGGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 788

Db   909 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 951
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RESULT 11
US-10-000-986-7
Sequence 7, Application US/10000986
Publication No. US20030096247A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 7
LENGTH: 968
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..31
NAME/KEY: CDS
LOCATION: 32..748
NAME/KEY: 3'UTR
LOCATION: 749..968
NAME/KEY: polyA_signal
LOCATION: 928..933
NAME/KEY: polyA_site
LOCATION: 953..968
US-10-000-986-7

Query Match   26.7%; Score 523; DB 15; Length 968;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 488

Qy   828 GAACTGCCTCTGTTGTGTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 GAACTGCCTCTGTTGTGTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 548

Qy   888 GGAAGGTGGATAACGGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   549 GGAAGGTGGATAACGGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 608

Qy   948 GCAAGGACAGCAGCCTACAGCCTCAGCGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   609 GCAAGGACAGCAGCCTACAGCCTCAGCGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 668

Qy   1008 AACACAAAGTCTACGGCTGGAAGTCACCCATCAGGGGCTGAGCTCGCCCGTCACAAAGA 1067
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   669 AACACAAAGTCTACGGCTGGAAGTCACCCATCAGGGGCTGAGCTCGCCCGTCACAAAGA 728

Qy   1068 GCTTCAACAGGGAGGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   729 GCTTCAACAGGGAGGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 788

Qy   1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCTTATTGC 1187
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   789 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCTTATTGC 848

Qy   1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTTAATTATGCTAA 1247
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTTAATTATGCTAA 908

Qy   1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
             |||||||||||||||||||||||||||||||||||||||||||
Db   909 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 951

RESULT 12
US-09-822-830A-531
; Sequence 531, Application US/09822830A
; Patent No. US2002014952A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 631
; SEQ ID NO 531
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-531

Query Match   26.7%;   Score 522.8;   DB 11;   Length 913;
Best Local Similarity   99.6%;
Matches   524;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   766 AGGAACTGTGGCTGCACCATCGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   388 AAGAACTGTGGCGCGCACCATCGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 447

Qy   826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 507

Qy   886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   508 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 567

Qy   946 CAGCAAGGACAGCACCTACACGCCTGCGAAGTCAGCGCTGAGCAAAGCAGACTACGA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   568 CAGCAAGGACAGCACCTACACGCCTGCGAAGTCAGCGCTGAGCAAAGCAGACTACGA 627

Qy   1006 GAAACACAAAGTCTACGGCTGGAAGTGTTAGAGGGAGAGTGCCCCACCTGCTTCCAG 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   628 GAAACACAAAGTCTACGGCTGGAAGTGTTAGAGGGAGAGTGCCCCACCTGCTTCCAG 687

Qy   1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTACCCCTATT 1125
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Db   688 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCACCTGCTACCCCTATT 747

Qy   1126 CCTGACCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db   748 CCTGACCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 807

Qy   1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTTCCTTCCTTAATTATGCT 1245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   808 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTTCCTTCCTTAATTATGCT 867

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 1291
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Db   868 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCCCCTGTG 913

RESULT 13
US-09-859-053-37
; Sequence 37, Application US/09859053
; Patent No. US2002010265A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US2002010265BAluaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(32)
; NAME/KEY: CDS
; LOCATION: (33)...(740)
; NAME/KEY: 3'UTR
; LOCATION: (744)...(970)
; NAME/KEY: sig_peptide
; LOCATION: (33)...(92)
US-09-859-053-37

Query Match   26.4%;   Score 518.4;   DB 11;   Length 970;
Best Local Similarity   99.8%;   Pred. No. 1.3e-121;
Matches   519;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db   419 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 478

Qy   826 TGGAACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 TGGAACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 538

Qy   886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 598

Qy   946 CAGCAAGGACAGCACCTACAGCCTCAGCGCTGAGCAAGCCTGAGCAAGCAGACTACGA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 CAGCAAGGACAGCACCTACAGCCTCAGCGCTGAGCAAGCCTGAGCAAGCAGACTACGA 658

Qy   1006 GAAACACAAAGTCTACGGCTGCGAAGTCACCCATCAGGGCTCGCCCGTCACAAA 1065
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Db   659 GAAACACAAAGTCTACGGCTGCGAAGTCACCCATCAGGGCTCGCCCGTCACAAA 718

Qy   1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCCCACCTGCTCCTCCAGTTCCAG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   719 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAGTGCCCCCCACCTGCTCCTCCAGTTCCAG 778

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Qy  1126 CCTGACCCCTCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db   779 CCTGACCCCTCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 838

Qy  1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTCCTTTAATTATGCT 1245
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Db   839 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTCCTTTAATTATGCT 898

Qy  1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db   899 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 938
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RESULT 14
US-09-859-053-29

; Sequence 29, Application US/09859053
; Patent No. US2002010265BA1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US2002010265BA1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match   26.4%; Score 518.4; DB 11; Length 974;
Best Local Similarity   99.8%; Pred. No. 1.3e-121;
Matches   519; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 484

Qy   826 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGATAACTTCTATCCCAGAGAGGCCAAAGTACA 544

Qy   886 GTGGAAGGTGGATAACGCCCTCAGCCTGTAACTCCCAGAGAGTGTCACAGAGCAGGA 945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545 GTGGAAGGTGGATAACGCCCTCAGCCTGTAACTCCCAGAGAGTGTCACAGAGCAGGA 604

Qy   946 CAGCAAGGACAGCAGACCTACAGCCTGAGCTGGCAAAGCAGACTACGA 1005
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Db   605 CAGCAAGGACAGCAGACCTACAGCCTGAGCTGGCAAAGCAGACTACGA 664

Qy  1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTCGCCCGTCACAAA 1065
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Db   665 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTCGCCCGTCACAAA 724

Qy  1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGAGGAAGTGCCCCCACCTGTTCCAG 1125
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Db   725 GAGCTTCAACAGGGGAGAGTGTTAGAGGAGGAAGTGCCCCCACCTGTTCCAG 784

Qy  1126 CCTGACCCCTCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Qy  1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTCCTTTAATTATGCT 1245
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Db   845 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTCCTTTAATTATGCT 904

Qy  1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db   905 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 944
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RESULT 15
US-09-800-729-79

; Sequence 79, Application US/09800729
; Patent No. US2002006319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (908)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-79

Query Match   26.4%; Score 518.4; DB 10; Length 990;
Best Local Similarity   99.8%; Pred. No. 1.3e-121;
Matches   519; Conservative   0; Mismatches   1; Indels   1; Gaps   0;

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Qy   766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db   388 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 447

Qy   826 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 TGGAACTGCCTCTGTTGTGTGCCTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 507

Qy   886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCGGTAACTCCCAGAGAGTGTCACAGAGCAGGA 945
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Db   508 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCGGTAACTCCCAGAGAGTGTCACAGAGCAGGA 567

Qy   946 CAGCAAGGACAGCAGACCTACAGCCTGAGCTGGCAAAGCAGACTACGA 1005
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   568 CAGCAAGGACAGCAGACCTACAGCCTGAGCTGGCAAAGCAGACTACGA 627

Qy  1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTCGCCCGTCACAAA 1065
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Db   628 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTCGCCCGTCACAAA 687

Qy  1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGAGGAAGTGCCCCCACCTGTTCCAG 1125
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Db   688 GAGCTTCAACAGGGGAGAGTGTTAGAGGAGGAAGTGCCCCCACCTGTTCCAG 747

Qy  1126 CCTGACCCCTCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   748 CCTGACCCCTCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 807
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Sat Jul 19 10:01:44 2003

us-09-627-896b-21.rnpb

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Qy   1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db    808 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCCTCCTCCTTGGCTTTAATTATGCT 867

Qy   1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db    868 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 907
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            GenCore version 5.1.6
     Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title:          US-09-627-896B-21
Perfect score:  1960
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                Gapop 10.0 , Gapext 1.0

Searched:       441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:    882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	1611.8	82.2	8858	4	US-09-247-352-6	Sequence 6, Appli
2	1611.8	82.2	8858	4	US-09-466-635-6	Sequence 6, Appli
3	1429.4	72.9	1701	2	US-07-916-098A-54	Sequence 54, Appl
4	1429.4	72.9	1701	2	US-07-916-098A-55	Sequence 55, Appl
5	1184.2	60.4	13999	4	US-08-444-644-24	Sequence 24, Appl
6	1184.2	60.4	13999	4	US-08-232-246A-24	Sequence 24, Appl
7	1181.4	60.3	1276	2	US-07-916-098A-53	Sequence 53, Appl
8	1181.2	60.3	1241	2	US-07-916-098A-51	Sequence 51, Appl
9	1091.2	55.7	1708	4	US-09-227-595-31	Sequence 31, Appl
10	1044	53.3	3881	4	US-09-042-353-369	Sequence 369, App
11	1044	53.3	3881	4	US-08-758-417A-217	Sequence 217, App
12	709.4	36.2	3819	4	US-09-042-353-393	Sequence 393, App
13	709.4	36.2	3819	4	US-08-758-417A-243	Sequence 243, App
14	698	35.6	8068	4	US-09-301-593-27	Sequence 27, Appl
15	667.6	34.1	8068	4	US-09-301-593-35	Sequence 35, Appl
16	518.4	26.4	931	3	US-09-049-672A-19	Sequence 19, Appl
17	518.4	26.4	958	3	US-09-049-672A-15	Sequence 15, Appl
18	518.4	26.4	1066	1	US-08-157-101A-4	Sequence 4, Appli
19	450	23.0	1149	3	US-08-477-460B-5	Sequence 5, Appli
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22	450	23.0	1149	4	US-08-485-372A-5	Sequence 5, Appli
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25	450	23.0	1149	5	PCT-US93-07422-5	Sequence 5, Appli
26	353.4	18.0	468	1	US-08-236-311-11	Sequence 11, Appl
27	353.4	18.0	468	3	US-08-457-918-11	Sequence 11, Appl
28	334.6	17.1	940	1	US-08-353-400-24	Sequence 24, Appl
29	324.8	16.6	1576	5	PCT-US95-1140S-34	Sequence 34, Appl
30	323.4	16.5	711	4	US-08-487-283A-15	Sequence 15, Appl
31	323.4	16.5	726	4	US-08-487-283A-9	Sequence 9, Appli
32	323.4	16.5	726	4	US-08-487-283A-13	Sequence 13, Appl
33	323.4	16.5	726	4	US-08-487-283A-14	Sequence 14, Appl
34	322.4	16.4	2143	3	US-09-097-309-5	Sequence 5, Appli
35	322.4	16.4	2143	4	US-09-097-171A-9	Sequence 9, Appli
36	322.4	16.4	2143	4	US-09-460-587-5	Sequence 5, Appli
37	322.4	16.4	2178	1	US-08-463-587A-24	Sequence 24, Appl
38	322.4	16.4	2178	3	US-08-463-667A-2	Sequence 2, Appli
39	322.4	16.4	2178	3	US-08-923-854-24	Sequence 24, Appl
40	322.4	16.4	2178	5	PCT-US91-09133-25	Sequence 25, Appl
41	322.4	16.4	6550	4	US-09-422-712B-1	Sequence 1, Appli
42	322.4	16.4	6550	4	US-09-607-756-1	Sequence 1, Appli
43	322.4	16.4	7305	1	US-08-286-740-4	Sequence 4, Appli
44	322.4	16.4	7305	5	PCT-US95-09576-4	Sequence 4, Appli
45	321.8	16.4	3169	3	US-08-630-820-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-09-247-352-6
; Sequence 6, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
;  APPLICANT: Aruffo, Alejandro A.
;  APPLICANT: Siadak, Anthony W.
;  APPLICANT: Berry, Karen K.
;  APPLICANT: Harris, Linda
;  APPLICANT: Thorne, Barbara A.
;  APPLICANT: Bajorath, Jurgen
;  APPLICANT: Huse, William D.
;  APPLICANT: Wu, Herren
;  APPLICANT: Watkins, Jeffry D.
;  TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
;  FILE REFERENCE: DB2a SEQUENCE
;  CURRENT APPLICATION NUMBER: US/09/247,352
;  CURRENT FILING DATE: 1999-02-10
;  EARLIER APPLICATION NUMBER: 09/026,291
;  EARLIER FILING DATE: 1998-02-19
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;  LENGTH: 8858
;  TYPE: DNA
;  ORGANISM: Human and Mouse
US-09-247-352-6

Query Match             82.2%;  Score 1611.8;  DB 4;  Length 8858;
Best Local Similarity   90.6%;  Pred. No. 0;
Matches 1783;  Conservative 0;  Mismatches 137;  Indels 49;  Gaps 4;

Qy      9 ACCATGGATTCACAGGCCCAGGTTCTATATTGCTGCTGCGTATGGTATCTGGCACCTGT 68
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Qy     69 GGGGACATTGTGTGACACAGCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCC 128
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Db  1284 AGTATCAACAGTGTGGAACCTGAAGATGTTGGAATTTATTACTGTCAACATGTCACAGC 1343
Qy   367 -ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGT--------- 414
Db  1344 TTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGTCGAGTCTCT 1403
Qy   415 --------AGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGGGGTCGGATGACG 462
Db  1404 AGATAACCGGTCAATCGGTCAATCGATTGGAATTCTAAACTCTGAGGGGTCGGATGACG 1463
Qy   463 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAGCATGCAAAGCCC 522
Db  1464 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAGCATGCAAAGCCCC 1523
Qy   523 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTATTAAGGAATAGGGGG 582
Db  1524 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTATTAAGGAATAGGGGG 1583
Qy   583 AAGCTAGGAAGAAGAAACTCAAAAATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT 642
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Db  1644 AATTATCTGGGATAAGCATGCTGTTTCTGTCGTCCCTAACATGCCC-----TTATCCG 1698
Qy   703 CAAACACACACCCAGGGCAGAACTTGTTACTTAAAACACCATCTGTTTGCTCTTTC 762
Db  1699 CAAACACACACCCAGGGCAGAACTTGTTACTTAAAACACCATCTGTTTGCTCTTTTC 1758
Qy   763 CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 822
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Qy   823 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 882
Db  1819 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 1878
Qy   883 ACAGTGGAAGGTGGATAACGCCCCTCCAATCGGTAACTCCCAGGAGAGTGTCACAGAGCA 942
Db  1879 ACAGTGGAAGGTGGATAACGCCCCTCCAATCGGTAACTCCCAGGAGAGTGTCACAGAGCA 1938
Qy   943 GGACAGCAAGGACACAGCACCTACGCCTGCAGCGCCTGAGCGCAAAGCAGACTA 1002
Db  1939 GGACAGCAAGGACACAGCACCTACGCCTGCAGCGCCTGAGCGCAAAGCAGACTA 1998
Qy  1003 CGAGAAAACACAAAGTCTACGCGTCACGCGGCCTCGCCCGTCAC 1062
Db  1999 CGAGAAAACACAAAGTCTACGCGTCACGCGGCCTCGCCCGTCAC 2058
Qy  1063 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTC 1122
Db  2059 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTC 2118
Qy  1123 CAGCCTGACCCCCCCATCCTTTGGCCTCTGACCAGGGGACCTACCCCT 1182
Db  2119 CAGCCTGACCCCCCCATCCTTTGGCCTCTGACCAGGGGACCTACCCCT 2178
Qy  1183 ATTGCGGTCCTCCAGCTCACCTCACCTCATCTTTGGCTTAATTAT 1242
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Qy  1243 GCTAATGTTGGAGGAGAATGAATAAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTT 1302
Db  2239 GCTAATGTTGGAGGAGAATGAATAAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTT 2298
Qy  1303 TCCTCATTTAATTATTATTATCTGTTGTTTTACCAACTACTCAATTTCTTTCTCTTATAAGGGA 1362
Db  2299 TCCTCATTTAATTATTATTATCTGTTGTTTTACCAACTACTCAATTTCTTTCTCTTATAAGGGA 2358
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Db  1363 CTAAATATGTAGTGCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATT 1422
Db  2359 CTAAATATGTAGTGCATCCTAAGGCACGTAACCATTTATAAAAATCATCCTTCATTCTATT 2418
Qy  1423 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCAAACCCACAAGCCTTCTGTCCTCAC 1482
Db  2419 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCAAACCCACAAGCCTTCTGTCCTCAC 2478
Qy  1483 AGTCCCCTGGGCCATGTAGGAGAGACTTGCTTCCCTCCTTCTTCCCCTCCTCAGCAAGCCC 1542
Db  2479 AGTCCCCTGGGCCATGTAGGAGAGACTTGCTTCCTCCTTCTTCCCCTCCTCAGCAAGCCC 2538
Qy  1543 TCATAGTCCTTTTTAAGGGTGACAGTCTTACAGTCGTCATATATCCTTGATTCAATTCCCT 1602
Db  2539 TCATAGTCCTTTTTTAAGGGTGACAGTCTTACAGTCTTACAGTCATATATCCTTTGATTCAATTCCCT 2598
Qy  1603 GGGAATCAACCAAAGCAAATTTTCAAAAGAAGAAACCTGCTATAAAGAGAAATCATTCAT 1662
Db  2599 GAGAATCAACCAAAGCAAATTTTCAAAAGAAGAAACCTGCTATAAAGAGAAATCATTCAT 2658
Qy  1663 TGCAACATGATATAAAATAACAACACAATAAAAGCAATTAATAAACAAACAATAGGGAA 1722
Db  2659 TGCAACATGATATAAAATAACAACACAATAAAAGCAATTAATAAACAAACAATAGGGAA 2718
Qy  1723 ATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTT 1782
Db  2719 ATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTT 2778
Qy  1783 AAACAGGTACTGAGGGACTCCTGTCTGCGCAAGGGCCCGTATTGAGTACTTTCCACAACCTA 1842
Db  2779 AAACAGGTACTGAGGGACTCCTGTCTGCGCAAGGGCCCGTATTGAGTACTTTCCACAACCTA 2838
Qy  1843 ATTTAATCCACTATACTGTGAGATTAAAAACATTCATTAAAAATGTTGCAAAGGTTCTA 1902
Db  2839 ATTTAATCCACTATACTGTGAGATTAAAAACATTCATTAAAAATGTTGCAAAGGTTCTA 2898
Qy  1903 TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCCACTTCTAG 1951
Db  2899 TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCCACTTCTAG 2947
```

RESULT 2
US-09-466-635-6
; Sequence 6, Application US/09466635
; Patent No. 6413514
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2 SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/466,635
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-466-635-6

Query Match   82.2%;
Best Local Similarity 90.6%;
Matches 1783; Conservative 0; Mismatches 0; Indels 137; Gaps 4;
Score 1611.8; DB 4; Length 8858;
Pred. No. 0;

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Db   1062  GGAGACATTGTGCTGACTCAGTCTCCAGCACCCTGTCTGTGACTCCAGGAGATAGTC 1121

Qy    129  ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTG  188
           |||  |||||  ||   |||  |||  |||||                          
Db   1122  TCTCTTTCCTGCAGGGCCAGCCAGAGTATTAGC--------------GACTACTTA    1163

Qy    189  GCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGCATCCACT  248
           ||  || ||  |||||||  || ||  || | ||     ||| |||  ||  |||  | 
Db   1164  CACTGGGTATCAACAAAAATCAGTCTCCTCATCTCATCAAAATATGCTTCCCAT      1223

Qy    249  AGGGAATCTGGGGTCCCTGATCGTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTC  308
           | || |||| |||||   |    ||  ||  ||  ||    || ||  |||||||||||
Db   1224  TCCATCTCTGGGATCCCCTCCAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTC 1283

Qy    309  ACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA-- 366
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Db   1284  AGTATCAACAGTGTGGAACCTGAAGATGTTGGAGTTTATTACTGCAGCATGTCAACATGGTCAACAGC 1343

Qy    367  -ATCTTTACACAGTTCGGAGGGGGGACCAAGGTGGAAATAAAACGTAAGT----------  414
            |  |||||||||| |  ||  ||||||||||||||||||  ||  ||| 
Db   1344  TTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGTAAGTCTGGAGTCTCT 1403

Qy    415  --------AGTCTCTCAACTCTAGAATTCTAAACTCTGAGGGGGTCGGATGACG  462
                   | ||  ||||  ||||  | |||  | |||||||||  ||||  | || 
Db   1404  AGATAACCGGTCAATGGATGGAATTGATATGGAATTCTAAACTCTGAGGGGGTCGGATGACG 1463

Qy    463  TGGCCAATTCTTTGCCTAAAGCATTGAGTTTACTGCAGGTCAAGGTCAGAAAAGCATGCCCC  522
           |||||||||||||||||||| |||| ||| |||||||||  ||| |||||||||||| ||||
Db   1464  TGGCCAATTCTTTGCCTAAAGCATTGAGTTTACTGCAGGTCAAGGTCAGAAAAGCATGCCCC 1523

Qy    523  TCAGAATGGCTGCGAAAGAGCTCCAACAAACAATTTGTTATTAAGGAATAGGGGG  582
           ||||||||||||||||||||||||| ||||||||  ||||||| ||||||||||| 
Db   1524  TCAGAATGGCTGCGAAAGAGCTCCAACAAACAATTTATTATTTAAGGAATAGGGGG 1583

Qy    583  AAGCTAGGAGGAAGAACTCAAAACTCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT  642
           ||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||| 
Db   1584  AAGCTAGGAGGAAGAACTCAAAACTCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT 1643

Qy    643  AATTTATCTGGATAAGCATGCTGTGTTTCTGTCCCTAACATGCCGTGATTATCCG  702
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Db   1644  AATTTATCTGGATAAGCATGCTGTGTTTCTGTCCCTAACATGCC-----TTATCCG 1698

Qy    703  CAAACACACCCAGGGCAGAACTTGTTACTTAAACACCATCCTGTTTTGCTTCTTTC  762
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Db   1699  CAAACACCACCCAGGGCAGAACTTGTTACTTAAACACCATCCTCTGTTTGCTTCTTTC 1758

Qy    763  CTCAGGAACTGTGGCTGCACCATCATCTGTCTCATCCATCTGATGAGCAGTTGAA  822
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Db   1759  CTCAGGAACTGTGGCTGCACCATCATCTGTCTCATCCATCTGATGAGCAGTTGAA 1818

Qy    823  ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGTGTCACAGAGCA  882
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1879  ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCGGGTAACTTCTATCCCAGAGAGGTGTCACAGAGCA 1938

Qy    883  ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCGG  942
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Db   1939  GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1998

Qy    943  GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1002
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1063  AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGGAGA  1122
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Db   2059  AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGGAGAGAAGTGCCCCACCTGCTCCTCAGTTC 2118

Qy   1123  CAGCCTGACCCCTCCATCTCGTTTTTCCACAGGGGGACCTACCCCT 1182
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Db   2359  CTAAATATGTAGTCATCCTAAGGCACGTAACCATTTATAAAAATCATCCTTCATTCTATT 2418

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Db   2419  TTACCCTATCATCCTCTGCAAGACAGTCCTTCCTTGCTTCTCGTCCTCAC 2478

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Db   2479  AGTCCCCTGGGCCCATGGTAGGGACAGTTGCTTCCCCTCCCTCAGCAAGCCC 2538

Qy   1543  TCATAGTCCTTTTTAAGGTGCACAGGTCTTACAGTCATATCCTTGATTCAATTCCCT 1602
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Db   2539  TCATAGTCCTTTTTAAGGTGCACAGGTCTTACAGTCATATCATATCCTTGATTCAATTCCCT 2598

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           ||||||||||||||||||||||||||||||||||||||||||| 
Db   2719  ATGTTTAAGTTCATCATGTACTTGAGTACTTTTTACATTTTTT 2778

Qy   1783  AAACAGGTACTGAGGGAGGGACTCCTGTCTCTGCCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 1842
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Db   2779  AAACAGGTACTGAGGGAGGGACTCCTGTCTCTGCCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 2838

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Db   2839  ATTTAATCCACACTACTACTGTGAGATTAAAAACATTCATTCAAAATGTTGCAAAGGTTCTA 2898

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RESULT 3
US-07-916-098A-54
; Sequence 54, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
;   APPLICANT: BURKLY, LINDA C.
;   APPLICANT: CHISHOLM, PATRICIA L.
;   APPLICANT: THOMAS, DAVID W.
;   APPLICANT: ROSA, MARGARET D.
;   APPLICANT: ROSA, JOSEPH J.
;   TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;   TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
;   STREET: 10 SOUTH WACKER DRIVE
;   CITY: CHICAGO

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;  STATE: ILLINOIS
;  COUNTRY: U.S.A.
;  ZIP: 60606
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: WORD PERFECT 5.1
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/916,098A
;  FILING DATE: July 24, 1992
;  CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: PCT/US91/08843
;  FILING DATE: NO. 5871732ember 27, 1991
;  CLASSIFICATION: 424
;  APPLICATION NUMBER: 07/618,542
;  FILING DATE: NO. 5871732ember 27, 1990
;  CLASSIFICATION: 424
;  ATTORNEY/AGENT INFORMATION:
;  NAME: JOHN J. MC DONNELL
;  REGISTRATION NUMBER: 26,949
;  REFERENCE/DOCKET NUMBER: 92,310-G
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (312) 715-1000
;  TELEFAX: (312) 715-1234
;  TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 54:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 1701 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: DNA (genomic)
;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: 1
;  OTHER INFORMATION: /note= "pMDR1006 insert"
US-07-916-098A-54
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Query Match         72.9%;  Score 1429.4;  DB 2;  Length 1701;
Best Local Similarity 93.1%;  Pred. No. 0;  Indels 17;  Gaps 3;
Matches 1534;  Conservative 0;  Mismatches 96;
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Qy     11 CATGGATTCACAAGGCCCAGGTTCTTATATTGCTGCTATGGGTATCTGCACCTGTGG  70
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Db     40 CATGGAGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTCGGCTGCTGCCAGGTGCCAGAGG 99

Qy     71 GGACATGTGTCTGACACAGTCTCAGAGTCTCAGAGTCTGCTCAACAGTAGACCCGAGA  130
          | ||| |   |     ||||||  |  || ||||   |||||  ||  | |  || ||
Db    100 TGATATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTGTCACTTGGACAGAGGGCTAC 159

Qy    131 TATTAGCTGCAAATCCAGTCAGAGTCTCGTCAGAGTTGCTCAACAGTGACCCGAGACTTGGC  190
          || |  || |  ||| |   ||||   ||     |  ||    |   |  |   |||||
Db    160 TATAAACTGCAAGTCCAGTGGGAGCCCTTTATAGTAGACCAATCAAAAGAACTACTTGGC 219

Qy    191 TTGGTACCAGCAGAAACCAGGCAGCCCTCCTAAACTGCTACTGGCCATCCACTAG  250
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Db    280 GGAATCTGGGGTCCCTGATCGCCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC 339
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Qy    431 GAAATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCTAAAGCATTGAGT  490
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Db    449 ---TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCTAAAGCATTGAGT  504

Qy    491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGCTGCAAAGAGCTCCAACAA  550
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Db    505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGCTGCAAAGAGCTCCAACAA  564

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 AACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAACTCAAAACATCAAG  624

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Db    625 ATTTTAAATACGGCTCCTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC  684

Qy    671 TGTCTGTCCCTAACATGCCCTGTGATATCCGCAAACAACACACCCAAGGCCAGAACTTT  730
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Db    685 TGTCTGTCCCTAACATGCCCTGTGATATCCGCAAACAACACACCCAAGGGCCAGAACTTT  744

Qy    731 GTTACTTAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGCCACCATCTGTC  790
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Db    745 GTTACTTAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGCGCCACCATCTGTC  804

Qy    791 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTCTTGTTGTGTGCCTG  850
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Db    865 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA  924

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    985 AGCAGCACCCTGACGCTGAGCAAAGCAGCTACGAGAAACACAAAGTCTACGCCTGCGAA  1044

Qy   1031 GTCACCCATCAGGGCCTGAGCTCCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG  1090
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Db   1045 GTCACCCATCAGGGCCTGAGCTCCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG  1104

Qy   1091 AGGGAGAGTGCCCCACCCTGCTCCTCAGTTCCAGCCTGACCCCCTCCATCCTTTGGCC  1150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1105 AGGGAGAGTGCCCCACCCTGCTCCTCAGTTCCAGCCTGACCCCCTCCATCCTTTGGCC  1164

Qy   1151 TCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCTTCACC  1210
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 TCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCTTCACC  1224

Qy   1211 TCACCCCCTCCTCCTCCTGGCTTAATTATGCTAATGTTGGAGGAATGAATAAAATA  1270
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 TCACCCCCTCCTCCTCCTGGCTTAATTATGTTGGAGGAGAATGAATAAAATA  1284

Qy   1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTCCTC-ATTTAATAATTATCTGTTG  1329
          ||||||||||||||||||||||||||||||||||||  ||| |||| |||||||||
Db   1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTCCTCAATTTAATAATTATCTGTTG  1344

Qy   1330 TTTTACCAACTACTCAATTTCTTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCA  1389
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Db   1345 -TTTACCAACTACTCAATTTCTTCTTATAAGGACTAAATATGTAGTCATCCTAAGGCGCA  1403

Qy   1390 TAACCATTTATAAAAATCATCCTCATTCATTTACCCTATCATCCTCCGCAAGACAGT  1449
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Db   1404 TAACCATTTATAAAAATCATCCTCATTCATTTACCCTATCATCCTCTGCAAGACAGT  1463

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Db   1464 CCTCCCTCAAACCCACCACAGCCTTCTGTCTCCTCCACAGTTCCCTGGGCCGTGGTAGGAGAGAC  1523
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Qy  1510 TTGCTTCCTGTGTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGT 1569
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Db  1524 TTGCTTCCTGTGTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTAAGGGTGACAGGT 1583

Qy  1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
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RESULT 4
US-07-916-098A-55
; Sequence 55, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871173ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871173ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1701 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 35..100
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(101..437, 782..1101)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 438..781
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "pMDR1007 insert: pre-5A8
; OTHER INFORMATION: humanized light chain"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 35..436
; FEATURE:
; NAME/KEY: exon
; LOCATION: 782..1101
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(35..437, 782..1101)
US-07-916-098A-55

Query Match   72.9%;   Score 1429.4;   DB 2;   Length 1701;
Best Local Similarity   93.1%;   Pred. No. 0;
Matches 1534;   Conservative   0;   Mismatches   96;   Indels   17;   Gaps   3;

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Db   40 CATGGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTATCCGGCACCTGTGCCAGTGCCAGAGG 99

Qy   71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC 130
         ||| | ||||||||||||||||||| ||||||||||||| ||||||||||||||| |
Db 100 TGATATGTAATGACACCAGTCTCCAGACTCCCCAGCTGTGTCACTTGGAGAGAGGGGCTAC 159

Qy 131 TATTAGCTGCAAATCCAGTCAGAGTGTTGCTCACAGTAGAACCCGAGAGAACTACTTGGC 190
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Db 160 TATAAACTGCAAGTCCAGTCCCAGTGGGAGCCCTTTATATAGTACCAATCAAAAGAACTACTTGGC 219

Qy 191 TTGGTACCAGCAGAAAACCAGGGCAGCCTCCTAAAACTGCTGATCTACTGGCCATCCACTAG 250
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Db 220 CTGGTACCAGCAGAAAACCAGGGCAGCCTCCTAAAACTGCTGATTTACTGGGCATCCACTAG 279

Qy 251 GGAATCTGGGGTCCCTGATCGCTCAGTTGCGGACAGATTCACTCTCAC 310
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Db 280 GGAATCTGGGGTCCCTGATCGCTCTCAGGCAGTCGGGACAGATTTCACTCTCAC 339

Qy 311 CATCAGCAGTCTGCAGGCTGAGCAGTGGCAGTTTATTACTGCGCAATCTTATAAATCT 370
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Db 340 CATCAGCAGTTTGCAGGCTGAGCAGTGGCAGTTTATTACTGTGCAGCAATATTATAGCTA 399

Qy 371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTA 430
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Db 400 TCGGACGTTCGGTGCGAGGGACCAAGCTGGAGATCAAAACGTAAGTAGTGCACT---------- 448

Qy 431 GAAATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 490
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Db 449 ----TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 504

Qy 491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 550
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Db 505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACA 564

Qy 551 AACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGGAAGAAACTCAAAACATCAAG 610
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Db 565 AACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGGAAGAAACTCAAAACATCAAG 624

Qy 611 ATTTAAATACGGTTCTTGGTCTCCTTGCTATATTATTCTGGATAAGCATGCTGTTTTC 670
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 625 ATTTAAATACGGTTCTTGTGTCTCCTTGCTATATTATTCTGGATAAGCATGCTGTTTTC 684

Qy 671 TGTCTGTCCCTAACATGCCCTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 730
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Db 685 TGTCTGTCCCTAACATGCCCTGATTATCCGCAAACAACACACCCAAGGGCAGAGAACTTT 744

Qy 731 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 745 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 804
```

```
ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
STREET:  Two Militia Drive
CITY:  Lexington
STATE:  MA
COUNTRY:  USA
ZIP:  02173
COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/444,644
    FILING DATE:
    CLASSIFICATION:  424
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/232,246
    FILING DATE:  07-JUL-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/800,458
    FILING DATE:  26-NOV-1991
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/US90/05077
    FILING DATE:  07-SEP-1990
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/404,089
    FILING DATE:  07-SEP-1989
ATTORNEY/AGENT INFORMATION:
    NAME:  Wagner, Richard W.
    REGISTRATION NUMBER:  34,480
    REFERENCE/DOCKET NUMBER:  ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (617) 861-6240
    TELEFAX:  (617) 861-9540
INFORMATION FOR SEQ ID NO:  24:
SEQUENCE CHARACTERISTICS:
    LENGTH:  13999 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  circular
MOLECULE TYPE:  DNA (genomic)
IMMEDIATE SOURCE:
    CLONE:  pAG4611
FEATURE:
    NAME/KEY:  misc_feature
    LOCATION:  1..13999
    OTHER INFORMATION:  /note= "Function = "Expression
    OTHER INFORMATION:  Vector Coding Sequence""
US-08-444-644-24
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Query Match          60.4%;  Score 1184.2;  DB 3;  Length 13999;
Best Local Similarity 99.5%;  Pred. No. 2.1e-298;
Matches 1208;  Conservative  0;  Mismatches  4;  Indels  2;  Gaps  2;
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Qy    433 AATTCTAAACTCGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTT  492
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Db   8087 AATTCTAAACTCGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTT 8146

Qy    493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA  552
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Db   8147 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 8206

Qy    553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT  612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8207 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT 8266

Qy    613 TTTAAATACGGTTCTTGGTCTCCTTGCTCTATAATTATCTGGATAAGCATGCTGTTTTCTG  672
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Db   8267 TTTAAATACGGTTCTTGGTCTCCTTGCTCTATAATTATCTGGATAAGCATGCTGTTTTCTG 8326

Qy    673 TCTGTCCCTAACATGCCCTGATTATCCGCAAACAACACCACCAAGGGCAGAACTTTGT  732
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Db    865 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA  924

Qy    911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGCACCTACAGCCTC  970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGCACCTACAGCCTC  984

Qy    971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1030
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Db   1165 TCTGACCCTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1224

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Db   1225 TCACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1284

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Db   1285 AAGTGAATCTTTGCACCTGTGTTCTCTCTTCCTCAATTTAATAATTATTATCTGTTG 1344

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Qy   1390 TAACCATTTATAAAAATCATCCTATTTTACCCTATCTATTTTACCCTATCCTCTGCAAGACAGT 1449
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Db   1404 TAACCATTTATAAAAATCATCCTATTTTATTTTACCCTATCATCCTCTGCAAGACAGT 1463

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Db   1524 TTGCTTCCTTCTGTTTTCCCCCTCCAGCCCTCATAGTCCTTTTAAGGGTGACAGGT 1583

Qy   1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
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Db   1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA 1643

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Db   1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670
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RESULT 5
US-08-444-644-24
; Sequence 24, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
;   APPLICANT:  Friden, Phillip M.
;   TITLE OF INVENTION:  TRANSFERRIN RECEPTOR SPECIFIC
;   TITLE OF INVENTION:  ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
;   TITLE OF INVENTION:  CONJUGATES
;   NUMBER OF SEQUENCES:  46
;   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
  STREET: Two Militia Drive
  CITY: Lexington
  STATE: MA
  COUNTRY: USA
  ZIP: 02173
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/232,246A
  FILING DATE: 04-MAY-1994
  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/800,458
  FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US90/05077
  FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/404,089
  FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
  NAME: Wagner, Richard W.
  REGISTRATION NUMBER: 34,480
  REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617) 861-6240
  TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 24:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 13999 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: circular
  MOLECULE TYPE: DNA (genomic)
  IMMEDIATE SOURCE:
  CLONE: pAG4611
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 1..13999
  OTHER INFORMATION: /note= "Function = "Expression
  OTHER INFORMATION: Vector Coding Sequence""

US-08-232-246A-24

Query Match   60.4%;   Score 1184.2;   DB 4;   Length 13999;
Best Local Similarity 99.5%;   Pred. No. 2.1e-298;
Matches 1208;   Conservative   0;   Mismatches   4;   Indels   2;   Gaps   2;

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Db   8387 TACTTAAACACCATCCTGTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 8446

Qy    793 CATCTTCCCGCCATCGATGAGCAGTTGAAATCTGGAACTGGAACTGGAAATCTGGAACT  852
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Db   8447 CATCTTCCCGCCATCGATGAGCAGTTGAAATCTGGAACTGGAACTGGAAATCTGGAACT 8506

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Db   8567 GGGTAACTTCCCAGGAGAGTGTCACAGAGCAGGAGGACCAGCAGCACCTACAGCCTCAG 8626

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Db   8687 CACCCATCAGGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 8746

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Db   8747 GGAGAAGTGCCCCACCTGCCTACCCCATTGCGGTCTCCTCCAGCTCATCTTCACCTC 8806

Qy   1153 TGACCCTTTTTCACAGGGGACCTACCCCTATTGCGGTTCCCATCCATCCTTTGGCCTC 1212
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Db   8807 TGACCCTTTTTCACAGGGGACCTACCCCTATTGCGGTTCCCATCCATCCTTTGGCCTC 8866

Qy   1213 ACCCCCCTCCTCCTCTCCTCCTTAATATGCTAATGTGGAGGAGAATGAATAAATAAA 1272
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Db   8867 ACCCCCCTCCTCCTCTCCTCCTTAATATGCTAATGTGGAGGAGAATGAATAAATAAA 8926

Qy   1273 GTGAATCTTGCACCTGTGGTTCTCTGTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   8927 GTGAATCTTGCACCTGTGGTTCTCTGTTCCTCTCCCAATTTAATAATTATTATCTGTTG-T 8985

Qy   1332 TTACCAACTACTCAATTTCTCAATTTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8986 TTACCAACTACTCAATTTCTCAATTTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 9045

Qy   1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9046 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 9105

Qy   1452 TCCCTCAAACCCACAAGCCTTCTGTCCCACAGTCCCCTGGGCCATGTGGGCCGTGGTAGGAGAGACTT 1511
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Db   9106 TCCCTCAAACCCACAAGCCTTCTGTCCCACAGTCCCCTGGGCCGTGTGGTAGGAGAGACTT 9165

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Db   9166 GCTTCCTTGTTTTCCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 9225

Qy   1572 TACAGTGCATATATCCTTTGATTCAACTCAACCAAAGACAAATTTTTCAAAA 1631
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Qy   1632 GAAGAAACCTGCTA 1645
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Db   9286 GAAGAAACCTGCNA 9299
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RESULT 6
US-08-232-246A-24
; Sequence 24, Application US/08232246A
; Patent No. 6329508
GENERAL INFORMATION:
  APPLICANT: Friden, Phillip M.
  TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

Qy   433 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTT 492
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Db   8087 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTGCCTAAAGCATTGAGTT 8146

Qy   493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGCTGCAAAGAGCTCCAACAAA 552
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Db   8147 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGCTGCAAAGAGCTCCAACAAA 8206

Qy   553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT 612
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8207 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAACATCAAGAT 8266

Qy   613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG 672
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Db   8267 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG 8326

Qy   673 TCTGTCCCTAAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGCAGACACTTTGT 732
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
  ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
  STREET: 10 SOUTH WACKER DRIVE
  CITY: CHICAGO
  STATE: ILLINOIS
  COUNTRY: U.S.A.
  ZIP: 60606
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/916,098A
  FILING DATE: July 24, 1992
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US91/08843
  FILING DATE: No. 5871732ember 27, 1991
  CLASSIFICATION: 424
  APPLICATION NUMBER: 07/618,542
  FILING DATE: No. 5871732ember 27, 1990
  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
  NAME: JOHN J. MC DONNELL
  REGISTRATION NUMBER: 26,949
  REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (312) 715-1000
  TELEFAX: (312) 715-1234
  TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 53:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 1276 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 1
  OTHER INFORMATION: /note= "pMDR986 insert"
US-07-916-098A-53

Query Match   60.3%; Score 1181.4; DB 2; Length 1276;
Best Local Similarity   98.9%; Pred. No. 3.9e-298;
Matches 1210; Conservative   0; Mismatches 11; Indels 2; Gaps 2;

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Qy  435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTCTTGCCTAAAGCATTGAGTTAC 494
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Db   24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTCTTGCCTAAAGCATTGAGTTAC 83

Qy  495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
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Db 8327 TCTGTCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 8386
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Db 8447 CATCTTCCCGCCATCCATCGATGAGCAGTGAAATCTGAAATCTGGAACTGCCTCGTTGTGTGCCTGCT 8506
Qy  853 GAATAACTTCTATCCCAGAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Qy  913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGCAGGACAGCAAGGACACCACTACAGCCTCAG 972
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Db 8567 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGCAGGACAGCAAGGACACCACTACAGCCTCAG 8626
Qy  973 CAGCACCCTGACGCGTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Db 8747 GGAGAAGTGCCCCACCTGCTCCAGTTCCAGCTGACCCCCTCCCATCCTTGGCCTC 8806
Qy 1153 TGACCCTTTTCCACAGGGACCTACCCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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Db 8867 ACCCCCCCTCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAATGAATAAATAAA 8926
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RESULT 7
US-07-916-098A-53
; Sequence 53, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.

GENERAL INFORMATION:
  APPLICANT: BURKLY, LINDA C.
  APPLICANT: CHISHOLM, PATRICIA L.
  APPLICANT: THOMAS, DAVID W.
  APPLICANT: ROSA, MARGARET D.
  APPLICANT: ROSA, JOSEPH J.
  TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
  TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
  NUMBER OF SEQUENCES: 61
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
    STREET: 10 SOUTH WACKER DRIVE
    CITY: CHICAGO
    STATE: ILLINOIS
    COUNTRY: U.S.A.
    ZIP: 60606
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WORD PERFECT 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/07/916,098A
    FILING DATE: July 24, 1992
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/US91/08843
    FILING DATE: No. 5871732ember 27, 1991
    CLASSIFICATION: 424
    APPLICATION NUMBER: 07/618,542
    FILING DATE: No. 5871732ember 27, 1990
    CLASSIFICATION: 424
  ATTORNEY/AGENT INFORMATION:
    NAME: JOHN J. MC DONNELL
    REGISTRATION NUMBER: 26,949
    REFERENCE/DOCKET NUMBER: 92,310-G
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (312) 715-1000
    TELEFAX: (312) 715-1234
    TELEX: 910/221-5317
  INFORMATION FOR SEQ ID NO: 51:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1241 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
  FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 1
    OTHER INFORMATION: /note= "pSAB153 insert"
  US-07-916-098A-51

Query Match   60.3%;   Score 1181.2; DB 2; Length 1241;
Best Local Similarity   99.6%;   Pred. No. 4.4e-298;
Matches 1205; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy   435 TTCTAAACTCTGAGGGGGTCGGATGACGGGCCATTCTTCGCCTAAAGCATTGAGTTTTAC 494
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Db   84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

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Qy   675 TGTCCCTAACATGCCCTGTGATTATCCGCAAAACAACACACCCAAGGGCGAGAACTTGTTA 734
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Qy   855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
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Qy   1095 AGAAGTGCCCCCACCTGCTCCTGACCCCCCATCCTCCCATCCTTCTTGGCCTCTG 1154
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Db   684 AGAAGTGCCCCCACCTGCTCCTGACCCCCCATCCTCCCATCCTTCTTGGCCTCTG 743

Qy   1155 ACCCTTTTTCCACAGGGGACTACCCCGTATTGCGGTCCTCCCAGTCATCTTCACCTCAC 1214
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Db   744 ACCCTTTTTCCACAGGGGACTACCCCGTATTGCGGTCCTCCCAGTCATCTTCACCTCAC 803

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Qy   1574 CAGTCATATATCCTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAGA 1633
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RESULT 8
US-07-916-098A-51
; Sequence 51, Application US/07916098A
; Patent No. 5871732

; Sequence 31, Application US/09227595
; Patent No. 6444792
; GENERAL INFORMATION:
;   APPLICANT: Gray, Gary S., et al.
;   TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
;   TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
;   NUMBER OF SEQUENCES: 32
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 60 State Street, suite 510
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/227,595
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/595,590
;   FILING DATE: February 2, 1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Amy E. Mandragouras
;   REGISTRATION NUMBER: 36,207
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)227-7400
;   TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1708 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-09-227-595-31

Query Match   55.7%; Score 1091.2; DB 4; Length 1708;
Best Local Similarity   99.6%; Pred. No. 1.4e-274;
Matches 1115; Conservative   0; Mismatches   3; Indels   2; Gaps   2;

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Db   890 CTGGAACTGCCTCGTTGTGTGCCTGCGAATAACTTCTATCCCAGGAGAGTGTCACAGAGCAGG 949

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Db   204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263

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Db   264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy   735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCCGAGAACTGGTCGCCACCATCTGTCTTCA 794
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Db   324 TCTTAAACACCATCCTGTTTGCTTCTTTCCTCCGAGAACTGGTCGCCACCATCTGTCTTCA 383

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Db   384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCCTGTGA 443

Qy   855 ATAACTTCTATCCCAGAGAGTGGCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCG 914
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Db   444 ATAACTTCTATCCCAGAGAGTGGCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCG 503

Qy   915 GTAACTCCCAGGAGAGTGTCACAGAGGACAGCAGCAAGGACAGCACCTACAGCCTCAGCA 974
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Db   504 GTAACTCCCAGGAGAGTGTCACAGAGGACAGCAGCAAGGACAGCACCTACAGCCTCAGCA 563

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Db   564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAAACACAAAGTCTACGCCTGCGAAGTCA 623

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Db   804 CCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

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Qy   1334 ACCAACTACTCAATTTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATATAC 1393
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Db   923 ACCAACTACTCAATTTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 982

Qy   1394 CATTTATAAAAATCATCCTTCATTCTATTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   983 CATTTATAAAAATCATCCTTCATTCTATTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy   1454 CCTCAAACCCACCAGCCTTCTGTCTCCTCACAGTCCCCATGGCCATGGTAGGAGAGACTTGC 1513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 CCTCAAACCCACCAGCCCTCTGTCTCCTCACAGTCCCCGGCCGTGGTAGGAGAGACTTGC 1102

Qy   1514 TTCCTTGTTTCCCCTCCTCAGCAAGCCCTCATAGTGCCTTTTTAAGGGGTGACAGTCTTA 1573
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1103 TTCCTTGTTTCCCCTCCTCAGCAAGCCCTCATAGTGCCTTTTTAAGGGGTGACAGTCTTA 1162

Qy   1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1163 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1222

Qy   1634 AGAAACCTGC 1643
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Db   1223 AGAAACCTGC 1232

RESULT 9
US-09-227-595-31

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Qy   945 ACAGCAAGGACAGCAGCACCTACAGCCTCAGCAGCGCCTGACGCTGAGCAAGCAGACTACG 1004
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1010 ACAGCAAGGACAGCAGCACCTACAGCCTCAGCAGCGCCTGACGCTGAGCAAGCAGACTACG 1069

Qy  1005 AGAAACACAAAGTCACGCCTGCGGAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA  1064
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1070 AGAAACACAAAGTCACGCCTGCGGAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACACA 1129

Qy  1065 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCGTCCTCCAGTTCCA  1124
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Db  1130 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCGTCCTCCAGTTCCA   1189

Qy  1125 GCCTGACCCCCTCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGGACCTACCCCTAT   1184
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1190 GCCTGACCCCCTCCATCCTTGGCCTCTGACCCTTTTCCACAGGGGGACCTACCCCTAT   1249

Qy  1185 TGCGGTCCTCCAGCTCATCTTCACCTCACCCCCCCTCCTTGGCTTAATTATGC       1244
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Db  1250 TGCGGTCCTCCAGCTCATCTTCACCTCACCCCCCCTCCTTGGCTTAATTATGC       1309

Qy  1245 TAATGTTGGAGGAGAATGAAATAAATAAAGTGAATCTTTGCACCTGTGTTTCTCTCTTTC 1304
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  1310 TAATGTTGGAGGAGAATGAAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1369

Qy  1305 CTC-ATTTAATAATTATTATTATCTGTTGTTTTACCAACTACTCAATTCTTCTTATAAGGAC 1363
         ||| ||||||||||||||||||||||| ||||||||||||||| |||||||||||||
Db  1370 CTCAATTTAATAATTATTATTATCTGTTG-TTTACCAACTACTCAATTTCTCTTATAAGGAC 1428

Qy  1364 TAAATATGTAGTCATCCTAAGGCGGCATAACCATTATAAAAATCATCCTTCATTCTATTT  1423
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1429 TAAATATGTAGTCATCCTAAGGCGGCATAACCATTATAAAAATCATCCTTCATTCTATTT  1488

Qy  1424 TACCCTATCATCCTCTGCAAGACAGTCCTCCCCTCAAACCCACAAGCCTTCTGTCCTCACA 1483
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  1489 TACCCTATCATCCTCTGCAAGACACAGTCCTCCCCTCAAACCCACAAGCCTTCTGTCCTCACA 1548

Qy  1484 GTCCCCTGGGCCCATGGTAGGAGGAGACTTGCTTCCCTGTGTTTCCCCTCAGCAAGCCCT  1543
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  1549 GTCCCCTGGGCCGTGGTAGGAGGAGACTTGCTTCCCTGTGTTTCCCCTCCAGCAAGCCCT  1608

Qy  1544 CATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCTG  1603
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1609 CATAGTCCTTTTTAAGGGTGACAGGTCTTACGGTCATATATCCTTTGATTCAATTCCCTG  1668

Qy  1604 GGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGC 1643
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Db  1669 GGAATCAACCAAGGCAAATTTTTCAAAAGAAGAAACCTGC 1708
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RESULT 10
US-09-042-353-369
; Sequence 369, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 369:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3881 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-042-353-369

Query Match   53.3%; Score 1044; DB 4; Length 3881;
Best Local Similarity 99.8%; Pred. No. 3.8e-262;
Matches 1066; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy   433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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; Sequence 217, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
;  APPLICANT: Lonberg, Nils
;              Kay, Robert M.
;  TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                       Producing Heterologous Antibodies
;  NUMBER OF SEQUENCES: 417
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/758,417A
;   FILING DATE: 02-Dec-1996
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/728,463
;   FILING DATE: 10-OCT-1996
;   APPLICATION NUMBER: US 08/544,404
;   FILING DATE: 10-OCT-1995
;   APPLICATION NUMBER: US 08/352,322
;   FILING DATE: 07-DEC-1994
;   APPLICATION NUMBER: US 08/209,741
;   FILING DATE: 09-MAR-1994
;   APPLICATION NUMBER: US 08/165,699
;   FILING DATE: 10-DEC-1993
;   APPLICATION NUMBER: US 08/161,739
;   FILING DATE: 03-DEC-1993
;   APPLICATION NUMBER: US 08/155,301
;   FILING DATE: 18-NOV-1993
;   APPLICATION NUMBER: US 08/096,762
;   FILING DATE: 22-JUL-1993
;   APPLICATION NUMBER: US 08/053,131
;   FILING DATE: 26-APR-1993
;   APPLICATION NUMBER: US 07/990,860
;   FILING DATE: 16-DEC-1992
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Serafini, Andrew T.
;   REGISTRATION NUMBER: 41,303
;   REFERENCE/DOCKET NUMBER: 014643-009030US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 217:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 3881 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 217:
; US-08-758-417A-217
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Query Match             53.3%;   Score 1044;   DB 4;   Length 3881;
Best Local Similarity   99.8%;   Pred. No. 3.8e-262;
Matches  1066;          Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    433 AATTCTAAACTCTGAGGGGTCGGATGACGTGCCATTCTTCTTGCCTAAAGCATTGAGTTT 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2555 AATTCTAAACTCTGAGGGGTCGGATGACGTGCCATTCTTCTTGCCTAAAGCATTGAGTTT 2614

Qy    493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674
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RESULT 11
US-08-758-417A-217

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Db   2555 AATTCTAAACTCTGAGGGGTCGGATGACGTGCCATTCTTCTTGCCTAAAGCATTGAGTTT 2614
Qy    493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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Db   2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy    553 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGGAAGAAACTCAAAACATCAAGAT 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2675 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGGAAGAAACTCAAAACATCAAGAT 2734

Qy    613 TTTAAATACGCTTCTGTCTCCTTGCTATAATTATCTGGATAATCTGTTTTCTG 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2735 TTTAAATACGCTTCTGTCTCCTTGGTCTCCTTGCTATAATTATCTGGATAATCTGTTTTCTG 2794

Qy    673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy    733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Db   2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy    793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCGTGTTGTGTGGCCTGCT 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCGTGTTGTGTGGCCTGCT 2974

Qy    853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy    913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Db   3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy    973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy   1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db   3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy   1093 GGGAAGTGCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db   3215 GGGAAGTGCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy   1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACCTC 1212
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Db   3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACCTC 3334

Qy   1213 ACCCCCCTCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAAATAAATAAA 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3335 ACCCCCCTCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAAATAAATAAA 3394

Qy   1273 GTGAATCTTTGCACCTGTGTTTCTCTCTTCCTC-ATTTAATAATTATTATTCTGTTGT 1331
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Db   3395 GTGAATCTTTGCACCTGTGTTTCTCTCTTCCTCAATTTAATAATTATTATTCTGTTG-T 3453

Qy   1332 TTACCAACTACTCAATTCTCTAATAAGGGACTAAATATGTAGTCATCCTAAGGGCGCATA 1391
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Db   3454 TTACCAACTACTCAATTCTCTAATAAGGGACTAAATATGTAGTCATCCTAAGGGCGCATA 3513

Qy   1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy   1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
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Db   3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621
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TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend and Crew LLP
  STREET: Two Embarcadero Center, Eighth Floor
  CITY: San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94111-3834
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/042,353
  FILING DATE: 13-MAR-1998
  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/810,279
  FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/853,408
  FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/904,068
  FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/990,860
  FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/053,131
  FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/096,762
  FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/155,301
  FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/161,739
  FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/165,699
  FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/209,741
  FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/352,322
  FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/544,404
  FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/728,463
  FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US96/16433
  FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/758,417
  FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US97/21803
  FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: . (415) 576-0200

Qy   553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAGAAAACTCAAAAACATCAAGAT 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAGAAAACTCAAAAACATCAAGAT 2734

Qy   613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGCTGTTTTCTG 2794

Qy   673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACACACCCAAGGCAGAAACTTTGT 732
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Db   2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACACACCCAAGGCAGAAACTTTGT 2854

Qy   733 TACTTAAACACCATCCTGTTGTTGCTTCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2855 TACTTAAACACCATCCTGTTGTTGCTTCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy   793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGGAAATCTGAACTGGAACTTCCTGTTGTGTCCTGCT 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGAACTGGAAATCTGAACTGGAACTTCCTGTTGTGTCCTGCT 2974

Qy   853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGATAACGCCCTCCAATC 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGATAACGCCCTCCAATC 3034

Qy   913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAG 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACACCTACAGCCTCAG 3094

Qy   973 CAGACACCCTGAGCGTGAGCAAGCAAGCAGACTACGACGACTCTACGCCTGCGAAGT 1032
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3095 CAGACACCCTGAGCGTGAGCAAGCAAGCAGACTACGACGACTCTACGCCTGCGAAGT 3154

Qy   1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAGAG 1092
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTTAGAG 3214

Qy   1093 GGAGAAGTGCCCCACCTGCTCCTGTTCCAGTTCCAGCTCCCATCCTCCCATCCTTTGGCCTC 1152
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3215 GGAGAAGTGCCCCACCTGCTCCTGTTCCAGTTCCAGCTCCCATCCTCCCATCCTTTGGCCTC 3274

Qy   1153 TGACCCTTTTTCCACAGGGGACCTACCCCGGTCCTCCAGCTCATCTTCACCTC 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3275 TGACCCTTTTTCCACAGGGGACCTACCCCGGTCCTCCAGCTCATCTTCACCTC 3334

Qy   1213 ACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
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Db   3335 ACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

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Db   3395 GTGAATCTTGCACCTGTTGGTTTCTCTCTTCCTCCCAATTTAATAATTATTATCTGTTG-T 3453

Qy   1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy   1392 ACCATTTATAAAAATCATCCTTCATTCATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3514 ACCATTTATAAAAATCATCCTTCATTCATTTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy   1452 TCCCTCAAACCCACAAGCCTTCGTCCTCACAGTCCCCTGGGCCATGG 1499
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   3574 TCCCTCAAACCCACAAGCCTTCGTCCTCACAGTCCCCTGGGCCATGG 3621

RESULT 12
US-09-042-353-393
; Sequence 393, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils
;   APPLICANT: Kay, Robert M.

```
;    TELEFAX:   (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 393:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:   3819 base pairs
;      TYPE:   nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: DNA
US-09-042-353-393

Query Match           36.2%;  Score 709.4;  DB 4;  Length 3819;
Best Local Similarity 99.6%;  Pred. No. 4.9e-175;
Matches   732;  Conservative  0;  Mismatches   0;  Indels  2;  Gaps  2;

Qy    766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2826 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 2885

Qy    826 TGGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2886 TGGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 2945

Qy    886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2946 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 3005

Qy    946 CAGCAAGGACAGCAGCACCTACAGCTTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3006 CAGCAAGGACAGCAGCACCTACAGCTTCAGCAGCACCCTGAGCGCTGAGCAAAGCAGACTACGA 3065

Qy   1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTCGAGTCGCCCGTCACCAAA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3066 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTCGAGTCGCCCGTCACCAAA 3125

Qy   1066 GAGCTTCAACAGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3126 GAGCTTCAACAGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAG 3185

Qy   1126 CCTGACCCCCTCCCATCTTTGGCCTCTGACCCTTTTCCACAGGGACCTACCCCTATT 1185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3186 CCTGACCCCCTCCCATCTCCATCTTTGGCCTCTGACCCTTTTCCACAGGGACCTACCCCTATT 3245

Qy   1186 GCGGTCCTCCAGTCATCTTCACCTCACCCCCCCTCCTTCCTTGGCTTTAATTATGCT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3246 GCGGTCCTCCAGTCATCTTCACCTCACCCCCCCTCCTTCCTTGGCTTTAATTATGCT 3305

Qy   1246 AATGTTGAGGAGGAGAATGAATAAAATAAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCCTTTCC 1305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3306 AATGTTGAGGAGGAGAATGAATAAAATAAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCCTTTCC 3365

Qy   1306 TC-ATTTAATAATTATTATTCGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGACT 1364
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3366 TCAATTTAATAATTATTATTATTCGTTG-TTTACCAACTACTCAATTTCTCTTATAAGGGACT 3424

Qy   1365 AAATATGTAGTCATCCTAGGGCCATAACCATTTATTAAAAATCATCCTTCATTCTATTTT 1424
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3425 AAATATGTAGTCATCCTAGGGCCATAACCATTTATTAAAAATCATCCTTCATTCTATTTT 3484

Qy   1425 ACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCTCCTCACAG 1484
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3485 ACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCTCCTCACAG 3544

Qy   1485 TCCCCTGGGCCATGG 1499
          |||||||||||||||
Db   3545 TCCCCTGGGCCATGG 3559


RESULT 13
US-08-758-417A-243
; Sequence 243, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
;    APPLICANT: Lonberg, Nils
```

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;    Kay, Robert M.
;  TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                     Producing Heterologous Antibodies
;  NUMBER OF SEQUENCES: 417
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Townsend and Townsend and Crew LLP
;    STREET: Two Embarcadero Center, Eighth Floor
;    CITY: San Francisco
;    STATE: California
;    COUNTRY: USA
;    ZIP: 94111-3834
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC Compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0,  Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/758,417A
;    FILING DATE: 02-Dec-1996
;    CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 08/728,463
;    FILING DATE: 10-OCT-1996
;    APPLICATION NUMBER: US 08/544,404
;    FILING DATE: 10-OCT-1995
;    APPLICATION NUMBER: US 08/352,322
;    FILING DATE: 07-DEC-1994
;    APPLICATION NUMBER: US 08/209,741
;    FILING DATE: 09-MAR-1994
;    APPLICATION NUMBER: US 08/165,699
;    FILING DATE: 10-DEC-1993
;    APPLICATION NUMBER: US 08/161,739
;    FILING DATE: 03-DEC-1993
;    APPLICATION NUMBER: US 08/155,301
;    FILING DATE: 18-NOV-1993
;    APPLICATION NUMBER: US 08/096,762
;    FILING DATE: 22-JUL-1993
;    APPLICATION NUMBER: US 08/053,131
;    FILING DATE: 26-APR-1993
;    APPLICATION NUMBER: US 07/990,860
;    FILING DATE: 16-DEC-1992
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Serafini, Andrew T.
;    REGISTRATION NUMBER: 41,303
;    REFERENCE/DOCKET NUMBER: 014643-00903OUS
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (415) 576-0200
;    TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 243:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 3819 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: DNA
;    SEQUENCE DESCRIPTION: SEQ ID NO: 243:
US-08-758-417A-243

Query Match           36.2%;  Score 709.4;  DB 4;  Length 3819;
Best Local Similarity 99.6%;  Pred. No. 4.9e-175;
Matches   732;  Conservative  0;  Mismatches   1;  Indels  2;  Gaps  2;

Qy    766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2826 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 2885

Qy    826 TGGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2886 TGGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 2945

Qy    886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2946 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 3005
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Qy      7  CCACCATGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCGGCACCT    66
           ||||||||||||||||||||||||||||||||| |||||| || ||||||||| || |||
Db   1594  CCACCATGATTCACAGGCCCAGGTTCTTATATGTTACTGCCGCTATGGGTATCTGGTACCT  1653

Qy     67  GTGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTGTCTGTAAGCTGAGAGGG   126
           |||||||||||||| ||| ||||||||| | ||||| ||||||||| || |||||||| ||
Db   1654  GTGGGACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGG   1713

Qy    127  CCACTATTAGCTGCAAATCAGTCAGAGTGTTATATTCTTTATATTGTCAACAGAACTACT   186
           ||| |||| ||||||||| || ||||||| | || | |  | ||||| ||| ||| ||||
Db   1714  TTACTATGAGCTGCAAGTCCAGTCAGAGCCTTTATATTCTAGAAATCAAAAGAACTACT   1773

Qy    187  TGGCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCA   246
           |||| |||||||||||||| ||||| |||| |||||||||| || |||  |||||||||||
Db   1774  TGGCCTGGTACCAGCAGAAGCCAGGGCAGTCTCCTAAACTGCTGATTTTCTGGGCATCCA   1833

Qy    247  CTAGGGAATCTGGGGTCCCTGATCGCCTTCAGTGGCAGTGGATCTGGGACACAGATTCACTC   306
           |||||||||||||||||||||| || ||||||||| ||||| |||||  |||| ||||||||
Db   1834  CTAGGGAATCTGGGGTCCCTGATCGCCTTCACAGGCAGTGGATTTGGGACGGATTTCAATC   1893

Qy    307  TCACCATCAGCAGTCTGCAGGCTGAGAGCTGCTTATTACTGCAGCCAATCTTATA       366
           ||||||||||||||||||||| || ||| ||| ||||||||||| ||| |||| |||
Db   1894  TCACCATCAGCAGTCTGCAGGCTGAGAGCTGCCAGTTTATGACTGTCAGCAATAATTTA  1953

Qy    367  ---ATCTTTACACGTTCGGAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTC   423
              | || || |||||| ||||| ||||||||||||||||||||||||||
Db   1954  GCTATCCCGCTCACGTTCGGTGGGACCAAGCTGGAGCTGAAACGTGAGTGG-------   2006

Qy    424  AACTCTAGAAATTCTAAACTCTGAGGGGTCGGTGGCCATTCTTTGCCTAAAGC       483
           ||||||||||||||||||| |  ||||||||||||||||||||||||||||||||
Db   2007  -------------------------------------------------------   2006

Qy    484  ATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCT   543
           ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   2007  ------------------------------------------------------------   2006

Qy    544  CCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGAAGAAACTCAAAA   603
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2007  ------------------------------------------------------------   2006

Qy    604  CATCAAGATTTAAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGC   663
                                                            ||||||||||||||||
Db   2007  -----------------------------------ATCCATCTGGGATAAGCATGC   2027

Qy    664  TGTTTTCTGTCGTCCCTAACATGCCCTGATTATCCGCAAACACACCCAAGGGCA   723
           ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2028  TGTTTTCTGTCGTCCCTAACATGCCCTGATTATGCCCAAACAACACCCAAGGGCA   2087

Qy    724  GAACTTGTTACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTGCACC   783
           |||||||||| || ||||||||||||||| || ||||||||||||||||||||||||||
Db   2088  GAACTTGTTACTTAAACACCATCCTGTTTGCTTCTTCCTCAGGAACTGTGGCTGCACC   2147

Qy    784  ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGGCCTCTGTGT   843
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2148  ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGGCCTCTGTGT   2207

Qy    844  GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGC   903
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2208  GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGC   2267

Qy    904  CCTCCAATCGGGTAACTCCAGGAGAGTGTCACAGGAGCAGGACAGCAAGGACAGCACCTA   963
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2268  CCTCCAATCGGGTAACTCCAGGAGAGTGTCACAGGAGCAGGACAGCAAGGACAGCACCTA   2327

Qy    964  CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGC  1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2328  CAGCCTCAGCAGCACCCTGAGCCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGC   2387

Qy   1024  CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGA  1083
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   2388  CTGCGAAGTCACCCATCAGGGCCTCAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGA   2447

Qy   1084  GTGTTAGGGAGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCC  1143
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Qy    946  CAGCAAGGACAGCAGCACTTCAGCGCTGAGCCTGAGCGCTGAGCAAAGCAGCAGACTACGA  1005
           ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   3006  CAGCAAGGACAGCAGCACTTCAGCGCTGAGCCTGAGCGCTGAGCAAAGCAGCAGACTACGA  3065

Qy   1006  GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA  1065
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3066  GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA  3125

Qy   1066  GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAG  1125
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   3126  GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCACCTGCTCCTCAGTTCCAG  3185

Qy   1126  CCTGACCCCCTCCCATCTCTTGGCCTCTGACCCTTTTCCACAGGGACCTACCCCTATT  1185
           ||||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||
Db   3186  CCTGACCCCCTCCCATCTCTTGGCCTCTGACCCTTTTCCACAGGGACCTACCCCTATT  3245

Qy   1186  GCGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTGGCTTAATTATGCT  1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3246  GCGGTCCTCCAGCTCATCTTCACCTCACCCCCTCCTCCTGGCTTAATTATGCT  3305

Qy   1246  AATGTTGGAGGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCC  1305
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   3306  AATGTTGGAGGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCC  3365

Qy   1306  TC-ATTTAATAATTATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTATAAGGGACT  1364
           || |||||||||||||| |||||||||||  |||||||||||||||||||| ||||||||||
Db   3366  TCAATTTAATAATTATTATTATCTGTTG-TTTACCAACTACTCAATTTCTCTATAAGGGACT  3424

Qy   1365  AAATATGTAGTTCATCTCCTAAGGCGCATAACCATTATAAAAATCATCCTTCATTCTATTTT  1424
           |||||||||||||||||||||||||| ||||||||||||| |||||||||||||||||||
Db   3425  AAATATGTAGTTCATCTCCTAAGGCGCATAACCATTATAAAAATCATCCTTCATTCTATTTT  3484

Qy   1425  ACCTATCATCCTCTGCAAGACAGTCCTCCCCCAAACCCACAAGCCTTCTGTCCTCCACAG  1484
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   3485  ACCTATCATCCTCTGCAAGACAGTCCTCCCCCAAACCCACAAGCCTTCTGTCCTCCACAG  3544

Qy   1485  TCCCCTGGGCCATGG  1499
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Db   3545  TCCCCTGGGCCATGG  3559
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Query Match   35.6%; Score 698; DB 4; Length 8068;
Best Local Similarity   76.5%; Pred. No. 6.4e-172;
Matches 992; Conservative 0; Mismatches 75; Indels 229; Gaps 2;

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Db   1954 GCTATCCGGCTCACGTTCGGACAAGGGGACCAAGGTGGAAATAAAACGTGAGTGG------ 2006
Qy    424 AACTCTTAGAGAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGC 483
Db   2007 ------------------------------------------------------------ 2006
Qy    484 ATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCT 543
Db   2007 ------------------------------------------------------------ 2006
Qy    544 CCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAGGAGAAACTCAAAA 603
Db   2007 ------------------------------------------------------------ 2006
Qy    604 CATCAAGATTTTAAATACCGTTCTTCTTGGTCTCCTTGCTATAATTATCTGGATAAGCATGC 663
Db   2007 ----------------------------ATCCATCTGGATAAGCATGC 2027
Qy    664 TGTTTTCTGTCTGTCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCA 723
Db   2028 TGTTTTCTGTCTGTCCTAACATGCCCTGTGATTATGCCGCAAACAACACACCCAAGGGCA 2087
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    724 GAACTTTGTTACTTAAACACCATCCTCTTCCTTCCTCAGGAACTGTGGCTGCACC 783
Db   2088 GAACTTTGTTACTTAAACACTATCCTCTTGCTTCCTTCCTCAGGAACTGTGGCTGCACC 2147
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    784 ATCTGTCTTCATCTTCCCGCATCGATGAGCAGTTGAAATCTGGAACTGCCCTGTGTTGT 843
Db   2148 ATCTGTCTTCATCTTCCCGCATCGATGAGCAGTTGAAATCTGGAACTGCCCTGTGTTGT 2207
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    844 GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGC 903
Db   2208 GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGC 2267
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    904 CCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACAGCACCTA 963
Db   2268 CCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAGGACAGCACCTA 2327
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    964 CAGGCTCAGCAGCACCCGACGTGAGCGTGAGCAAAGAGACTACGAGAAACAAGTCTACGC 1023
Db   2328 CAGCCTCAGCAGCACCCGACGTGAGCGTGAGCAAAGAGACTACGAGAAACAAAGTCTACGC 2387
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1024 CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGA 1083
Db   2388 CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGA 2447
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1084 GTGTTAGAGGGAGAAGTGCCCCACCCACCTCCAGTTCCAGCCCCTCCATCC 1143
Db   2448 GTGTTAGAGGGAGAAGTGCCCCACCCACCTCCAGTTCCAGCCCCTCCATCC 2507
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1144 TTTGGCCCTCGACCCTTTTCCCAGGGGACCTACCCGTCCTCCAGCTCATC 1203
Db   2508 TTTGGCCCTCGACCCTTTTCCCAGGGGACCTACCCGTCCTCCAGCTCATC 2567
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1204 TTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGA 1263
Db   2568 TTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGA 2627
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1264 ATAAATAAAGTGAATCTTTGCACCTGTGTTTCTCT 1299
Db   2628 ATAAATAAAGTGAATCTTTGCACCTGTGGTGGATCT 2663
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Search completed: July 18, 2003, 19:59:00
Job time : 109.931 secs

RESULT 15
US-09-301-593-35
; Sequence 35, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 8068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-301-593-35

Query Match   34.1%;
Best Local Similarity   75.1%;   Score 667.6; DB 4; Length 8068;
Matches 973; Conservative   0; Mismatches 94; Indels 229; Gaps 2;
                                                    Pred. No. 5.2e-164;

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Qy      7 CCACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGTATGGTATCTGGCACCT 66
           |||||||||||||||||||||||||||||| || ||| | |||||||||||||
Db   1594 CCACCATGGAGACAGACACACTCCTGCTATGGGTGCTCTCGGTTCTGGGTTCCAGGTTCCT 1653
Qy     67 GTGGGGACATTGTGCTGACACAGTCTCCAGCTCCCTGCTGTAAGCTTGAGAGAGAGGG 126
           |||||||| || ||||||||||||||||||||| | ||
Db   1654 CCGGAGACATTGTGATGACCCAATCTCCAGCTCTTTGGCTGTGTCTCTAGGGGAGGAGGG 1713
Qy    127 CCACTATTAGCTGCAAATCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACT 186
           |||||||| ||||| ||| || ||||||| ||
Db   1714 CCACCATCAACTGCAAGTCCAGTCAGAGCCTTTTATATTCTAGAAATCAAAGAACTACT 1773
Qy    187 TGGCTTGTACCAGCAGAAAACAGGGCAGCCTCCAAAACTGCTGATCTACTGGGCATCCA 246
           |||||||| ||||||||||||| ||||||| ||| ||||||| |||||||
Db   1774 TGGCCTGGTATCAGCAGAAACCAGGACAGAACCCAAAACTCCTCATCTTTTGGGCTAGCA 1833
Qy    247 CTAGGGAATCTGGGGTCCCTGAT 306
           ||||||||||||||||| |||||||
Db   1834 CTAGGGAATCTGGGGTACCTGATAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCC 1893
Qy    307 TCACCATCAGCAGTCTGCAGGCT 366
           |||||||||| ||||||||||
Db   1894 TCACCATTAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTTTA 1953
Qy    367 ---ATCTTTACACGTTCCGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTC 423
              |||  ||||||||| ||||||| |||||||||||||||
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 18, 2003, 04:46:48 ; Search time 6294.87 Seconds
(without alignments)
10397.705 Million cell updates/sec

Title: US-09-627-896B-23
Perfect score: 2249
Sequence: 1 tctagaccaccatgggttgg.........ccgggtaaatgagtgaattc 2249

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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14: gb_vi:*
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16: em_fun:*
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35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_hrgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	80.2	2560	6	AR035228	AR035228 Sequence
2	1793.2	79.7	2010	9	HSA250170	AJ250170 Homo sapi
3	1787.6	79.5	2009	9	HUMIGCD1	J00230 Human Ig ge
4	1765.2	78.5	563102	2	AC084717	AC084717 Homo sapi
5	1752.8	77.9	2193	9	AF237584	AF237584 Homo sapi
6	1651.6	73.4	2287	6	AR029004	AR029004 Sequence
7	1651.6	73.4	2287	6	AR037308	AR037308 Sequence
8	1651.6	73.4	2287	6	BD000539	BD000539 Antibody
9	1651.6	73.4	2287	6	I90051	I90051 Sequence 1
10	1638	72.8	4694	6	AX088865	AX088865 Sequence
11	1638	72.8	4694	6	AX478055	AX478055 Sequence
12	1613	71.7	2028	6	HUMIGCD2	K01316 Human Ig ge
13	1611.8	71.7	4723	6	AR161379	AR161379 Sequence
14	1611.8	71.7	4723	6	AX088864	AX088864 Sequence
15	1611.8	71.6	4723	6	AX478054	AX478054 Sequence
16	1610.8	71.6	2029	6	AR035227	AR035227 Sequence
17	1610.8	71.6	2802	9	HSIGG1CP	Z17370 H.sapiens g
18 c	1607.6	71.5	169802	9	CNS01DT2	AL122127 Human chr
19	1584.6	70.5	2482	6	AR100741	AR100741 Sequence
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21	1584.6	70.5	2482	6	AR130196	AR130196 Sequence
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23	1561	69.4	2033	9	AF237586	AF237586 Homo sapi
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25	1547.2	68.8	2009	9	AX327474	AX327474 Sequence
26	1547.2	68.8	2009	6	E06998	E06998 DNA encodin
27	1547.2	68.8	2009	9	HUMIGCC4	J00228 Homo sapien
28	1547.2	68.8	3133	6	I08115	I08115 Sequence 1
29	1545.6	68.7	2009	6	E10971	E10971 DNA sequenc
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32	1516.2	67.4	1980	6	I16572	I16572 Sequence 4
33	1465.8	65.2	3108	6	E10974	E10974 Intron-incl
34	1465.8	65.2	3147	6	E10975	E10975 Intron-incl
35	1463.4	65.1	2071	6	E40080	E40080 Drug contai
36	1463.4	65.1	2071	6	E40888	E40888 Humanized a
37	1463.4	65.1	2071	6	E43434	E43434 Humanized a
38	1458.6	64.9	2077	6	E40055	E40055 Drug contai
39	1458.6	64.9	2077	6	E40863	E40863 Humanized a
40	1458.6	64.9	2077	6	E43409	E43409 Humanized a
41	1455.4	64.7	2073	6	E40910	E40910 Humanized a
42	1455.4	64.7	2073	6	E40911	E40911 Humanized a
43	1455.4	64.7	2077	6	E43441	E43441 Humanized a
44	1453.8	64.6	2073	6	E40912	E40912 Humanized a
45	1438.6	64.0	3282	6	AR038306	AR038306 Sequence

ALIGNMENTS

RESULT 1
AR035228
LOCUS   AR035228   2560 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 44 from patent US 5871732.
ACCESSION   AR035228
VERSION   AR035228.1 GI:5951896
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 2560)
AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
TITLE   Anti-CD4 antibody homologs useful in prophylaxis and treatment of
            AIDS, ARC and HIV infection
JOURNAL   Patent: US 5871732-A 44 16-FEB-1999;

Pred. No. is the number of results predicted by chance to have a

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FEATURES          Location/Qualifiers
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                  /organism="unknown"
BASE COUNT     848 a     544 c     720 g     448 t
ORIGIN

Query Match      80.2%;   Score 1804;   DB 6;   Length 2560;
Best Local Similarity   89.2%;   Pred. No. 0;
Matches 2049;   Conservative   0;   Mismatches 185;   Indels 64;   Gaps 7;

Qy      8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGTACAGGTGTGCACTC 67
          |||||||| |||||| | |||||||||||| || |||| | ||||||| |||||||
Db      8 CACCATGGACTGGACCTGGAGGGTCTTCTGCTTGCTGGTCGTAGCACCAGGTGCCCACTC 67

Qy     68 CCAGGTCCAGCTGCGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGAGCTCAGTGAAGGT 127
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Db     68 CCAGGTCCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGGT 127

Qy    128 GTCCTGCAAAGTTCCGGCTACACATTCACTGATTATGCTATACAGTGTGGTGGACAGGC 187
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Db    128 GTCCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATACACTGGGTGAGGCAGGC 187

Qy    188 TCCTGGACAGGGCCTGAGTGGATTGGAGTTATTAATAATTACTATGATAATACAAACTA 247
          ||||| ||||||||||| ||||| |||| |||| || |  || || || || ||| |||
Db    188 GCCTGGGCAGGGCCTGAGTGGATGGGATATATATTTTTAACATGATGGTACTGACTA 247

Qy    248 CAACCAGAAGTTAAGGCAAGGCCACAAATGACTGTAGACAAGTCGACAGCACAGCCTA 307
          |||| ||| ||| || ||||| ||| |  |||| |||||||  |||||| ||||||||
Db    248 CGATGAGAAGTTCAAAGGCAAGGCCACACTGACTGTAGACAAATCCTCCAACACAGCCTA 307

Qy    308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAG----363
          ||||||| ||| ||  || ||||| |||| || ||||| |||||||||||| ||||
Db    308 CATGGAGCTCAGCAGCCTGAGGTCTGAGGACACTGCAGTCTATTACTGTGCAAGAGAGAA 367

Qy    364 ------CGGCTCTGTATATGGACTACTGCGGGTCAAGGTCACCCTGTCACCCT 409
                  |||  ||||| | |||||||||||| ||||||||||||||||||
Db    368 GGATAACTACGCGGACGGGGGCTGGTTGCTTACTGGGGCCAAGGGACCCTGGTCACCGT 427

Qy    410 CTCCTCAGGTGAGTCCTAAA--------ACCT 434
          |||||||||||||||
Db    428 CTCCTCAGGTGAGTCCTAAGCTTGGTACCGGGAATTCAGATCTGCAGCATGCGGCAGCT 487

Qy    435 CTAG------AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGCAGGAGTGGG 489
          ||||       ||||| ||||||||||||||||||||| |||||||||||||||||||
Db    488 CTAGATATCAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTG-GGGGCAGGAGGGGG 546

Qy    490 CTAAGGTGAGGCAGGTGGCGCAGCCAGCCAGGGGCCTCTGAGCCCCAGACACT 549
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Db    547 CTAAGGTGAGGCAGGTGGCGCAGCCAGCCAGGTCTCACCCCATGAGCCCAGACACT 606

Qy    550 GGACCCTGCCTGGACCGTGGATGGAATGACAAGAACCGAGGGGCCTCTGGGCC 609
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Db    607 GGACCCTGCCATGGACCATCGCGGATAGAACAAGAACCGAGGGGCCTCTGGGCCC 666

Qy    610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTTCGAGCCTTCCACCAGGGCC 669
          ||||||||||||||| |||||||| ||||||||||||||||| ||||||||||||||
Db    667 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTTCCAGCTTCCACCAGGGGCC 726

Qy    670 CATCGGTCGTTCTCCCCCGGCTCTGGCGGCCCTGCTCCGAGAGCCCAGCCGCGCCCTGG 729
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Db    727 CATCCGGTCGTTCTCCCCGGCTCTGGCGGCCCTGCTCCGAGAGCCACAGCCCGCCTGG 786

Qy    730 GCTGCCTTGGTCAAGGACTACTTCCCCGAACCGGTGTCGTGGAACTCAGGCGCTC 789
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Db    787 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGTCGTGGAACTCAGGCGCCTC 846

Qy    790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTTCCCTCCTCCCTCA 849
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Qy    850 GCAGGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    907 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACACCTGCAACGTAG 966
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Qy    910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
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Db    967 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCAGCAGGGAG 1026

Qy    970 GGAGGGTGTTGCTGAAGCCAGGTCAGCCTCCTGCTGGACGCACCCGGCTGTGCA 1029
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAGGGTGTTGCTGGACGCCAGCTCAGCCTCCTGCTGGACGCACCCGGCTGTGCA 1086

Qy   1030 GCCCCAGCCCAGGGGAGCAAGGCAGCGCAGCCCCATCTGTCCTCACCCGGAGGCCTCGCCC 1089
          || ||| |||||| |||| |||||||||||||||||||||||||||||||||| ||| |||
Db   1087 GCCCCAGCCCAGGCCAGCAGCAAGGCAGCATGCCCCATCTGTCTCTCTGTCCTCACCCGGAGGCCTCTGACC 1146

Qy   1090 GCCCCACTCATGCTCAGGAGGGTCTTCGGCTTTTCCACCGGCTCCAGGCAGGCA 1149
          |||| ||||||||||| |||||| |||| |||||||||||||||||||||||||
Db   1147 ACCCCACTCATGCTCAGGAGAGGGTCTTCTGGATTTTTCCACCAGGTCCCCGGCA-CCA 1205

Qy   1150 CAGGCTGGGTGCCCCTACCCCAGCGCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
          ||||| || ||||||||||||||||||||| ||||||||||||||  |||||||||||||
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Qy   1210 TGCCAAAAGCCATATCCGGAGGAGCACCCTGCCCCTGACCTAAGCCGACCCAAAGGCCAAA 1269
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Db   1265 TGCCAAGAGCCATATCCGGAGGAGCACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 1324

Qy   1270 CTGTCCACTCCCCAGCTCGGACACTTCTCTCTCCCCAGATCGGAGTAACTCCCAATCT 1329
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Db   1325 CTCTCCACTCCCCAGCTCAGACACACTTCTCTCTCCCCAGATCTGAGTAACTCCCAATCT 1384

Qy   1330 TCTCTCTGGAGCGCAAAATGTTGTCGAGTGCCACCGTGCCCAGTGAAGCCAGCCCA 1389
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Db   1385 TCTCTCTGCAGAGTCCAAAATATGGTCCCCGAGTGCCCATCATGCCCAGTGAAGCCAACCCA 1444

Qy   1390 GGCCTCGCCCTCCAGCTCAAGGCGGACAGGTGCCTGCCCTAGAGTAGCCTGCATCCAGGGGACA 1449
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Db   1445 GGCCTCGCCCTCCAGCTCAAGGCGGACAGGTGCCTGCCCTAGAGTAGCCTGCATCCAGGGACA 1504

Qy   1450 GGCCCCAGCTGGGTGCTGCACGTCCGACCTCCATCTCTTCCTCAGCACC--ACCTGCGG 1506
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Qy   1507 CAGCACCGTCAGTCTTCCTCCTTCCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGA 1566
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Db   1565 GGGGACCATCAGTCTTCCTGTTCCCCCCAAAAACCAAGGACACTCTCATGATCTCCCGGA 1624

Qy   1567 CCCCTGAGGTCACGTGCGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
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Db   1625 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1684

Qy   1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
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Db   1685 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1744

Qy   1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
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Db   1745 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTCGTGCACCAGGACTGGCTGAACG 1804

Qy   1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCTCCCAGCCCCCATCCGAGAAAACCA 1806
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Qy   1807 TCTCCAAAACCAAAGGTCAGGACTGGTGACGTGTCGTGGAACTCAGGCGCTC 1866
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Db   1865 TCTCCAAAGCCAAAGGTCAGGACCCACACGGGTGCGAGGGGCCACACGCCAGCAGCCAGCTC 1924

Qy   1867 GGCCACCCTCGTGCCCTGGAGACCGTGTCCTGCTGCTGTCCTACTCCCTCA 1926
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Db   1925 GGCCACCCTCTGCCCTGGAGTGCACCGTGTCCTGCTGCTGTCCTACTCCCTCA 1984

Qy   1927 CGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGAGGATGACCGAGGTC 1986
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Db   1985 CGAGAGCCAGCAGTGTACACCGTGCCCCCATCCCGGGAGGATGACCGAGATGACCAGGTC 2044
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Qy   1987  AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC  2046
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Db   2045  AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC  2104

Qy   2047  AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC  2106
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Db   2105  AATGGGCAGCCGGAGAACAACTACAAGACCACACCGCCCGTCCTGGACTCCGACGGCTCC  2164

Qy   2107  TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC  2166
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Db   2165  TTCTTCCTCTACAGCAGCCTAACCGTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTC  2224

Qy   2167  TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG  2226
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Db   2225  TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACAGAGAAGAGCCTCTCCCTG  2284

Qy   2227  TCCCCGGGTAAATGAGTG  2244
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Db   2285  TCTCTGGGTAAATGAGTG  2302


RESULT 2
HSA250170
LOCUS       HSA250170               2010 bp    DNA     linear   PRI 22-NOV-2001
DEFINITION  Homo sapiens partial IgG2 gene for immunoglobulin heavy chain
            constant region IgG2, exons 1-4.
ACCESSION   AJ250170
VERSION     AJ250170.1  GI:10799663
KEYWORDS    constant region; IgG2 gene; immunoglobulin; immunoglobulin heavy
            chain.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ellison,J. and Hood,L.
  TITLE     Linkage and sequence homology of two human immunoglobulin gamma
            heavy chain constant region genes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
   MEDLINE   82197621
   PUBMED    6804948
REFERENCE   2  (bases 1 to 2010)
  AUTHORS   Hougs,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1999) Hougs L., Dept. of Clinical Immunology,
            sect. 7631, National University Hospital, Rigshospitalet, Tagensvej
            20, DK-2200 Copenhagen N., DENMARK
  AUTHORS   Hougs,L., Sveigaard,A. and Barington,T.
  TITLE     The first constant-domain (CHI) exon of human IGHG2 is polymorphic
            and in strong linkage disequilibrium with the CH2 exon polymorphism
            encoding the G2m(n+) allotype in Caucasians
  JOURNAL   Immunogenetics 52 (3-4), 242-248 (2001)
   MEDLINE   21115140
   PUBMED    11220626
COMMENT     Related sequences Z49801 and Z49802.
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                     /sex="female"
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                CVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDG
                MEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKT
                KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM
                LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"
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     intron          938..1055
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     exon            1056..1382
                     /gene="IgG2"
                     /number=3
     intron          1383..1479
                     /gene="IgG2"
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     exon            1480..1803
                     /gene="IgG2"
                     /number=4
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                     /note="PCR 3' primer"
BASE COUNT      413 a    702 c    566 g    329 t
ORIGIN

Query Match             79.7%;  Score 1793.2;  DB 9;  Length 2010;
Best Local Similarity   99.6%;  Pred. No. 0;
Matches 1798;  Conservative    0;  Mismatches   8;  Indels    0;  Gaps    0;

Qy    439  AGCTTTCTGGGGCGGCCTGACTTTGGCTTTGGGCAGGGAGTGGGCAGGGAGTGGGCTAAGGTGA  498
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Db      1  AGCTTTCTGGGGCGGCCTGACTTTGGCTTTGGGCAGGGAGTGGGCAGGGAGTGGGCTAAGGTGA   60

Qy    499  GGCAGGTGGCGCCAGGTGCAGTGCACCAATGCCCGTGAGCCCAGCACTGACCCCTGC  558
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GGCAGGTGGCGCCAGGTGCAGTGCACCAATGCCCGTGAGCCCAGCACTGACCCCTGC  120

Qy    559  CTTGGACCCTCGTTGGATAGACAGAAGAACCGAGGGGCCCTCGCGCCTCCGGCCTCGTC  618
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Db    121  CTTGGACCCTCGTTGGATAGACAGAAGAACCGAGGGGCCCTCGCGCCTCCGGCCTCGTC  180

Qy    619  CCACACCGGTCACATGGCACCATGGCACCTCCTTCTGCAGCCTCCACCAAGGGCCCATCGGTCT  678
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CCACACCGGTCACATGGCACCATGGCACCTCCTTCTGCAGCCTCCACCAAGGGCCCATCGGTCT  240

Qy    679  TCCCCCTGGCCGCCTGCTCCAGGAGCACCTCCGAGAGCACACAGCGGCCCTGGGCTGCTGG  738
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Db    241  TCCCCCTGGCCGCCTGCTCCAGGAGCACCTCCGAGAGCACACAGCGGCCCTGGGCTGCTGG  300

Qy    739  TCAAGGACTACTTCCCGAACCGGTCACGGTGTCGTGGAACTCAGGGCGCTCTGACCAGCG  798
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Db    301  TCAAGGACTACTTCCCCGAACCGGTCACGGTGTCGTGGAACTCAGGGCGCTCTGACCAGCG  360

Qy    799  GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG  858
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Db   661  ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG  720

Qy  1159  TGCCCCTACCCCAGGCCCTTCACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAG  1218
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RESULT 3

HUMIGCD1

LOCUS   HUMIGCD1   2009 bp   DNA   linear   PRI 11-APR-2001
DEFINITION Human Ig germline H-chain G-E-A region B: gamma-2 constant region,
            3' end.
ACCESSION   J00230 V00554
VERSION   J00230.1 GI:184750
KEYWORDS   .
SEGMENT   1 of 7
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 896 to 1256; 1749 to 1937)
AUTHORS   Krawinkel,U. and Rabbitts,T.H.
TITLE   Comparison of the hinge-coding segments in human immunoglobulin
            gamma heavy chain genes and the linkage of the gamma 2 and gamma 4
            subclass genes
JOURNAL   EMBO J. 1 (4), 403-407 (1982)
MEDLINE   84235992
PUBMED   6329676
REFERENCE   2 (bases 1 to 2009)
AUTHORS   Ellison,J. and Hood,L.
TITLE   Linkage and sequence homology of two human immunoglobulin gamma
            heavy chain constant region genes
JOURNAL   Proc Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
MEDLINE   82197621
PUBMED   6804948
REFERENCE   3 (bases 475 to 1071; 1179 to 1330; 1461 to 1524)
AUTHORS   Takahashi,N., Ueda,S., Obata,M., Nikaido,T., Nakai,S. and Honjo,T.
TITLE   Structure of human immunoglobulin gamma genes: implications for
            evolution of a gene family
JOURNAL   Cell 29 (2), 671-679 (1982)
MEDLINE   83001943
PUBMED   6811139
COMMENT   On Mar 2, 2000 this sequence version replaced gi:32759.
            [2] also reports sequences for gamma-3, gamma-4, and a gamma
            pseudogene. Most of this sequence is 95% homologous with gamma-4.
            The hinge exons are only 70% homologous. The authors estimate that
            gamma-2 and gamma-4 diverged 6.6 million years ago. The authors in
            [1] speculate that intron-mediated domain transfer played an
            important role in the evolution of human gamma genes. They also
            report the hinge regions of gamma-1, gamma-3, gamma-4, and a
            pseudo-gamma gene. [1] estimates the divergence of the human gamma
            genes to be between 7.7 and 4.4 million years ago. This entry is
            part of a multigene region containing the gamma-2, gamma-4,
            epsilon-1, and alpha-2 genes. The relative locations of the four
            genes were determined by Flanagan and Rabbits (Nature 300, 709-713

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              (1982)". They refer to this gene group as region B. The region A
              genes are gamma-3, gamma-1, pseudo-epsilon, alpha-1. Flanagan and
              Rabbits also determined the general locations of the two regions.
              They place region A between the JH/mu/delta region and region B.
              Complete source information:
              Human fetal liver DNA, library of T. Maniatis [3] and Lawn et al
              [2], [1]; clones p-gamma-2RPA3 [2], 5A [3], and Ig-gamma-2-15 [1].

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Best Local Similarity   99.7%;   Pred. No. 0;
Matches 1801;  Conservative  0;  Mismatches  4;  Indels  1;  Gaps  1;

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RESULT 4
AC084717

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LOCUS        AC084717              56310 bp    DNA     linear   HTG 15-JAN-2001
DEFINITION   Homo sapiens clone RP11-815P21, WORKING DRAFT SEQUENCE, 3 unordered
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ACCESSION    AC084717
VERSION      AC084717.2  GI:12229387
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE       Homo sapiens
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 56310)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE      Homo sapiens, clone RP11-815P21
  JOURNAL    Unpublished
REFERENCE    2  (bases 1 to 56310)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
             Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
             Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
             Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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             FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
             Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
             Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
             Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.,
             Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
             McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
             Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
             O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,
             Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
             Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
             Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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             Tirrell,A., Travers,M., Triglio,J., Vassiliev,H., Viel,R., Vo,A.,
             Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
             Zimmer,A. and Zody,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (08-NOV-2000) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      On Jan 15, 2001 this sequence version replaced gi:11112056.
             All repeats were identified using RepeatMasker:
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: WIBR
    Web site: http://www-seq.mit.edu
    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
    Center project name: L11499
    Center clone name: 815_P_21
------ Summary Statistics
    Sequencing vector: Plasmid; n/a; 100% of reads
    Chemistry: Dye-terminator Big Dye; 100% of reads
    Assembly program: Phrap; version 0.960731
    Consensus quality: 55130 bases at least Q40
    Consensus quality: 55883 bases at least Q30
    Consensus quality: 56050 bases at least Q20
    Insert size: 61000; agarose-fp
    Insert size: 56110; sum-of-contigs
    Quality coverage: 7.9 in Q20 bases; agarose-fp
    Quality coverage: 8.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*   1   46566: contig of 46566 bp in length
*   46567   46666: gap of   100 bp
*   46667   50756: contig of 4090 bp in length
*   50757   50856: gap of   100 bp
*   50857   56310: contig of 5454 bp in length.

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="RP11-815P21"
                     /clone_lib="RPCI-11 Human Male BAC"
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                     clone_end:T7
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BASE COUNT   13780 a   15160 c   15160 g   12010 t   200 others
ORIGIN

Query Match   78.5%; Score 1765.2; DB 2; Length 56310;
Best Local Similarity   98.9%; Pred. No. 0;
Matches 1787; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

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exon   1183..1218
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BASE COUNT   468 a   589 g   740 c   389 t   7 others
ORIGIN

Query Match   77.9%;   Score 1752.8;   DB 9;   Length 2193;
Best Local Similarity   89.2%;   Pred. No. 0;
Matches 1954; Conservative   7; Mismatches 109; Indels 120; Gaps   2;

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Db      2 AGGTSMARCTGCAGSAGTCNGGGACTGTGCTGGCAAGGCCTGGGCTTCCGTGAGGATGT 61

Qy    130 CCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTC 189
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Qy    190 CTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAAACTACA 249
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Db    122 GAGAACAACTACAAGACCACACACCTCCCATGCTGGACTCCCGACACGGCTCCCTCCTCTAC 181

Qy    250 ACCAGAAGTTAAGGGCAAGGCCCACAATGACTGTAGACAAGTCAGCAGCACAGCCTATA 309
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Db    182 CCCAGAGGTTTAAGGACAAGACAAGCCAAACTGACTGAGTCACATCAGCCCAACACTGCCTACA 241

Qy    310 TGGAACTTAGTTCTTTGAGATCTGAAGGATACGGCGTTTATTACTGTGCAA-------- 360
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Db    242 TGGAGTCTCAGCAGCCTGACAAATGAGACTCTGCGGTCTATTACTGTTCAATCATCATCTACT 301

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Db    302 TTGATTACGCCGACTTTATTATGGACTACTGGTCAAGGGACCACACGGTCACCGTCTCGA 361

Qy    415 CAGGTGAGTCCTAAAACCTCTAGAGCTTTCTGGGGCGAGCCGGAGCCTGACTTTGGCTTT 474
          ||||  ||| |  ||||||| ||||||||||| |||| |||  |||||||| ||||||||
Db    362 CAGGTGAGTGC------------------------------------------GGCC 372

Qy    475 GGGGCAGGGAGTGGGCTAAGTGAGGCAGGTGGGCCGGCCAGCCAGTGCACACCCAATGCCC 534
          ||||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||
Db    373 -------------------------------------------------------GGCC 376

Qy    535 GTGAGCCAGACACTGGACCCTGCCTGGGACCCTGGATAGACAAGAACCGAGGGGCCT 594
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Db    377 GCGAGCCAGACACTGGACCCTGCCTGGGACCCTGGATAGACAAGAACCGAGGGGCCT 436

Qy    595 CTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGTCACATGGCAGTCACATGGCGCCACCAYCTCTTGCAG 654
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Db    437 CTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGTCACATGGCAGTCACATGGCGRCCAYCTCYCTTGCAG 496

Qy    655 CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCTGTCCCGAGAGCACCTCCGAGA 714
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Db    497 CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCTGTCCCGAGAGCACCTCCGAGA 556

Qy    715 GCACACGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTCACGGTGTCGT 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 GCACACGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTCACGGTGTCGT 616
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RESULT 5
AF237584

LOCUS   AF237584   2193 bp   DNA   linear   PRI 14-MAY-2001
DEFINITION Homo sapiens recombinant IgG2 heavy chain gene, partial cds.
ACCESSION   AF237584
VERSION   AF237584.1 GI:9857754
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2193)
AUTHORS   Vidarsson,G., van der Pol,W.L., van den Elsen,J.M.H., Vile,H.,
            Jansen,M., Duijs,J., Morton,H.C., Boel,E., Daha,M.R., Corthesy,B.
            and van de Winkel,J.G.J.
TITLE   Activity of human IgG and IgA subclasses in immune defense against
            Neisseria meningitidis serogroup B
JOURNAL   J. Immunol. 166 (10), 6250-6256 (2001)
MEDLINE   21240692
PUBMED   11342648
REFERENCE   2 (bases 1 to 2193)
AUTHORS   Vidarsson,G., Jansen,M., Boel,E. and van de Winkel,J.G.J.
TITLE   Direct Submission
JOURNAL   Submitted (22-FEB-2000) Department of Immunology, University
            Medical Center Utrecht, Rm. KC.02-085.2, Lundlaan 6, Utrecht 3584
            EA, The Netherlands
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Db  24967 AGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAACCA 25026

Qy   1819 AAGGTGGGACCCCGGCGGGTATGAGGGCCACATGGACAGAGGCCGGCTGGCCCACCCTCT 1878
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Db  25027 AAGGTGGGACCCCGGCGGGTATGAGGGCCACATGGACAGAGGCCGGCTGGCCCACCCTCT 25086

Qy   1879 GCCCTGGGAGTGACGCCGGTGTGCCAACCTCTGTCCCTACAGGGCCAGCCCCGAGAACCACAG 1938
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Db  25087 GCCCTGGGAGTGACGCCGGTGTGCCAACCTCTGTCCCTACAGGGCCAGCCCCGAGAACCACAG 25146

Qy   1939 GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC 1998
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Db  25147 GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC 25206

Qy   1999 CTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG 2058
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Db  25207 CTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG 25266

Qy   2059 GAGAACAACTACAAGACCACACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTAC 2118
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Qy   2119 AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG 2178
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Db  25327 AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG 25386

Qy   2179 ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 2238
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Qy   2239 TGAGTG 2244
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Qy   1855  AGAGGCCGGCTCGGCCACCCTGCCTGGGAGTGACCGCCGCTGTGCCAACCTCTGTCCCT  1914
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Db   1697  AGAGGCCGGCTCGGCCACCCTGCCTGGGAGTGACCGCCGCTGTGCCAACCTCTGTCCCT  1756

Qy   1915  ACAGGGCAGCCCGAGAACCACAGTGTACACCTGCCCCATCCCGGGAGGAGATGACC  1974
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Db   1757  ACAGGGCAGCCCGAGAACCACAGTGTACACCTGCCCCATCCCGGGAGGAGATGACC  1816

Qy   1975  AAGAACCAGGTCAGCCTGACCTGCCTGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG  2034
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Db   1817  AAGAACCAGGTCAGCCTGACCTGCCTGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG  1876

Qy   2035  GAGTGGGAGAGCAATGGCCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGAC  2094
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Db   1877  GAGTGGGAGAGCAATGGCCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGAC  1936

Qy   2095  TCCGACGGCTCCTTCCTTCACAGCAAGCTGACAAGAGCAGGTGGCAGCAG  2154
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Db   1937  TCCGACGGCTCCTTCCTTCACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG  1996

Qy   2155  GGGAACGTCTTCATGTCCGTGATGAGGCTCTGCACAACTACACGCAGAAG  2214
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Db   1997  GGGAACGTCTTCATGTCCGTGATGAGGCTCTGCACAACTACACGCAGAAG  2056

Qy   2215  AGCCTCTCCCTGCCCCGGGTAAATGAGTG  2244
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Db   2057  AGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2086
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RESULT 6
AR029004

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LOCUS       AR029004                2287 bp    DNA    linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5858983.
ACCESSION   AR029004
VERSION     AR029004.1  GI:5940977
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2287)
  AUTHORS   Seed,B. and Walz,G.
  TITLE     Inhibition of cell adhesion protein-carbohydrate interactions
  JOURNAL   Patent: US 5858983-A 1 12-JAN-1999;
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ORIGIN
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Query Match   73.4%; Score 1651.6; DB 6; Length 2287;
Best Local Similarity   87.2%; Pred. No. 3e-311;
Matches 1998; Conservative   0; Mismatches 219; Indels 75; Gaps 14;

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Db      7  ACCACCATGGACTGGACCTGGAGGGTTCCTCTTCTTTGTCGTGGCAGCTACAGGTGTC  66

Qy     63  CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG  122
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Db     67  CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCCGGTG  126

Qy    123  AAGGTGTCCTGCAAAGCTTCCGGCTACACCTTCACTGATTATGCTATACAGTGGGTGAGA  182
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Db    127  AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA  186

Qy    183  CAGGCTCCTGGACAGGGGCCTGAGTGGATGGGATTATTATTACTATGATAATACCA  242
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Db    187  CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTATAATGGTAACACA  246

Qy    243  AACTACAACCAGAAGTTTAAGGGCAGGCCACAATGACTGTAGACAAGTCACGAGCACA  302
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Qy    775  GGAACTCAGGCGCTGCTGAGCAGGGGCTGCACACCTTCCCAGCTGTCCTACAGTCCTCAG  834
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Db    617  GGAACTCAGGCGCTGCTGAGCAGGGGCTGCACACCTTCCCAGCTGTCCTACAGTCCTCAG  676

Qy    835  GACTCTACTCCCTCCTTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCT  894
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Db    677  GACTCTACTCCCTCCTTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCT  736

Qy    895  ACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGA  954
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Db    737  ACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGA  796

Qy    955  GGCCAGCTCAGGAGGAGGGGTGTCTGCTGGAAGCTCAGCCTCAGCCTCCTGCGACG  1014
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Db    797  GGCCAGCTCAGGAGGAGGGGTGTCTGCTGGAAGCCAGGCTCAGCCTCCTGCCTGACG  856

Qy   1015  CACCCCGCGTGTGCAGCCCCAGCGAGCAGCAGCAGCAGCCCCATCGTGTCTCCTCACC  1074
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Db    857  CACCCCGTGTGCAGCCCCAGCGAGCAGCAGCAGCAGCCCCATCGTGTCTCCTCACC  916

Qy   1075  CGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCA  1134
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Db    917  CGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCA  976

Qy   1135  GGCTCCAGGCAGGCAACGGGTCGGTGCCCTCACCCCCAGGCCCTTCACACAGGGGCAGG  1194
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Db    977  GGCTCCAGGCAGGCAACGGGTCGGTGCCCTCACCCCCAGGCCCTTCACACAGGGGCAGG  1036

Qy   1195  TGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCCTGCCCCTGACCTAAGCCG  1254
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Qy   1255  ACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCTCCCAGATCCG  1314
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Qy   1315  AGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTGTGTCGAGTGCCCACCGTGCCC  1374
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Db   1157  AGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCC  1216

Qy   1375  AGGTAAGCCAGCCAGGCCCTCGCCCTTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGC  1434
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Qy   1435  CTGCATCCAGGGACAGGCCCAGCTGGGTGCTGACACGTGCACCTCACCTCCTCTTCCTCAG  1494
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Db   1277  CTGCATCCAGGGACAGGCCCAGCTGGGTGCTGACAGTCCACCTCACCTCCTCTTCCTCAG  1336

Qy   1495  CACCACCTGCGCGCAGCAGCCGTCAGTCTTCTCCCCTCCCCCAAAAACCAAGGACACCCTCA  1554
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Qy   1555  TGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCG  1614
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Db   1397  TGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCG  1456

Qy   1615  AGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCAC  1674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1457  AGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCAC  1516

Qy   1675  GGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGG  1734
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Db   1517  GGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGG  1576

Qy   1735  ACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCA  1794
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Qy   1795  TCGAGAAAACCATCTCCAAAAACCAAAGGTGGGACCCGCGGGTATGAGGGCCACATGGAC  1854
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Qy    303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA 362
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Db    307 GCCTACATGGAGCTGAGCAGCCTGAGCAGCACGGCCCGTGTATTACTGTGCGAGA 366

Qy    363 GCCG------------------------------CCTGGTATATGGACTACTGGGGT 389
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Db    367 GATAATGAGCGGGTATTGTAGTGGTGTAGTGGTTCGGGGCTGGTCGACCCCTGGGGC 426

Qy    390 CAAGGTACCCCTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
          ||  ||||||||||||||||||||||||||| | ||||||||  ||
Db    427 CAGGGAACCCCTGTCACCGTCTCTTCAGGTGAGTACTGAATTCT----AGCTTTCTGGG 481

Qy    450 GCGAGCCGGGCCGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGCTAAGGTGAGGCAGGTGGCG 509
          ||  | || ||||| | |||  ||||||||||||||||
Db    482 GCAGGCCCAGCGGCCTTGGCCTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 541

Qy    510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCGTGGACCCTGCCTGGACCCCTCG 569
          ||||||||||||||||| |||||||||
Db    542 CCAG-CAGTGCACACCCAATGCCCAGACACTGGACGCGCT-----GAACCTCG 595

Qy    570 TGGATAGACAAGAACCGAGGGGCCCTTGTCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
          ||||||||||||||||||||||||||||
Db    596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGGCCCAGCTCTGTCCCACACCGCGG 654

Qy    630 TCACATGGCACCACCTCTTGCAGCCTCCACCAGGGCCCATGGGCGTCTTCCCCTGGCG 689
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Db    655 TCACATGGCACCACCTCTTGCAGCCCTTCCACCAGGGCCCATGGGCGTCTTCCCCTGGCA 714

Qy    690 CCCTGCTCCAGGAGCACCTCCAGAGCACAGCCGGTGCGTGTCTGGAACTCAGGACTAC 749
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Db    715 CCCTGCTCCTCCAAAGAGCACCTCTGGGGACAGCAGCCGGTGCGTGTCTGGAACTCAGGACTAC 774

Qy    750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
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Db    775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy    810 TTCCCAGCTGTCTCTACAGTCCTCAGGACTCTACTCCTCCCTCAGCAGCGTGGTGACCGTGCCC 869
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Db    835 TTCCCGGCTGTCTCTACAGTCCTCAGGACTCTACTCCTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy    870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
          |||||||||||||||||||
Db    895 TCCAGCAGTCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy    930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTGCTGGAAGC 989
          ||||||||||||||||||||||||||||
Db    955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTGCTGGAAG- 1013

Qy    990 CAGGCTCAGCGCCCCTGCCTGGACGCGCACCCCGGTGCACCCCGGCTATGCAGCCCGACTCC 1049
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Db   1014 CAGGCTCAGCGCCCTGCCTGGACGCACCCCCGGCTATGCAGCCCGACTCC 1073

Qy   1050 GGCAGGCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCGCCCCACTCATGCTCAGGGA 1109
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Db   1074 GGCAGGCCCGTCTGCCTCTGCCCCGGA-GCCTCTGCCGCCCCCACTCATGCTCAGGGA 1132

Qy   1110 GAGGGTCTTCTGGCTTTTTTTGCCACCAGGCTCCAGGCAGGCACCAGGCTCGGTGCCCTACCC 1169
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Db   1133 GAGGGTCTTCTGCTTTTTC---CCAGGCTCTGGGCAGGCACAGCTAGGTGCCCCTAACC 1190

Qy   1170 CAGGGCCCTCACACACAGGGGCAGGTGCTGCTTGGCTCAGACCCTGCCAAAAGCCATATCCGGG 1229
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Db   1191 CAGGGCCCTGCACACAAAGGGGCAGGTGCTGGCTCAGCCCTGCCAAGACCATATCCGGG 1250

Qy   1230 AGGACCCCTGCCCCTGACCTAAGCCGACACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
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Db   1251 AGGACCCCTGCCCCTGACCTAAGCCCAAACTCCCACTCCCTCAGCTCG 1310

Qy   1290 GACACCTTCTCTCCTCCCAGAATCGAGTAACTCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
          |||||||||||||||||||||
Db   1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370

Qy   1350 GTTGTGTCGA-------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
          |||| | |
Db   1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy   1401 CCAGCTCAAGGCGGGACCAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
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Db   1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy   1461 GGTGCTGACACGTCCACCTCCATCTTCCTCAGCACC----ACCTGCGGCAGCACCGTCA 1517
          |||||||||||| | | ||||||||
Db   1491 GGTGCTGACAGTCCACCTCCATCTCTCCTCAGCACCGTCA-----ACCTCTGGGGGACCGTCA 1550

Qy   1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577
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Db   1551 GTCTTCCTCT-----AGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGGCCTGGGGAC 1605

Qy   1578 ACGTGCGT-----GGTGGTGACGTGAGCGACGACGAGACCCGAGGTCCAGTTCAACTGGT 1632
          |||||||
Db   1606 TCCAGTGTACGCACCTGGTGACGTGAGCGACGAGACCCTGAGTTCAAGTTCAACTGGT 1665

Qy   1633 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACA 1692
          |||||||||||||||||||||
Db   1666 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 1725

Qy   1693 GCACGTTCCGTGTGGTGAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG 1752
          |||||||||||||||||||||||
Db   1726 GCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 1785

Qy   1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1812
          |||||||||||||||||||||||
Db   1786 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1845

Qy   1813 AAACCAAAGGTGGACCCGCGGGGTATGAGGGTGCCACTGACAGCAGACGCCGGCTCCGAGAA 1872
          |||||||||||||||||||||||
Db   1846 AAGCCAAAGGTGGACCCGTGGGGTGCGAGGGTGCCACTGACAGCAGACGAGGCCGGCTCCGAGAA 1905

Qy   1873 CCCTCTGCCCCTGGAGTGACCGCTGTCCAACCTCTGTCCTCACAGGGCAGCCCCGAGCTGCTG 1932
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Db   1906 CCCTCTGCCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAA 1964

Qy   1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGATGACCTCAAGAACCAAGGTCAGCCTG 1992
          |||||||||||||||||||||
Db   1965 CCACAGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTG 2024

Qy   1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2052
          |||||||||||||||||||||||
Db   2025 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084

Qy   2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112
          |||||||||||||||||||||||
Db   2085 CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC 2144

Qy   2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
          |||||||||||||||||||||||
Db   2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2204

Qy   2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG 2232
          |||||||||||||||||||||||
Db   2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG 2264

Qy   2233 GGTAAATGAGTG 2244
          |||||||||||
Db   2265 GGTAAATGAGTG 2276
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RESULT 7
AR037308

LOCUS   AR037308   2287 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5801044.
ACCESSION   AR037308
VERSION   AR037308.1 GI:5955164
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.

REFERENCE   1 (bases 1 to 2287)
AUTHORS   Seed,B. and Walz,G.
TITLE   Nucleic acid encoding an antibody that inhibits cell adhesion
             protein-carbohydrate interactions
JOURNAL   Patent: US 5801044-A 1 01-SEP-1998;
FEATURES   Location/Qualifiers
source   1..2287
             /organism="unknown"
BASE COUNT   478 a   739 c   667 g   403 t
ORIGIN

Query Match   73.4%;   Score 1651.6; DB 6; Length 2287;
Best Local Similarity   87.2%;   Pred. No. 3e-311;
Matches 1998; Conservative   0; Mismatches 219; Indels 75; Gaps 14;

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Qy      6 ACCACCATGGGTTGGAACTGTA--TCATCTTCTTGTGGTTACCACAGCTACAGGTGTG     62
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Db      7 ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTCGTGGTGGCAGCTACAGGTGTC     66

Qy     63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG    122
            ||||||||||||||||||||||||  |||||| || |||  || || |||
Db     67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG    126

Qy    123 AAGGTGTCCTGCAAAGCTTCCGGCTACACCATTCACTGATTATGCTATACAGTGGGTGAGA    182
            ||||||||||||||||||||||||  ||||||||| ||||||||||||||| |||
Db    127 AAGGTCTCCTGCAAGGGTTCTGGATACACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA    186

Qy    183 CAGGCTCCTGGACAGGGGCCTGAGTGGATGGATTGGAGTGTTATTAATATTACTGATAATACA    242
            ||||||||||||||||||||||  |||||| |||  |||||  ||||||||||||||||
Db    187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCCATCTTTGGTACAGCA    246

Qy    243 AACTACAACCAGAAGTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGACGACA    302
            ||||| |||||||||  |||||||| ||| | ||||| |||||||||||||||||||||
Db    247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACACCTCCACGAGCACA    306

Qy    303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA    362
            |||||| |||| |   |||| ||||||||||||||||||||||||||||||||||||||
Db    307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA    366

Qy    363 GCCG-----------------------CCTGGTATATGGACTACTGGGGT          389
                                        |||||||||||||| |||||||
Db    367 GATAATGGAGCGATTGTAGTGGTAGCTGCTGCTACTGGGGTTCGACCCCTGGGGGC     426

Qy    390 CAAGGTACCCTGTCACCGTCTCCTCAGTGAGTCCTTAAACCTCTAGAGCTTTCTGGG    449
            ||||||| |||||| |||||||||||  |||| ||||||||   |||
Db    427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTCTGAGAATCT-----AGCTTTCTGGG     481

Qy    450 GCGAGCCCGGGCCTGACTTTGGCTTTGGGGCAGGTGGGCTTGAGGGCAGGTGGCG    509
            ||||| |||||||||||||||||  |||||||| ||||| |||
Db    482 GCAGGCCCAGGGCCTGACTTTGGCTTTGGGGCAGGGGCTTAAGGTGGCAGGTGGCG     541

Qy    510 CCAGCCAGTGCACACCAAATGCCGTGAGCCGTGAGAGCACTGGACCCTCG    569
            ||||| ||| ||| |||||||||||||||||||||||||||||| |||
Db    542 CCAG-CAGGTGCACACCAACTGCCCATGAGCCCATGAGGGGCTCAGACCCTCG-----GAACCTTCG     595

Qy    570 TGGATAGACAAGAACCGAGGGGCGTGTCGTGACGGTGTCTGACCACGCCTCGTCCCCACCGCGG    629
            ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||||
Db    596 CGGACAGTTAAGAACCCAGGGGCCTGCTGCG--CCTGGGGGCCCAGCTCTGTCCCACCACCGCGG     654

Qy    630 TCACATGGCACCACCCTCTTGCAGCCTTCCAGGCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG    689
            ||||| || ||| ||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db    655 TCACATGGCACCACCTCTTCTTGCAGCCTTCCAGGCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA     714

Qy    690 CCCTGCTCCAGGAGCACTCCAGGAGACGCAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC    749
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC     774

Qy    750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTGTCGTGACCAGCGGCGTGCACACC    809
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC     834

Qy    810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC    869
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC     894

Qy    870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC    929
            ||||||||||||||||| |||||||||||||| |||||||  |||||||||| ||||||
Db    895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC     954

Qy    930 AAGGTGGACAAGACAGTTGGTGAGAGGCAGTCAGCTCAGGAGGAGGGTGTCTGCTGGAAGC    989
            ||||||||||||| |  |||||||||||| |||||||||||||||||||||||||||||
Db    955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGCGGCCCAGCACCGGCCCAGCGACGCA    1013

Qy    990 CAGGCTCAGCCCTTCCTGCACCCTGTGCGACGCACCCGGCTGTGCAGCCCAGGGCAGCAA   1049
            |||||||||||||  ||| |||||||||||||||||||||||||||| ||||||| |||
Db   1014 CAGGCTCAGCGCTCGCTGCCGGCGACGTATCCGGCTGTCAGCCCATCCCCGGGAGCAA    1073

Qy   1050 GGGAGGCCCCATCGTCTGTCCCTCACCCCGAGGAGGCTCTGCGCCGCCCCCCACTCATGCTCAGGGA   1109
            ||||||||||||||||||||||||| |||||||| ||||||||||||||||| ||||||
Db   1074 GGGCAGGCCCCGTCTGCCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA    1132

Qy   1110 GAGGGTCTTCTGGCTTTTCCACCAGGCTCCAGGCTGAGGAGGAGCCTCAGTGTCCCCTACCC   1169
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Db   1133 GAGGGTCTTCTGGCTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC    1190

Qy   1170 CAGGCCCTTCACACACAGGGGCAGGTGCTGCTGGCTGCAGCCTGCAAAAGCCCATATCCGGG   1229
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Db   1191 CAGGCCCCTGCACAACACAAAGGGGCAGGTGCTGGGCTGCAGCCTGCAAGAGCCATATCCGGG    1250

Qy   1230 AGACCCTGCCCCTGACCTAAGCCAACCCCCAAAGGCCAAACTGTCCACTCCCTCAGCCTCG   1289
            ||||||||| |||| ||| || |  || || || |  | |||||||||| || ||||||||
Db   1251 AGACCCTGCCCCTGACCTAAGCCCAACCCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG    1310

Qy   1290 GACACCTTCTCTCCTCCATCCAGTATGACCAATCTCGGTAACTCCAATCTCTCTGAGCGGCAAAT   1349
            |||||||||||||||||||||||| |||||| ||||||| ||||||||||  |||| |||||
Db   1311 GACACCTTCTCTCCTCCCAGTTCCAGTACCCCAGATTCCAGTAACTCCAATCCCAATCCCAAAT    1370

Qy   1350 GTTGTGTCGA--------GTGCCACCGTGCCAGGTAAGCCAGGGCCTCGCCCT   1400
            |||||||| |        ||||||||||||| ||||||||||||||| |||||
Db   1371 CTTGTGCACAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGGCCTCGCCCT    1430

Qy   1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG   1460
            ||||||||||||||||||||||| |||| ||| |||||||||| ||||||||||||||||
Db   1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG    1490

Qy   1461 GGTGCTGACACGTCCACTTCCATCTCCTCAGCACC---ACCTGCGGCCAGCACCGTCA   1517
            ||| ||||||| ||||| ||| ||| ||||||||||   |||||| |||||| ||||||
Db   1491 GGTGCTGACACGTCCACCTCCCATCTCTTCAGCACTCTTCAGCACC    1550

Qy   1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTTCCCGACCCCTGAGGTC   1577
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Db   1551 GTCTTCCTCTTCCCTCCTTC-----AGGGGGTTTTGGTTCCTGTGTGGGTACTAGTACGGGGGAC    1605

Qy   1578 ACGTGCGT-------GGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT   1632
            ||||||||       ||| ||||| ||||||||||||||||||||||| ||||||||||
Db   1606 TCCAGTGTACGCACCTGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT    1665

Qy   1633 ACGTGGACGGCGTGGAGGTGCATAATGCAAGACAAAGCCACCGGGAGGAGCAGTTCAACA   1692
            ||||||||||||||||||||||||||||| ||||||  | ||||||||||||||||||||
Db   1666 ACGTGGACGGCGTGGAGGTGCATAATGCAAGACAAAGCCGCGGGAGGAGCAGTACAACA    1725

Qy   1693 GCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG   1752
            ||||| || |||||| ||||| |||||||| |||||| ||||||||||||||||||||||
Db   1726 GCACGTTCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG-    1785

Qy   1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA   1812
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Db   1786 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA    1845

Qy   1813 AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACACCGGGGTCTCGGGCCCA   1872
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Db   1846 AAGCCAAAGGTGGGACCCGCGGGGTGCGAGGGCCACACCGGGGTCTCGGGCCCA    1905

Qy   1873 CCCTTCGCCTGCTCGGGAGTCATCCCTGTGCTCCTACTCCCTGTCTCCAGCAGCGGTGACCTGCCC   1932
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Db   1873 ... 
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Db  1906  CCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAA 1964
                ||||||||||||||||||||||||||||||||| |||  ||||||||||||||||||
Qy  1933  CCACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCAGTCAGCCTG 1992
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1965  CCACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGTGCAGTGAGCTGAAGAGCCTG 2024

Qy  1993  ACCTGCCTGGTCAAAGGCTTCTACCCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2052
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Db  2025  ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084

Qy  2053  CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTC 2112
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Db  2085  CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC 2144

Qy  2113  CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
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Db  2145  CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2204

Qy  2173  TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG 2232
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2205  TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG 2264

Qy  2233  GGTAAAATGAGTG 2244
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Db  2265  GGTAAAATGAGTG 2276
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RESULT 8
BD000539

LOCUS   BD000539   2287 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION Antibody capable of being used for inhibition of interaction
            between cell adhesion protein and sugar ligand.
ACCESSION   BD000539
VERSION   BD000539.1 GI:18623652
KEYWORDS   JP 2000325092-A/1.
SOURCE   unidentified.
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 2287)
  AUTHORS   Brian,S. and Gard,W.
  TITLE   Antibody capable of being used for inhibition of interaction
            between cell adhesion protein and sugar ligand
  JOURNAL   Patent: JP 2000325092-A 1 28-NOV-2000;
            THE GENERAL HOSPITAL CORP
COMMENT   OS   Unidentified
            PN   JP 2000325092-A/1
            PD   28-NOV-2000
            PF   04-APR-2000 JP 2000102880
            PR   23-NOV-1990 US   07/618314
            PI   SHEED BRIAN,WARTZ GARD
            PC   C12N15/09,A61K39/395,A61P9/10,A61P17/06,A61P29/00,A61P29/00,
            PC   A61P43/00,
            PC   C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10,G01N33/53, PC
            C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key   Location/Qualifiers
            FT   source   1..2287
FEATURES   Location/Qualifiers
     source   1..2287
                     /organism="unidentified"
                     /organism='Unidentified'.
                     /db_xref="taxon:32644"
BASE COUNT   478 a   739 c   667 g   403 t
ORIGIN

Query Match   73.4%;   Score 1651.6; DB 6; Length 2287;
Best Local Similarity 87.2%; Pred. No. 3e-311;
Matches 1998; Conservative   0; Mismatches 219;   Indels 75; Gaps 14;

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Qy  6  ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACCAGGTACAGTGTG 62
              |||||||||||||||||||||     |||||||||||||||||||||||||||||||||
Db  7  ACCACCATGGACTGGACCTGGAGGGTCTTCTTTCTTCTTGTTGGTGGCAGCAGTACAGGTGTC 66
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The right column sequence alignment block (Qy/Db pairs, positions 63–1132):

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Qy   63  CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
               |||||||||||||||||||| ||| |||||| ||||||||||||   ||
Db   67  CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCCGGTG 126

Qy  123  AAGGTGTCCTGCAAAGCTTCCGGTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
               ||||||||||||||||||||| |||||||||||| |  |   ||
Db  127  AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy  183  CAGGCCTCTGGACAGGGCCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
               ||||||||||||||||||||| |||||||||||| ||  || |  ||
Db  187  CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCA 246

Qy  243  AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCAAGTGCAGCACA 302
               |||||| ||| ||  || |||| |||| |||   ||
Db  247  AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACAGAGCACA 306

Qy  303  GCCTATATGGAACTTAGTTCTTGAGATCTGAGACTGAGGATACGGCCGTTATTACTGTGCAAGA 362
               |||   |||||  | |  ||||| ||| ||||||
Db  307  GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 366

Qy  363  GCGG----------------------------------CCTGGTATATGGACTACTGGGGT 389
               ||||                                  ||     || |
Db  367  GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTTTGTGTACTCGGGTCGTTCGACCCCTGGGGC 426

Qy  390  CAAGGTACCCTGGTCACCGTCTCCTCAGGTGAGTCTTAAAACCTCTAAAACCTCTGAGTACTGAATTCT---- 449
               |||| ||||| ||| |||| |||| |||| ||||||     |||||
Db  427  CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT----AGCTTTCTGGG 481

Qy  450  GCGAGCCGGGCCTGACTTTGGCTTTGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
               |||||||||||||||||| ||||||||||||||||||
Db  482  GCAGGCCAGGGTGCACCTTGGCTTTGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 541

Qy  510  CCAGCCAGTGCACACCCCCAGAGCAGCTGACCCTGCTCGGGCCCTGGACCCTG 569
               |||||||| ||||||||||| ||||||||||  |
Db  542  CCAG-CAGGTGCACCACCAGACCCCAGAGACACTGGACGCT----GAACCTCG 595

Qy  570  TGGATAGACAAGAACCGAGGGGCCTCTGGGCCCAGTCTCGTCTCCACACCGCGG 629
               ||| ||| ||    || |||||  |
Db  596  CGGACAGTTAAGAACCCAGGGCCCTGCG--CCTCGGCCCCAGCTCTGTCCCACACCGCGG 654

Qy  630  TCACATGGCACCACCTCTTGCAGCTCAGAGGGCCATCGGTCTTCCCCCTGGCG 689
               |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  655  TCACATGGCACCACCTCTTGCAGCTCAGAGGGCCATCGGTCTTCCCCCTGGCA 714

Qy  690  CCCTGCTCCAGGAGCACCTCCAGAGCACAGCGGCCCTGGGCTGCGTTGAGCAGCGGCGTGCACACC 749
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  715  CCCTCCTCCAAGAGCACCTCCGGGGCACACTGGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy  750  TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTTCGACCAGCGGCGTGCACACC 809
               ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  775  TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy  810  TTCCCAGCTGTCCTACAGTCTCAGGACTTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  835  TTCCCGGCTGTCCTACAGTCTCAGGACTCCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy  870  TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
               |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  895  TCCAGCAGCTTGGGCACCCAGACCTACACCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy  930  AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGGAAGC 989
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Db  955  AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGGGAAG- 1013

Qy  990  CAGGCTCAGCGCTCCTGCCTGGACGCCACCCCGGCTGTGAGCGCCAGGGCAGCAA 1049
               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  1014 CAGGCTCAGCGCTCCTGCCTGGACCATCCCGGCTTGAGCGCCCCAGTCCAGGGCAGCAA 1073

Qy  1050 GGCAGGCCCCATCGTGTCTGCCTGCCTGCTTCACCCGGAGGCCTCTGCCCGCCCCCACTCATGCTCAGGGA 1109
               |||||||||||||||||| |||| ||||||||||||||||| ||||
Db  1074 GGCAGCGCCCCGTCCTGGCACCTGGACTGACCTGGAGGGTCCCCACTCCACTCATGCTCAGGGA 1132
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Db   2205 TCCTGATGCATGAGGCTCTGCACAACCACTACACGCGCAGAGAGAGCCCTCCCTGTCTCCG 2264
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||

Qy   2233 GGTAAATGAGTG 2244

Db   2265 GGTAAATGAGTG 2276


RESULT 9
I90051
LOCUS       I90051                  2287 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 1 from patent US 5723583.
ACCESSION   I90051
VERSION     I90051.1  GI:3409991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2287)
  AUTHORS   Seed,B. and Walz,G.
  TITLE     Antibody containing sialyl lewis X determinants
  JOURNAL   Patent: US 5723583-A 1 03-MAR-1998;
FEATURES             Location/Qualifiers
     source          1..2287
                     /organism="unknown"
BASE COUNT      478 a    739 c    667 g    403 t
ORIGIN

Query Match             73.4%;  Score 1651.6;  DB 6;  Length 2287;
Best Local Similarity   87.2%;  Pred. No. 3e-311;
Matches 1998;  Conservative    0;  Mismatches 219;  Indels   75;  Gaps   14;

Qy      6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTCTTCTTCGTTACCACAGCTACAGGTGTG 62
          |||||||||||||||||||||| |  ||||||| |||||| |||||| ||||||||||||||
Db      7 ACCACCATGGGTTGGAACTGTGAGGTTCATCTTCTTCTTGTGTGGTGGCAGCAGACAGGTGTC 66

Qy     63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
          |||||| |||||||||||||||||||||||| |||||||||||||| ||||||||||||
Db     67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCTTCGGTG 126

Qy    123 AAGGTGTCCTGCAAAGCTTCGGTACACATTCACTGTTATACAGTGGTGGTGAGA 182
          |||||||||||||| |||||||||||||||| |||||||||||||||| |||||
Db    127 AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy    183 CAGGCTCCTGGACAGGGCCTCGAGTGGTTAATGGAGTTATTGGTGATAATACA 242
          |||||| |||||||||||||||||||||| |||| ||||||||| |||||| |
Db    187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCCTATCTTTGGTACAGCA 246

Qy    243 AACTACACCAGAAGTTAAGGGCAAGCAAATGACTGTGACAAGTCGACGAGCACA 302
          |||| || | ||||| |||| ||||||||| |||||||||||||||||||||
Db    247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGGCGAATCCACGAGCACA 306

Qy    303 GCCTATATGGAACTTAGTTCTTGAGATCTGAAGA 362
          |||||||| || |||| ||||| |||||||||||
Db    307 GCCTACATGGAGCTGAGCAGCCTGACATCTGAGGA 366

Qy    363 GCCG----------------------CCTGTATATGACTACTGGGGT 389
          ||||                      |||||||||||||||||||
Db    367 GATAATGGAGTATTGTAGTGGTGGTAGCCGTCCTACTGGTACTGCAGCA 426

Qy    390 CAAGGTACCCTTGTCACCGTCTCCTCAGGGTGAGCTTCCTAAAACCTCTGG 449
          |||||||||||||||||||||||||| ||| ||||| |||||||||||
Db    427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT---AGCTTTCTGG 481

Qy    450 GCGAGCCGGCCTGGACTTTGGCTTGGGCAGGTGAGGTGGGCTAAGGTGAGGCAGGTGGCG 509
          |||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||
Db    482 GCAGGCCAGGCCTGGACTTTGGCTTGGGCAGGTGAGGTGGGCTAAGGTGAGGCAGGTGGCG 541

Qy    510 CCTACAGCTGCACCCAAATGCCCGTGACACTGGACGTCTTCTCATGC 569
          |||| ||| ||| |||||||||||||||||||||||||||||||||
Db    542 CCTACAGCTGCACCCAAATGCCCAATGCCATGAGCCCAGACACTGGACGCT-----GAACCTCG 595

Qy    570 TGGATAGACAAGAACCGAGGGGCCTCTGCAACCACTACACGCAGAGAGAGCCTCTGCCCACCACCGCGG 629
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RESULT 10
AX088865

LOCUS   AX088865   4694 bp   DNA   linear   PAT 17-MAR-2001
DEFINITION   Sequence 41 from Patent WO0114424.
ACCESSION   AX088865
VERSION   AX088865.1 GI:13337636
KEYWORDS
SOURCE   synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1 (bases 1 to 4694)
  AUTHORS   Korman,A.J., Halk,E.L. and Lonberg,N.
  TITLE   Human ctla-4 antibodies and their uses
  JOURNAL   Patent: WO 0114424-A 41 01-MAR-2001;
             MEDAREX, INC. (US)
FEATURES   Location/Qualifiers
     source   1..4694
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="gamma4 heavy chain plasmid pG4HE"
BASE COUNT   1068 a   1396 c   1248 g   982 t
ORIGIN

Query Match   72.8%;   Score 1638;   DB 6;   Length 4694;
Best Local Similarity 94.6%;   Pred. No. 1.2e-308;
Matches 1719;   Conservative 0;   Mismatches 95;   Indels 4;   Gaps 2;

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Qy   490  CTAAGGTGAGGCAGGTGGCGCGCAGCCAGTGCACACCCAATGCCCGTGAGCCCAGACACT  549
          |||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db    67  CTAAGGTGACGCAGGTGGCGCGCAGCCAGTGCACACCCAATGCCCAATGAGCCCAGACACT  126

Qy   550  GGACCCTGCCTGTGACCCTGGTGATAGACAAGAACCGAGGGGCGGGCCTTGCGCCCTGGGCC  609
          |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db   127  GGACCCTGCCTGTGACCATGGCGATAGACAAGAACCGAGTGGGGCCTTGCGCTGCCCTGGGCC  186

Qy   610  AGCTCTGTCCCACACCGCGGTCACATGGCACCACCCTCTTGCAGCCTCCACCAAGGGCC  669
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   187  AGTCTGTCCCACACCGCGGTCACCGGGTCACCATGCCACCACCCTCTTGCAGCCTCCACCAAGGGCC  246

Qy   670  CATCGGTCTTCCCCCTGGCCCTGCTCCAGGAGCACTCCGAGAGCACAGCGGCCCTG  729
          |||||||||||||||||||||||||||||||||||||||||||||
Db   247  CATCCGTCTTCCCCCTGGCCCCTGCTCCAGGAGCACTCCGAGAGCACAGCGCCCTG  306

Qy   730  GCTGCCTCAAGGACTACTTCCCCGAACCGGTGTGTGGAACTCAGGCCGTC  789
          ||||||||||||||||||||||||  |||||||||||||||||||||||
Db   307  GCTGCCTCAAGGACTACTTCCCCGAACCGGTGTGTGGAACTCAGGCCGTC  366

Qy   790  TGACCAGGCGGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGACTCTACTCCCTCA  849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   367  TGACCAGGCGGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGACTCTACTCCCTCA  426

Qy   850  GCAGGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG  909
          ||| ||||||||||||||||||||||||||||||||||||||||||
Db   427  GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGCAGACCTACACCTGCAACGTAG  486

Qy   910  ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGTTGGTGACAGAGGCCAGTCAGGGAG  969
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   487  ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCAGGGAG  546

Qy   970  GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGGACGCACCCCGGCTGTGCA  1029
          |||||||||||||||||||||||||||||||||||||||||||
Db   547  GGAGGGGTTGTCTGCTGGAAGCCAGGCTCAGCGCCCTGCCCTGGACGCACCCCGGCTGTGCA  606

Qy  1030  GCCCCAGCCCAGGGCAGCAGGCAGGCCCCATCGTGCTTCCTCCTCCCAGAGCCTCTGCCC  1089
          ||||||||||||||||||||  |||||||||||||||||||||||||
Db   607  GCCCCAGCCCAGGGCAGCAAGGCATGCCCCATCGTGCTTCCTCCTCCCAGAGCCTCTGACC  666

Qy  1090  GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGCTTTTTTCCACCAGGCTCCAGGCAGGCA  1149
          |||||||||||||||||||||||||  ||||||||||||||||
Db   667  ACCCCACTCATGCTCAGGGAGAGGGTCTTCTGATTTTTTCCACCAGGCTCCGGGCAGCCA  726

Qy  1150  CAGGGCTGGGTGCCCCTACCCCAGGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC  1209
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   727  CAGGGCTGAGTGCCCCTACCCCAGGGCCCTGCACATACAGGGGCAGGTGCTTGGCTCAGACC  786

Qy  1210  TGCCAAAAGCCATATCCGGGGAGGACCCTGCCCCTGACCTAAGGCCACCCCAAAGGCCAAA  1269
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   787  TGCCAAGAGCCATATCCGGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA  846

Qy  1270  CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTTCACTCCAATCT  1329
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Db   847  CTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTTCACTCCAATCT  906

Qy  1330  TCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCA  1389
          |||||||||||||||||  ||||||||||||||||||||||||||||
Db   907  TCTCTCTGCAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAGCCCA  966

Qy  1390  GGGCCTCGCCCCTGGAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA  1449
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   967  GGCCTCGCCCCTGCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA  1026

Qy  1450  GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCCTCTTCCTCAGCACC--ACCTGCGG  1506
          ||||||||||||||||||||  ||||||||||||||||||||||  |||||||
Db  1027  GGCCCCAGCCCGGGGTGACGGGGTGCTGACCATCCCATCCTCTTCCTCAGCACCTGAGTTCCTGG  1086

Qy  1507  CAGCACCGTCAGTTCTTCCTCTTCCCCTCCGTTGTTCCCCCCAAAAACCCACCCTCATGATCTCCCGGA  1566
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1087  GGGGACCATCAGTCTTCCTCTTCCCCCTCCGTTGTTCCCCCCAAAAACCCAAGGACCCTCATGATCTCCCGGA  1146
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(second column)

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Qy  1567  CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA  1626
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Db  1147  CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA  1206

Qy  1627  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGAGGAGCAGT  1686
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Db  1207  ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  1266

Qy  1687  TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG  1746
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  1267  TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG  1326

Qy  1747  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA  1806
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  1327  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCGTCCCATCGAGAAAAACA  1386

Qy  1807  TCTCCAAAAACCAAAGGTGGGACCCGGGGGTGATGAGGGCCACATGGACAGAGGCCGGCTC  1866
          ||||||||||||||||||||||||||||||||||||||||||
Db  1387  TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACATGGACAGAGGCCAGCTC  1446

Qy  1867  GGCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCCAGCCC  1926
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Db  1447  GGCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCCAGCCC  1506

Qy  1927  CGAGAACCACAGCGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC  1986
          |||||||||||||||||||||||||||||||||||||||||||||
Db  1507  CGAGAGCCACAGGCCACAGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC  1566

Qy  1987  AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC  2046
          |||||||||||||||||||||||||||||||||||||||||||
Db  1567  AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC  1626

Qy  2047  AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC  2106
          |||||||||||||||||||||||||||||||||||||||||||||
Db  1627  AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCATGCTGGACTCCGACGGCTCC  1686

Qy  2107  TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC  2166
          |||||||||||||||||||||||||||||||||||||||||||
Db  1687  TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC  1746

Qy  2167  TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGCAGAGCCTCTCCCTG  2226
          ||||||||||||||||||||||||||||||||||||||||||||
Db  1747  TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACAGAGAAGAGCCTCTCCCTG  1806

Qy  2227  TCCCCGGGTAAATGAGTG  2244
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Db  1807  TCTCTGGGTAAATGAGTG  1824
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RESULT 11
AX478055
LOCUS        AX478055                4694 bp      DNA        linear      PAT 12-AUG-2002
DEFINITION   Sequence 3 from Patent WO0243478.
ACCESSION    AX478055
VERSION      AX478055.1    GI:22217037
KEYWORDS     .
SOURCE       synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE    1
  AUTHORS    Tomizuka,K., Ishida,I., Lonberg,N. and Halk,E.
  TITLE      Transgenic transchromosomal rodents for making human antibodies
  JOURNAL    Patent: WO 024478-A 3 06-JUN-2002;
             Medarex, Inc. (US) ; KIRIN BEER KABUSHIKI KAISHA (JP)
FEATURES             Location/Qualifiers
     source          1..4694
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Gamma4 heavy chain plasmid~pG4HE"
BASE COUNT   1068 a   1396 c   1248 g   982 t
ORIGIN

Query Match    72.8%;    Score 1638;    DB 6;    Length 4694;
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Best Local Similarity   94.6%;   Pred. No. 1.2e-308;
Matches 1719;   Conservative   0;   Mismatches   95;   Indels   4;   Gaps   2;

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Qy    430 AACCTCTAGAGCTTCTCTGGGGCGGAGCCGGCCGGCCTGACTTGGCTTTGGGGCAGGGAGTGGG 489
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Db      8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCCGGCCCGGCCTGACTTTGGC-TGGGGCAGGGAGGGGGGG 66

Qy    490 CTAAGGTGAGGCAGGTGGCGCCAGCTAGGTCGCCAGTTCGCACACCCAATGCCCGTGAGCCCAGACACT 549
          |||||||| ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     67 CTAAGGTGACGCAGGTGCGCCAGCTAGGTGCGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 126

Qy    550 GGACCCTGCCTGGACCCCTGTGATAGACAAGAACCGAGGGGCTCTGCGCCCTGGCGCC 609
          ||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    127 GGACCCTGCATGCGATAGACCGGATAGACAACAACCGAGGGGCCTCTGCGCCCTGGCGCC 186

Qy    610 AGTCTGTCCCACACCCGGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
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Db    187 AGTCTGTCCCACACCCGGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 246

Qy    670 CATCGGTCTTCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCGCCCTGG 729
          |||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||
Db    247 CATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCGCCCTGG 306

Qy    730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCGTC 789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCGCC 366

Qy    790 TGACCAGCGGCGGTGCACACCTTCCCAGCTGTCCTACAGTCTCCAGGACTCTTCACTCCCTCA 849
          ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Db    367 TGACCAGCGGCGGTGCACACCTTCCCGGCTGTCCTACAGTCTCCAGGACTCTTCACTCCCTCA 426

Qy    850 GCAGCGGTGGTGACCGTGCCCTCAGCAACTTCGGCACCCAGACCTACACGTGCAACGTAG 909
          ||||||||||||||||||||||||||||| | ||||| |||||||||||||||||||||||
Db    427 GCAGCGGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACGTGCAACGTAG 486

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Db    547 GGAGGGTGTCTGCTGGTGGAGGCCAGGCCAGCGCACCCCGGCTGCCTGGACGCGTGTGCA 606

Qy   1030 GCCCCAGCCCAGGAGGCAGCAGAGGCCAAGGCACGGAGCCCTGCGCCCTGCGGAGGGCCTCTGCCC 1089
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Db    667 ACCCCACTCATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCGGGCAGCCA 726

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Db    787 TGCCAAGAGCCATATCCGGAGGACCCTGCCCGAGGACCCTGACCAGGAGGCCCCAAAGGCCAA 846

Qy   1270 CTGTCCACTCCCTCAGCTTCCCGGACACCTCTCTCCTCCCCCAGATCCGAGTAACTCCCAATCT 1329
          ||||||||||||||||||||| |||||||||| |||||||||||||||||||||||| |||||||
Db    847 CTCTCCACTCCCTCAGCTTCCCGGATCACCTCTCTCCTCCCCCAGATCGAGTAACTCCCCAATCT 906

Qy   1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGACCCCCACCGTGCCCAGGTAAGCCAGCCCA 1389
          ||||||||||||| ||||||| |||||||||||||||||||||||||||||||||||||
Db    907 TCTCTCTGCAGAGTCCAAATATGGTCCCCCATCATGCCCCAGGTAAGCCAGCCCA 966

Qy   1390 GGCCTCGCCCTCCAGCTCAAGGCCTCGAGGGCAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
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Db    967 GGCCTCGCCCTCCAGCTCAAGGCCGGGACAGGCCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1026

Qy   1450 GGCCCCAGCGTGGGTGCTGACACGTCCACCTCCACCTCTTCCTCAGCACC--ACCTGCGG 1506
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Db   1027 GGCCCCAGCGCCGGGTGCTGACGCGCATCCACCTCCATCTCTTCCTCAGCACCTCCATCTGTCCTCTGAGTTCCTGG 1086
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Qy   1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
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Qy   1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
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Qy   1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1746
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Db   1267 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1326

Qy   1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
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Qy   1807 TCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCAGGGGGAGGAGATGACCAAGAACCAGGTC 1866
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Qy   1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
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Qy   2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
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Db   1687 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTC 1746

Qy   2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
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Qy   2227 TCCCCGGGTAAATGAGTG 2244
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Db   1807 TCTCTGGGTAAATGAGTG 1824
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RESULT 12
HUMIGCD2
LOCUS   HUMIGCD2   2028 bp   DNA   linear   PRI 11-APR-2001
DEFINITION   Human Ig germline H-chain G-E-A region B: gamma-4 constant region,
               3' end.
ACCESSION   K01316
VERSION   K01316.1   GI:184751
KEYWORDS   .
SEGMENT   2 of 7
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2028)
AUTHORS   Ellison,J., Buxbaum,J. and Hood,L.
TITLE   Nucleotide sequence of a human immunoglobulin C gamma 4 gene
JOURNAL   DNA 1 (1), 11-18 (1981)
MEDLINE   83157104

PUBMED   6299662
REFERENCE   2 (bases 894 to 1106)
AUTHORS   Krawinkel,U. and Rabbitts,T.H.
TITLE   Comparison of the hinge-coding segments in human immunoglobulin
            gamma heavy chain genes and the linkage of the gamma 2 and gamma 4
            subclass genes
JOURNAL   EMBO J. 1 (4), 403-407 (1982)
MEDLINE   84235992
PUBMED   6329676
REFERENCE   3 (bases 1 to 2028)
AUTHORS   Ellison,J. and Hood,L.
TITLE   Linkage and sequence homology of two human immunoglobulin gamma
            heavy chain constant region genes
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
MEDLINE   82197621
PUBMED   6804948
REFERENCE   4 (bases 475 to 1069; 1180 to 1331; 1432 to 1655)
AUTHORS   Takahashi,N., Ueda,S., Obata,M., Nikaido,T., Nakai,S. and Honjo,T.
TITLE   Structure of human immunoglobulin gamma genes: implications for
            evolution of a gene family
JOURNAL   Cell 29 (2), 671-679 (1982)
MEDLINE   83001943
PUBMED   6811139
COMMENT   [1] reports that the human C-gamma-4 gene is equally homologous to
            the mouse gamma-1, gamma-2a, and gamma-2b genes (about 75%). [3]
            also reports partial sequences for human gamma-2, gamma-3, and a
            gamma pseudogene. [2] presents the gamma-1, gamma-2, gamma-3, and
            pseudo-gamma hinge regions.
            This entry is part of a multigene region (region B), which includes
            the gamma-2, gamma-4, epsilon-1, and alpha-2 genes. See segment 1
            for more comments.
            Complete source information:
            Human fetal liver DNA, library of T. Maniatis [3] and Lawn et al
            [1], [2]; clones 24B [1], lambda-HG4.1 [3], and Ig-gamma-4-2 [2].
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Query Match   71.7%; Score 1613; DB 9; Length 2028;
Best Local Similarity   94.7%; Pred. No. 9.9e-304;
Matches 1713; Conservative 0; Mismatches 90; Indels 6; Gaps 4;

Qy   439 AGCTTTCTGGGGCGGAGCCGGCCGGGCCTGACTTGGCTTTGGGGCGGGAGGAGTGGGCTAAGGTGA 498
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Db   1 AGCTTTCTGGGGCAGGCCGGCCGGGCCTGACTTTGGC-TGGGGCGGGAGGAGGGGGGCTAAGGTGA 59

Qy   499 GGCAGGTGCGCCAGGTGCACACCCAATGCCGTGAGCCCAGACACTGACCCTGC 558
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Db   60 CGCAGGTGCGCGCAGGTGCACACCCAATGCCAATGCCCAGACACTGACCCTGC 119

Qy   559 CTTGGACCCTCGTGGATAGACAAGAACCGGAGGGGCCTCTGCGCCCTGGGGCCCCAGCTCTGTC 618
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 ATTGGACCATCGCGGATAGACAAGAACCGGAGGGGCCTCTGCGCCCTGGGGCCCCAGCTCTGTC 179

Qy   619 CCACACCGGTCACATGGCACCTCCTTGCAGCCTCCACAAGGGCCCATCGGTCT 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   180 CCACACCGGTCACATGGCACCTCCTTGCAGCTTCCACAAGGGCCCATCCGTCT 239

Qy   679 TCCCCCTGCGCCCTGCTTCCGAGGAGCACCTCCGAGGAGCACGCGGCCCTGGGCTGCCTGG 738
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   240 TCCCCCTGCGCCCTGCTTCCGAGGAGCACCTCCGAGGAGCACACAGCCGCCCTGGGCTGCCTGG 299

Qy   739 TCAAGGACTACTTCCCGAACCGGTGACGGTGCGTGGTCGTGAACTCAGGCGCTCTGACCAGCG 798
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Db   300 TCAAGGACTACTTCCCGAACCGGTGACGGTGCGTGGTCGTGAACTCAGGCGCTCAGGACCAGCG 359

Qy   799 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 858
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Db   360 GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 419

Qy   859 TGACGGTGCCTCAGCAACTTCGGCACCAGGCTTCCTCCTGCGACCTACACCTGCGACGTAGATCACAAGC 918
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Db   420 TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGC 479

Qy   919 CCAGCAACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGAGGGGTGT 978
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Db   480 CCAGCAACCAAGGTGGACAAGAGTTGGTGAGAGGCCAGCAGCAGGGAGGGGGGTGT 539

Qy   979 CTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAGCGCACCCCGGTCGTGCAGCCCCAGCC 1038
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Db   540 CTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAGCGCACCCCGGTCGTGCAGCCCCAGCC 599

Qy   1039 CAGGGCAGCAAGGCAGAGGGCAGCGCCCATCGTCTCCTCCTCACCCCGGAGGCCTCCAGGCTC 1098
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Db   660 ATGCTCAGGGAGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCGGCA--CCACAGGCTGGA 718

Qy   1159 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCCAGGTGCTTGGCTAAGGCCGCACCCTGCCAAAAG 1218
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Db   719 TGCCCCTACCCCAGGCCCTGCCGCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAGAG 777

Qy   1219 CCATATCCGGAGGAGGACCCTGACCTAAGGCCCAAAACTGTCCACT 1278
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Db   778 CCATATCCGGAGGAGGACCCTGACCTAAGGCCCAAAACTCTCCACT 837

Qy   1279 CCCTCAGCTCGGACACCTTCTCCTCCGAGATCGCGAGTAACTCCCAATCTTCTCTCTGC 1338
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Db   838 CCCTCAGCTCGAGACACCTTCTCTCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTGC 897

Qy   1339 AGAGCCGCAAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGGCCTCGCC 1398
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Qy   1399 CTCCAGCTCAAGGGCGGGACAGGTGCCCTAGAGTGCTGCCATCCAGGACAGCAGCCCCAGCC 1458
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ORIGIN

Query Match            71.7%;  Score 1611.8;  DB 6;  Length 4723;
Best Local Similarity  94.3%;  Pred. No. 1.5e-303;
Matches 1722;  Conservative 0;  Mismatches 87;  Indels 18;  Gaps 4;
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Db   958 CTCCAGCTCAAGGCGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGAGACAGGCCCCAGC 1017

Qy  1459 TGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCCGGCAGCACCGT 1515
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Db  1018 CGGGTGCTGACGCGATCCACCTCCATCTCTTCCTCAGTTCCTGGGGGACCAT 1077

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Db  1078 CAGTCTTCCTGTTCCCCCCAAAACCCAGGACACTCTCATGATCTCCGGACCCCTGAGG 1137

Qy  1576 TCACGTGCGTGGTGGTGACGTGAGCCAGGAGACCCGAGGTCCAGTTCAACTGGTACG 1635
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Db  1198 TGGATGGGCGGTGCATAATGCCAAGACAAAGCCGCGGGAGAGCAGTTCAACAGCA 1257

Qy  1696 CGTTCCGTGGTGGTCAGCCTCCTCACCGTTGCACCAGGACTGGCTGAACGGCAAGGAGT 1755
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Db  1258 CGTACCGTGGTGGTCAGCCTCCTCACCGTCTGCACCGTGGCTGAACGGCAAGGAGT 1317

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Qy  1816 CCAAAGGTGGGACCCGCGGTGTATGAGGGCCACCATGGACAGGAGCACCTCGGCCACCC 1875
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Qy  1876 TCTGCCCTGGGAGTGACGTCGTGCCAACCTCGTCCCTACCAGGGGCAGCCCCGAGAACCA 1935
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Db  1438 TCTGCCCTGGGAGTGACCTCGTCGCCAACCTCGTCCCTACCAGGGGCAGCCCCGAGAGCCA 1497

Qy  1936 CAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACC 1995
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Qy  2176 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCGGGT 2235
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RESULT 13
AR161379
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DEFINITION  Sequence 370 from patent US 6255458.
ACCESSION   AR161379
VERSION     AR161379.1   GI:16227241
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4723)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     High affinity human antibodies and human antibodies against digoxin
  JOURNAL   Patent: US 6255458-A 370 03-JUL-2001;
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The Db alignment section (left portion):

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Qy   430 AACCTCTAGAGCTTTCTGGGGCAGCCGGCCTGACTTTGGCTTTGGGGCAGGGAGTGG 489
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Db   902 TCTCTCTGCGAGAGCCCCCAAATCTTGTGACAAAACTCGTGACAAAACTCACACATGCCCACCGTGCCCAGTAA 961
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AUTHORS    Korman,A.J., Halk,E.L. and Lonberg,N.
TITLE      Human ctla-4 antibodies and their uses
JOURNAL    Patent: WO 0114424-A 40 01-MAR-2001;
           MEDAREX, INC. (US)
FEATURES   Location/Qualifiers
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Db      8 AGCAGCTGAAGCTTTCTCGGGGGCAGCCGGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

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VERSION     AX088864.1  GI:13397635
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REFERENCE     1
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  TITLE       Transgenic transchromosomal rodents for making human antibodies
  JOURNAL     Patent: WO 0243478-A 2 06-JUN-2002;
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ACCESSION    AX478054
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Db   1502  GGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG  1561

Qy   1978  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG  2037
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1562  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG  1621

Qy   2038  TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC  2097
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1622  TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC  1681

Qy   2098  GACGGCTCTTCATCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG  2157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682  GACGGCTCTTCATCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG  1741

Qy   2158  AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  2217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1742  AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  1801

Qy   2218  CTCTCCCTGTCTCCGGGTAAATGAGTG  2244
           |||||||||||||||||||||||||||
Db   1802  CTCTCCCTGTCTCCGGGTAAATGAGTG  1828
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          GenCore version 5.1.6
     Copyright (c) 1993 -2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        July 18, 2003, 04:16:54 ; Search time 3897.3 Seconds
                                          (without alignments)
                                          9345.860 Million cell updates/sec

Title:         US-09-627-896B-23
Perfect score: 2249
Sequence:      1 tctagaccaccatgggtgg.........ccggtaaatgagtgagtgaattc 2249

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched:      1615406б seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1:  em_estba:*
               2:  em_esthum:*
               3:  em_estin:*
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               5:  em_estcv:*
               6:  em_estpl:*
               7:  em_estro:*
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               21: em_gss_vrt:*
               22: em_gss_fun:*
               23: em_gss_mam:*
               24: em_gss_mus:*
               25: em_gss_other:*
               26: em_gss_pro:*
               27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	533	23.7	856	13	BI768933	BI768933 603058055
2	530.4	23.6	974	12	BG398446	BG398446 602439729
3	506.4	22.5	757	12	BG674795	BG674795 602620925
4	505.8	22.5	990	12	BG756349	BG756349 602713669
5	504.2	22.4	871	12	BG753979	BG753979 602709506
6	504.2	22.4	965	12	BG754808	BG754808 602714385
7	504.2	22.4	983	14	BQ708975	BQ708975 AGENCOURT
8	503.2	22.4	941	14	BQ712021	BQ712021 AGENCOURT
9	502.6	22.3	873	14	BQ708562	BQ708562 AGENCOURT
10	502.6	22.3	925	14	BQ709152	BQ709152 AGENCOURT
11	502.6	22.3	947	14	BQ709771	BQ709771 AGENCOURT
12	501.6	22.3	973	14	BQ706204	BQ706204 AGENCOURT
13	501	22.3	919	14	BQ709339	BQ709339 AGENCOURT
14	500.2	22.2	797	12	BG741164	BG741164 602631842
15	499.6	22.2	843	13	BM007897	BM007897 603617582
16	497	22.1	813	14	BQ061039	BQ061039 AGENCOURT
17	495.2	22.0	914	14	BQ712363	BQ712363 AGENCOURT
18	494.2	22.0	784	14	BQ712730	BQ712730 AGENCOURT
19	494	22.0	897	14	BQ709144	BQ709144 AGENCOURT
20	493.2	21.9	881	14	BQ711291	BQ711291 AGENCOURT
21 (c)	493	21.9	954	12	BG746184	BG746184 602723696
22	492.2	21.9	892	12	BG397723	BG397723 602438784
23	492.2	21.9	897	13	BM008412	BM008412 603617406
24	491.8	21.9	856	14	BQ709859	BQ709859 AGENCOURT
25	489.6	21.8	967	14	BQ710768	BQ710768 AGENCOURT
26	488.6	21.7	909	14	BQ711117	BQ711117 AGENCOURT
27	488.4	21.7	940	14	BQ705928	BQ705928 AGENCOURT
28 (c)	488.4	21.7	951	12	BQ746233	BQ746233 602723760
29	488	21.6	584	12	BF880706	BF880706 QV3-ET017
30	485.6	21.6	961	14	BQ710233	BQ710233 AGENCOURT
31	483.8	21.5	977	14	BQ710532	BQ710532 AGENCOURT
32	483.6	21.5	941	14	BQ711680	BQ711680 AGENCOURT
33	483.4	21.5	926	12	BG755166	BG755166 602711488
34 (c)	482.8	21.5	1074	12	BG745803	BG745803 602723944
35	480.8	21.4	958	14	BQ706140	BQ706140 AGENCOURT
36	480.6	21.4	1014	14	BM914505	BM914505 AGENCOURT
37 (c)	480.2	21.4	815	12	BG745709	BG745709 602723815
38 (c)	478.8	21.3	781	14	BM674851	BM674851 UI-E-EJ0-
39	478	21.3	925	14	BQ709853	BQ709853 AGENCOURT
40 (c)	474	21.1	1034	12	BG745946	BG745946 602724146
41	473.4	21.0	817	12	BG678806	BG678806 602624701
42	473	21.0	894	12	BG745916	BG745916 602724102
43 (c)	470.8	20.9	764	14	BQ009025	BQ009025 UI-H-EI0-
44	468.2	20.8	987	14	BQ081933	BQ081933 AGENCOURT
45	468.2	20.8	1020	14	BQ062878	BQ062878 AGENCOURT

ALIGNMENTS

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RESULT 1
BI768933

LOCUS       BI768933                 856 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  6030S05055F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207605 5',
            mRNA sequence.
ACCESSION   BI768933
VERSION     BI768933.1  GI:15760511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: Life Technologies, Inc.
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be.
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11520 row: m column: 14
            High quality sequence stop: 797.
FEATURES             Location/Qualifiers
     source          1 ..856
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RESULT 2
BG398446
LOCUS   BG398446   602439729F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565862 5', mRNA sequence.   974 bp   mRNA   linear   EST 12-MAR-2001
DEFINITION 602439729F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565862 5',
            mRNA sequence.
ACCESSION   BG398446
VERSION   BG398446.1 GI:11291894
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 974)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1283 row: j column: 07
            High quality sequence stop: 801.
FEATURES   Location/Qualifiers
     source   1..974
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4565862"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT   231 a   315 c   272 g   155 t   1 others
ORIGIN

Query Match   23.6%;   Score 530.4; DB 12; Length 974;
Best Local Similarity   83.0%;   Pred. No. 9.2e-118;
Matches 722; Conservative   0; Mismatches   41; Indels 107; Gaps   6;

Qy   1371 GCCCAGGTAAGCACCACCAGGCCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAG 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2 GCCCAGGTAAGCACCACCAGGCCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAG 61

Qy   1431 TAGCCTGCATCCAGGGACAGGCCCCAGCTGGGGTGCTGACACGTCCACCTCCATCTCTTCC 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 TAGCCTGCATCCAGGGACAGGCCCCAGCTGGGGTGCTGACACGTCCACCTCCATCTCTTCC 121

Qy   1491 TCAGCACC---ACCTGCGCGACCAGCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 1547
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 TCAGCACCTGAACTCCTGGGGGGACCAGCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 181

Qy   1548 ACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGTGAGCCACGAA 1607
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGAGCCACGAA 241

Qy   1608 GACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAATGCCAAGACA 1667
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 301

Query Match   23.7%;   Score 533; DB 13; Length 856;
Best Local Similarity   85.8%;   Pred. No. 2e-118;
Matches 646; Conservative   0; Mismatches   97; Indels 10; Gaps   1;

BASE COUNT   209 a   281 c   228 g   138 t

Qy   1486 CTTCCTCAGCACCACCTGCGGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 1545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   92 CGTGCCCAGGCACCACCTGTGGCAGGAGCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 151

Qy   1546 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGTGACGTGAGCCACG 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   152 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGTGACGTGAGCCACG 211

Qy   1606 AAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212 AAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 271

Qy   1666 CAAAGCCACCGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTTCCTCACCGTTG 1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   272 CAAAGCCACCGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTTCCTCACCGTTG 331

Qy   1726 TGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCC 1785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   332 TGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCC 391

Qy   1786 CAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGC 1845
          |||||||||||||||||||||||||||||||||||||||
Db   392 CAGCCCCCATCGAGAAAACCATCTCCAAAACCAA------------------------ 425

Qy   1846 CACATGGACAGAGGCGGCGGCTCGGCCCACCCTCGCCCCCTCTGCCCTGGGAGTGACCGCGTGTGCCAACC 1905

Db   426 -- 425

Qy   1906 TCTGTCCCTACAGGGCAGCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCGGGAG 1965
          |||||||||||||||||||||||||||||||||||||||
Db   426 ---------AGGGCAGCAGCCCGAGAACCACCACCAGGTGTACACCCTGCCCCCATCCGGGAG 474

Qy   1966 GAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC 2025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 GAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC 534

Qy   2026 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCC 2085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCC 594

Qy   2086 ATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 2145
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   595 ATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 654

Qy   2146 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC 2205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC 714

Qy   2206 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 2238
          ||||||||||||||||||||||||| || ||
Db   715 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA 747

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                    /lab_host="DH10B (T1 phage-resistant)"
                    /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                    Average insert size 1.5kb. Library constructed by Life
                    Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT     187 a     248 c     203 g     118 t       1 others
ORIGIN

Query Match             22.5%;    Score 506.4;   DB 12;   Length 757;
Best Local Similarity   83.5%;    Pred. No. 5.5e-112;
Matches   629;  Conservative    0;  Mismatches   27;  Indels   97;  Gaps     1;

Qy   1492 CAGCACCACCTGCGCAGCACGTTCAGTCTTCCTTCCTTCCCCCAAAACCAAGGACACCC 1551
          |||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||
Db     68 CACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTTCCTTCCCCCAAAACCAAGGACACCC  127

Qy   1552 TCATGATCTCCCGACCCCTGAGTCACGTGGTGTGGACGTGAGCACGAAGACC 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 TCATGATCTCCCGACCCCTGAGTCACGTGGTGTGGACGTGAGCACGAAGACC  187

Qy   1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    188 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  247

Qy   1672 CACGGGAGGAGCAGTTCAACAGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCTCCCAGCCC 1731
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Db    248 CGCGGGAGGAGCAGTACAACAGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCTCCCAGCCC  307

Qy   1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCCTCCCAGCCC 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCCTCCCAGCCC  367

Qy   1792 CCATCGCGAAAACCATCTCCAAAACCAAGGTGGGACCCGGGGTATGAGGGCCACATG 1851
          |||||||||||||||||||||||||||||||||||||||||
Db    368 CCATCGCGAAAACCATCTCCAAAGCCAA                            395

Qy   1852 GACAGAGGCCGGCTCGGCCTCCGCCCTGGGAGTGACCGGTCGTGCCAACCTCTGTC 1911
          |||||||||||||||||||||||||||||||||
Db    396                                                          395

Qy   1912 CCTACAGGGCAGCCCCGAGAACCAGGACACCAGGTGTACACCCGTGCCCCCATCCCGGGAGGAGATG 1971
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 -----AGGGCAGCCCCGAGAACCAGGACACCAGGTGTACACCCGTGCCCCCATCCCGGGAGGAGATG  450

Qy   1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCGGCGACATCGCC 2031
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    451 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCGGCGACATCGCC  510

Qy   2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG  570

Qy   2092 GACTCCGACGGCTCTTCTTCCTCTTCCTCTATAGCAAGTCACCGTGGACAAGAGCAGGTGGCAG 2151
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GACTCCGACGGCTCTTCTTCCTCTTCCTCTATAGCAAGTCACCGTGGACAAGAGCAGGTGGCAG  630

Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAANCACTACACGCAG  690

Qy   2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
          |||||||||||||||||||||||||||||||||
Db    691 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG  723
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RESULT 4
BG756349
LOCUS   BG756349   990 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602713669F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853873 5',
            mRNA sequence.
ACCESSION   BG756349
VERSION   BG756349.1   GI:14067002

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Qy   1668 AAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTGGTCAGCGTCCTCACCGTTGTG 1727
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Db    302 AAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCAGCGTCCTCAGCGTCCTCACCGTCCTG  361

Qy   1728 CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCA 1787
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Db    362 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCCTCCCA  421

Qy   1788 GCCCCATGCGAGAAAACCATCTCCAAAACCAAGGTGGGACCCGCGGGTATGAGGGCCA 1847
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Db    422 GCCCCATGCGAGAAAACCATCTCCAAAGCCAA---------------------------  453

Qy   1848 CATGGACAGAGGCCGGCTCGGCCCACCCTCGCCCCTGGGAGTGACCGGTCGTGCCAACCTC 1907
          ---------------------------------------------------------
Db    454 -----------------------------------------------------------  453

Qy   1908 TGTCCCTACAGGGCAGCCCCGAGAACCAGGACCACCAGGTGTACACCCGTGCCCCCATCCGGGGAGGA 1967
          |||||||||||||||||||||||||||||||||||||||||||||
Db    454 ------AGGGCAGCCCCGAGAACCAGGACCACCAGGTGTACACCCGTGCCCCCATCCCGCCCGGGATGA  504

Qy   1968 GATGACCAAGAACCAGGTCAGCGCTGACCTGCCTGGTCAAAGGCTTCTACCCGGCGACAT 2027
          | ||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    505 GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCGGCGACAT  564

Qy   2028 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCAT 2087
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT  624

Qy   2088 GCTGGACTCCGACGGCTCCTTCTT--CCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 2145
          |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    625 GCTGGACTCCGACGGCTCCTTCTTTCCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGG  684

Qy   2146 TGG--CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 2203
          |||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 TGGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA-GCTCTGCACAAC--AT  741

Qy   2204 ACACGCAGAAGAGCCTCTCCCTGTCCCCGG 2233
          ||||||||||||||||||||||||||||||
Db    742 ACACGCAGAAGAGAGCCTCTCCCTGTTCTCCGG  771
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RESULT 3
BG674795
LOCUS   BG674795   757 bp   mRNA   linear   EST 01-MAY-2001
DEFINITION 602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4744150 5',
            mRNA sequence.
ACCESSION   BG674795
VERSION   BG674795.1   GI:13906191
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 757)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10594 row: b column: 07
            High quality sequence stop: 755.
FEATURES   Location/Qualifiers
     source   1..757
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                     /db_xref="taxon:9606"
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Db    363 ------AGGACAGCCCCGAGAACCACAGGTGTACACCCTGGTCAAAGGCTTCTACCCCCAGCGACATCGCC    417
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Qy   1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTGCAAAGGCTTCTACCCCCAGCGACATCGCC   2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCCAGCGACATCGCC    477

Qy   2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGCAACTACAAGACAACACACTTCCCATGCTG   2091
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Db    478 GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACAACTACAACACAACGCCTCCCATGCTG    537

Qy   2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG   2151
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Db    538 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG    597

Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG   2211
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Db    598 CAGGGGAACATCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCGCTTCACGCAG    657

Qy   2212 AAGAGCCTCTCCCCGTCCCCGGGTAAATGAGTG   2244
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Db    658 AAGAGCCCTCTCCCCGTCTCCGGGTAAATGAGTG    690
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RESULT 5
BG753979
LOCUS   BG753979   871 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION   602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5',
               mRNA sequence.
ACCESSION   BG753979
VERSION   BG753979.1 GI:14064632
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 871)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
               cDNA Library Preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM1686 row: k column: 02
               High quality sequence stop: 848.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4846201"
                     /clone_lib="NIH_MGC 48"
                     /tissue_type="primary B-cells from tonsils (cell line) "
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT   220 a   284 c   231 g   136 t
ORIGIN

Query Match   22.4%;   Score 504.2; DB 12; Length 871;
Best Local Similarity 83.4%;   Pred. No. 2e-111;

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Qy   1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGACACCC   1551
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Db     35 CACCTGAACTCCTGGGAGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGATACCC     94

Qy   1552 TCATGATCTCCCGGACCCCCTGAGGTCGCGTGGTGTGGTGGTGGACGTGAGCCACGAAGACC   1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     95 TTATGATTTCCCGGACCCCCTGAGGTCGCGTGGTGTGGTGGTGGACGTGAGCCACGAAGACC    154

Qy   1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC   1671
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Db    155 CCGAGGTCCAGTTCAAGTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC    214

Qy   1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTGTCAGGCTCCTCACCGTTGTGCACC   1731
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    215 CGCGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGTCAGCGTCCTCACCGTCCTGCACC    274

Qy   1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGGCCTCCCAGCCC   1791
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Db    275 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCTCCAACAAAAGCCTCCCAGCCC    334

Qy   1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGTATGAGGGCCACATG   1851
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Db    335 CCATCGAGAAAACCATCTCCAAAACCAA------------------------------    362

Qy   1852 GACAGAGGCCGGCTCGGCCACCCTCTGCCCTGGGAGTGACCACCGCTGTGCCAACCTCTGTC   1911
Db    363 ------------------------------------------------------------    362

Qy   1912 CCTACACGGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG   1971
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1702   row: i   column: 22
High quality sequence stop: 779.

FEATURES   Location/Qualifiers
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT   229 a   361 c   247 g   127 t   1 others
ORIGIN

Query Match   22.4%;   Score 504.2; DB 12; Length 965;
Best Local Similarity 83.4%;   Pred. No. 2.1e-111;
Matches   628; Conservative   0; Mismatches   28; Indels   97; Gaps   1;

Qy   1492 CAGCACCACCTGCGCAGCACCGTCAGTCTTCCTCTTCCCCCAAAACCAAGGACACACC 1551
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Db   68 CACCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCAAGGACACACC   67

Qy   1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGACGTGAGCGAGCCACGAAGACC 1611
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Db   68 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCGAGCCACGAAGACC 127

Qy   1612 CCGAGGTCAACTGGTACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
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Db   128 CTGAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 187

Qy   1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGTCAGCGTCCTCACCGTTGTGCACC 1731
          || |||||||||||||| ||||| |||||||||| ||| ||||||||||||| || |||
Db   188 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTTCACC 247

Qy   1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCC 1791
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Qy   1852 GACAGAGGCCGGCTCGGCCCCACCCTGCCCTGGGAGTGACCGCGTGTGCAACCTCTGTC 1911

Db   336 -- 335

Qy   1912 CCTACAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCTGGTCAAGGAGGAGGAGATG 1971
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Qy   1972 ACCAAGAACCAGGTCAGCGCCTGACCTGCCTGGTCAAGGGCTTCTACCCAGGACATCGGC 2031
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Db   391 ACCAAGAACCAGGTCAGCGCCTGACCTGCCTGGTCAAAGGCTTCATCCCAGGACATCGGC 450

Qy   2032 GTGGAGTGGGAGAGCAATGGCAATGGGCAGCCGCAGCCGGAGAACAACTACAAGACCACC 2091
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Db   451 GTGGAGTGGGAGAGCAATGGCAATGGGCAGCCGCAGCCGGAGAACAACTACAAGACCACG 510

RESULT 6
BG754808
LOCUS   BG754808   965 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602714385F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854621 5',
            mRNA sequence.
ACCESSION   BG754808
VERSION   BG754808.1 GI:14065461
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 965)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov

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Qy  2092  GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGAGCTCACCGTGGACAAGAGCAGTGGCAG  2151
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Db   511  GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGAGCTCACCGTGGACAAGAGCAGTGGCAG   570

Qy  2152  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG  2211
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Db   571  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG   630

Qy  2212  AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG  2244
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Db   631  AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG   663
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RESULT 7
BQ708975
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LOCUS       BQ708975             983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: k  column: 12
            High quality sequence stop: 604.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      251 a    306 c    265 g    161 t
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Query Match   22.4%; Score 504.2; DB 14; Length 983;
Best Local Similarity   83.4%; Pred. No. 2.1e-111;
Matches 628; Conservative   0; Mismatches 28; Indels 97; Gaps   1;

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Qy  1492  CAGCACCACCTGCGGCAGCACCCTCAGTCTTCCCTCTTCCCCCCAAAAACCCAAGGACACACCC  1551
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Db    55  CACCTGAACTCCTGGGGGACCCTCAGTCTTCCCTCTCCCCCCAAAAACCCAAGGACACACCC   114

Qy  1552  TCATGATCTCCCGGACCCCCTGAGGTCACGTCGTGTGGTGGACGTGACGTGACCACGAAGACC  1611
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Db   115  TCATGATCTCCCGGACCCCCTGAGGTCACATGCGTGTGGTGGACGTGGACGTGACCACGAAGACC   174

Qy  1612  CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  1671
          |  |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   175  CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC   234

Qy  1672  CACGGGAGGAGCAGTTCAACACGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC  1731
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Db   235  CCGCGGGAGGAGCAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC   294

Qy  1732  AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC  1791
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Db   295  AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC   354

Qy  1792  CCATCGAGAAAACCATCTCCAAAACCAAAGTGGGACCCCGGGTATGAGGGCCACATG  1851
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Qy  1852  GACAGAGGCCGGCTCGGCCCACCCCTCGCCCTGGGAGTGCCCTGGAGTGACCGGCGTGTGCCAACCTCGTC  1911
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Db   383  ---------   382

Qy  1912  CCTACGGGCCAGCCCCGAGAACCCAGAGGTCTACACCCTGCCCCCATCCCGGGAGGAGATG  1971
               |||||||||||||||||| |||||| |||||||||||||||||||||||| |||| |||
Db   383  -----AGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGGCTG   437

Qy  1972  ACCAAGAACCAGGTCAGCCTGCCTGCTCGTCAAAGGCTTCTACCCCCAGCGACATCGCC  2031
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Db   438  ACCAAGAACCAGGTCAGCCTGCCTGCTCGTCAAAGGCTTCTATCCCCAGCGACATCGCC   497

Qy  2032  GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCATGCTG  2091
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Db   498  GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACGCCTCCCGTGCTG   557

Qy  2092  GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGAGCTCACCGTGGACAAGAGCAGTGGCAG  2151
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Db   558  GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGAGCTCACCGTGGACAAGAGCAGTGGCAG   617

Qy  2152  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG  2211
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Db   618  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG   677

Qy  2212  AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG  2244
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RESULT 8
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LOCUS       BQ712021             941 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
            5', mRNA sequence.
ACCESSION   BQ712021
VERSION     BQ712021.1  GI:21850920
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474 row: c  column: 04
            High quality sequence stop: 638.
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DEFINITION   AGENCOURT_7977052 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215953
             5', mRNA sequence.
ACCESSION   BQ708562
VERSION   BQ708562.1 GI:21847461
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 873)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2385 row: 1 column: 02
             High quality sequence stop: 682.
FEATURES   Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   205 a   277 c   222 g   133 t   36 others
ORIGIN

Query Match   22.3%; Score 502.6; DB 14; Length 873;
Best Local Similarity 83.3%; Pred. No. 4.9e-111;
Matches 627; Conservative   0; Mismatches 29; Indels 97; Gaps   1;

Qy   1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTTCTCCCCCAAAACCAAGGACACCC 1551
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Db   22 CACCTGAACTCCTGGGGGACCGGTCAGTCTTCCTTCTCCCCCAAAACCAAGGACACCC 81

Qy   1552 TCATGATCTCCCGGACCCCCTGAGGTCACGTGGTGGTGACGTGAGCGTGAGCCACGAAGACC 1611
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Db   82 TCATGATCTCCCGGACCCCCTGAGGTCACATGCGTGGTGGTGACGTGAGCGTGAGCCACGAAGACC 141

Qy   1612 CCGAGGTCCAGTTCAACTGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
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Db   142 CTGAGGTCAAGTTCAACTGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 201

Qy   1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCGTGTGTGCACC 1731
           ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   202 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCGTGTGTGCACC 261

Qy   1732 AGGACTGGCTGAACGGCAAGGCTCTCCAACAAAGGCCTCCCAGCCC 1791
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Db   262 AGGACTGGCTGAATGGCAAGGAGTCTCCAACAAAGGCCTCCCAGCCC 321

Qy   1792 CCATCGAGAAAAACCATTCCAAAAACCAAGGTGGGACCCGCGGGTATGAGGGCCACATG 1851
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Db   322 CCATCGAGAAAAACCATTCCAAAGCCAA---------------------------- 349

Qy   1852 GACAGAGGCCGGCTCGGCCCACCCCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

RESULT 9
BQ708562

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Best Local Similarity   83.3%;   Pred. No. 5e-111;
Matches 627;   Conservative   0;   Mismatches  29;   Indels  97;   Gaps   1;

Qy   1492 CAGCACCACCTGGGCAGCAGCCGTCAGTCTTCCTCCTTCCCCCAAAACCCAAGGACACCC 1551
          ||  ||||||||||||||| |||| ||||||||||||| |||||||  ||||||||||||
Db     79 CACCTGAACTCTGGGGGACCCGTCAGTCTTCCTCTCCTTCCCCCAAAACCCAAGGACACCC 138

Qy   1552 TCATGATCTCCCGACCCCTGAGGTCACGTGGTGGTGAGCGCACGAGACC 1611
          ||||||| ||||||||||||||||||||||||| ||| ||||||||||||
Db    139 TCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGAGCGCACGAGACC 198

Qy   1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
          |  ||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    199 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 258

Qy   1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||
Db    259 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 318

Qy   1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
          ||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||
Db    319 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 378

Qy   1792 CCATCGAGAAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGTATGAGGGCCACATG 1851
          |||||||||| |||||||||||||||| ||||
Db    379 CCATCGAGAAAAACCATCTCCAAAGCCA------------------------------ 406

Qy   1852 GACAGAGGCCGGCTCGGCGCCACCCTCTGCCCTGGGAGTGACCGCGTGTGCCAACCTCTGTC 1911
Db    407 --------------------------------------------------------- 406

Qy   1912 CCTACAGGGAGCAGCCCGGAGAACCACCAGGTGTACACCCTGCCCCATCCCGGGAGAGATG 1971
          |||                  ||||||||||||||||||||| ||||||||||||||||||||
Db    407 ----AGGGCAGCCCGGAGAACCACCAGGTGTACACCCTGCCCCATCCCGGGATGAGCTG 461

Qy   1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    462 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 521

Qy   2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCACCCGTGCTG 581

Qy   2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    582 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 641

Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    642 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAG 701

Qy   2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
          |||||||||||||||||||||||||||||||||
Db    702 AAGAGCCTCTCCCTGTCCCGGGTAAATGAGTG 734
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RESULT 11
BQ709771
LOCUS       BQ709771              947 bp   mRNA    linear    EST 16-JUL-2002
DEFINITION  AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
            5', mRNA sequence.
ACCESSION   BQ709771
VERSION     BQ709771.1  GI:21848670
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 947)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
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Db    350 ------------------------------------------------------ 349

Qy   1912 CCTACAGGGAGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCATCCCGGGAGAGATG 1971
          |||                  |||||||||||||||||||||||||||||||||||||||||
Db    350 -----AGGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCATCCCGGGATGAGCTG 404

Qy   1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    405 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 464

Qy   2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCACCCGTGCTG 524

Qy   2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 584

Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    585 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAG 644

Qy   2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
          ||||||||||||||||| |||||||||||||||
Db    645 AAGAGCCTCTCCCTGTCCCGGGTAAATGAGTG 677
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RESULT 10
BQ709152
LOCUS       BQ709152              925 bp   mRNA    linear    EST 16-JUL-2002
DEFINITION  AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
            5', mRNA sequence.
ACCESSION   BQ709152
VERSION     BQ709152.1  GI:21848051
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 925)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516   row: m   column: 22
            High quality sequence stop: 739.
FEATURES            Location/Qualifiers
     source         1..925
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6301245"
                    /clone_lib="NIH_MGC_113"
                    /lab_host="DH10B (phage-resistant)"
                    /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
BASE COUNT     230 a    292 c    225 g    144 t    34 others
ORIGIN
Query Match    ,    22.3%;    Score 502.6;    DB 14;    Length 925;
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Db    731  GACTCCGACGGCTCCTTCCTTCCTCACGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG   790

Qy   2152  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTTCGCACAACCACTACACGCAG  2211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCATGCATGCGACCACCACTACACGCAG   850

Qy   2212  AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG  2244
           ||||||||||||||||||||||||||||||||
Db    851  AAGAGCCCTCTCCCTGTCCCCGGGTAAATGAGTG   883

RESULT 12
BQ706204
LOCUS        BQ706204          973 bp    mRNA      linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
             5', mRNA sequence.
ACCESSION    BQ706204
VERSION      BQ706204.1  GI:21845103
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 973)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2464 row: d  column: 09
             High quality sequence stop: 640.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT       255 a     310 c     256 g     146 t
ORIGIN

Query Match          22.3%;  Score 501.6;  DB 14;  Length 973;
Best Local Similarity  83.1%;  Pred. No. 9e-111;
Matches  626;  Conservative   0;  Mismatches  30;  Indels  97;  Gaps   1;

Qy   1492  CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTTCCCCCAAAACCCAAGGACACCC  1551
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Db    139  CACCTGAACTCCTGGGGGACCGTCAGTCTTCCTTCCCCCAAAAACCCAAGGACACCC   198

Qy   1552  TCATGATCTCCCGACCCCTGAGGTCACGTGCGTGGTGGACGTGAGCGTGGACGAAGACC  1611
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199  TCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCGTGGACGAAGACC   258

Qy   1612  CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGCATAATGCCAAGACAAAGC  1671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259  CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC   318
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.Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2466 row: m  column: 16
High quality sequence start: 3
High quality sequence stop: 675.

FEATURES             Location/Qualifiers
     source          1..947
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278583"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT       225 a     320 c     252 g     150 t
ORIGIN

Query Match          22.3%;  Score 502.6;  DB 14;  Length 947;
Best Local Similarity  83.3%;  Pred. No. 5.1e-111;
Matches  627;  Conservative   0;  Mismatches  29;  Indels  97;  Gaps   1;

Qy   1492  CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTTCCCCCAAAACCCAAGGACACCC  1551
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Db    228  CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTTCCCCCAAAAACCCAAGGACACCC   287

Qy   1552  TCATGATCTCCCGACCCCTGAGGTCACGTGCGTGGTGGACGTGAGCGTGGACGAAGACC  1611
           ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    288  TCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCGTGGACGAAGACC   347

Qy   1612  CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  1671
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348  CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC   407

Qy   1672  CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC  1731
           || ||||||||||||||||||||||| || ||||||||||||||||||||||||||||
Db    408  CGCGGGAGGAGCAGTACAACAGCACGTACCGTGGTCAGCGTCCTCACCGTTGTGCACC   467

Qy   1732  AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCC  1791
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Db    468  AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC   527

Qy   1792  CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGACCCGGGGTATGAGGGCCACATG  1851
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Db    528  CCATCGAGAAAACCATCTCCAAAGCCAA   555

Qy   1852  GACAGAGCCGGCTCGGCCCACCCTGCCCTGGGAGTGACCGCGTGCCAACCTCTGTC  1911
Db    556  --------------------------------------------   555

Qy   1912  CCTACAGGGCAGCCCGGAGAACCACAGTGTACACCCTGCCCCCATCCGGGAGGAGATG  1971
           |  |||||||||||||||||||||||||||||||||||||||||||||
Db    556  -----AGGGCAGCCCGGAGAACCACAGTGTACACCCTGCCCCCATCCGGGATGGAGCTG   610

Qy   1972  ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC  2031
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611  ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC   670

Qy   2032  GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACCACCTCCCATGCTG  2091
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                    /clone_lib="NIH_MGC_113"
                    /lab_host="DH10B (phage-resistant)"
                    /note="organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT    234 a    297 c    229 g    150 t      9 others
ORIGIN

Query Match        22.3%;  Score 501;  DB 14;  Length 919;
Best Local Similarity  83.1%;  Pred. No. 1.2e-110;
Matches  626;  Conservative   0;  Mismatches  30;  Indels  97;  Gaps   1;

Qy   1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCAAAACCAAGGACACCC 1551
          |||              |||||   ||||||||||||||| ||||||||||||||||
Db     88 CACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCTCTTCCCCCAAAACCAAGGACACCC 147

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Qy   1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 267

Qy   1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTGTGCACC 1731
          | |||||||||||||| |||||||||| |||||||||||||||||||||||||||||||
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Qy   1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCAAGGTCAACAAAGGCCTCCCAGCCC 1791
          |||||||| |||| ||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    379 AGGACTGCTGAATGGCAAGGAGTACAAGTGCAAGGTCAAGGTCAACAAAGCCCTCCCAGCCC 438

Qy   1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGACCCGCGGGTATGAGGGCCACATG 1851
          |||||||||||||||||||||||||| |||
Db    439 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------ 466

Qy   1852 GACAGAGGCCGGCTCGGCCCACCCCTGCCCTGGAGTGACCGGTGTGCCAACCTCTGTC 1911
          
Db    416 --------------------------------------------------------- 415

Qy   1912 CCTACAGGGCAGCCCCAGAACCACAGGTGTACACCTGCCCCATCCCGGGAGGAGATG 1971
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Db    416 -----AGGGCAGCCCCAGAACCACAGGTGTACACCTGCCCCATCCCGGGGATGAGCTG 470

Qy   1972 ACCAAGAACCAGGTCAGCGTGACCTGCCTGGTCAAGGGCTTCTACCCCAGCGACATCGCC 2031
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Db    471 ACCAAGAACCAGGTCAGCGTGACCTGCCTGGTTCTATCCCAGCGACATCGCC 530

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
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Qy   2092 GACTCCGACGGCTCCTTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGGCTCTGCACAACCACTACACGCAG 2211
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Db    651 CAGGGGAACGTCTTCTCGTGATGCATGAGGGCTCTGCACAACCACTACACGCAG 710

Qy   2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 14
BG741164
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RESULT 13
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BQ709339
LOCUS       BQ709339                 919 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
            5', mRNA sequence.
ACCESSION   BQ709339
VERSION     BQ709339.1  GI:21848238
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2381 row: m column: 11
            "High quality sequence stop: 576.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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DEFINITION  602631842F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776923 5',
            mRNA sequence.
ACCESSION   BG741164
VERSION     BG741164.1  GI:14051817
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10630 row: d  column: 12
            High quality sequence stop: 782.
FEATURES             Location/Qualifiers
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                     /clone_lib="NCI_CGAP_Skn3"
                     /lab_host="DH10B (T1_phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.5kb. Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP library."
BASE COUNT    203 a    262 c    210 g    122 t
ORIGIN

Query Match            22.2%;  Score 500.2;  DB 12;  Length 797;
Best Local Similarity  84.3%;  Pred. No. 1.8e-110;
Matches  618;  Conservative  0;  Mismatches  18;  Indels  97;  Gaps  1;

Qy   1505 GGCAGCACCGTCAGTCTTCCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 1564
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Db     12 GGGGGGACCGTCAGTCTTCCTTCCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 71

Qy   1555 GACCCCTGAGGTCACGTGCGTGGTGACGTGAGCCACGAGACACCCGAGGTCCAGTT 1624
               |||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db     72 GACCCCTGAGGTCACATGCGTGGTGACGTGAGCCACGAGACACCCGAGGTCAAGTT 131

Qy   1625 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCA 1684
               |||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db    132 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 191

Qy   1685 GTTCAACAGCACGTTCCGTGTGGTCAGCGTGCTCACCGTTGTGCCACCAGGACTGGCTGAA 1744
             ||  |||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db    192 GTACAACAGCACGTACCGTGTGGTCAGCGTGCTCACCGTTGTGCCACCAGGACTGGCTGAA 251

Qy   1745 CGGAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAAC 1804
             |  |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db    252 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 311

Qy   1805 CATCTCCAAAACCAAAGTGGGACCCCGCGGGTATGAGGGCCACATGGACAGAGGCCCGGC 1864
             ||||||||  ||||
Db    312 CATCTCCAAAGCCAA------------------------------------------ 326

Qy   1865 TCGGCCCCACCCTGCCCTGGGACGTGACCGCTGTGCCCAACCTCTGTCCCTACAGGGCAGC 1924
                                                              |||||||
Db    327 A-------------------------------------AGGGCAGC 334

Qy   1925 CCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGG 1984
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    335 CCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGG 394

Qy   1985 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCGAGCGACATCGCCGTGGAGTGGGAGA 2044
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Db    395 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCGAGCGACATCGCCGTGGAGTGGGAGA 454

Qy   2045 GCAATGGGCAGCCGGAGAACAACTACAAGACCACACCGCCTCCCATGCTGGACTCCGACGGCT 2104
             |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db    455 GCAATGGGCAGCCGGAGAACAACTACAAGACCACACCGCCTCCCGTGCTGGACTCCGACGGCT 514

Qy   2105 CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT 2164
             |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db    515 CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT 574

Qy   2165 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC 2224
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    575 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC 634

Qy   2225 TGTCCCCGGGTAA 2237
             |||||||||||||
Db    635 TGTCCCCGGGTAA 647

RESULT 15
BM007897
LOCUS       BM007897                843 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
            mRNA sequence.
ACCESSION   BM007897
VERSION     BM007897.1  GI:1522238
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939 row: d  column: 22
            High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1..843
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    207 a    277 c    227 g    132 t
ORIGIN

Query Match            22.2%;  Score 499.6;  DB 13;  Length 843;
Best Local Similarity  83.2%;  Pred. No. 2.6e-110;
Matches  624;  Conservative  0;  Mismatches  29;  Indels  97;  Gaps  1;

Qy   1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTTCCTTCCCCCCAAAACCCAAGGACACCC 1551
             ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    139 CACCTGAACTCCTGGGGACCGTCAGTCTTCCTCTTCCCCCAAAAACCCAAGGACACCC 198
          ||  ||      ||   | | |||||||||||||||||||||||||||||||||||||
Qy   1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCCTGGTGGTGACGTGAGCGCACGAGGACC 1611
          ||||||||||||||||||||||||||||||| |||||  |||  ||| |||||||||||
Db    199 TCATGATCTCCCGGACCCCTGAGGTCACATGCCTGGTGGTGACGTGAGCCACGAAGACC 258

Qy   1612 CCGAGGTCCAGTTCAACTGGTACGTGACGGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
          |||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||
Db    259 CTGAGGTCAAGTTCAACTGGTACGTGGACGGGCGTGGAGGTGCATAATGCCAAGACAAAGC 318

Qy   1672 CACGGGAGGAGCAGTTCAACACGCAGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
          ||||||||||| ||||||||||||||| |||   ||||||||||||  |||||| |||||
Db    319 CGCGGGAGGAGCAGTACAACAGCACGTACCCGTGGTGGTCAGCGTCCTCACCGTCCTGCACC 378

Qy   1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
          ||||||||||| |||||||||||||||||||||||||| |||||||| ||||||||||||
Db    379 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 438

Qy   1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGACCCGCGGGGTATGAGGGCCACATG 1851
          ||||||||||||| |||| ||||||||||||  |||
Db    439 CCATCGAGAAAACCATCTCCAAAGCCAA                              466

Qy   1852 GACAGAGAGGCCGGCTCGGCCCACCCTCTGCCCTCGGAGTGACCGGCTGTGCCAACCTCTGTC 1911
Db    467 --------------------------------------------------------  466

Qy   1912 CCTACAGGGCCAGCCCCGAGAACCACACAGTGTACACCCTGCCCCATCCCGGGAGGAGATG 1971
              ||||||||||||||||||||||||| |||||||||||||||  ||||||||||||
Db    467 -----AGGGCAGCCCCGAGAACCACACAGGTGTACACCCCTGCCCCATCCCGGGATGAGCTG 521

Qy   1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
          ||||||||||||||||||||||||||||||||||| |||||||| |||||||||||| ||
Db    522 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGCTTCTATCCCAGCGACATCGCC 581

Qy   2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACCTCCCATGCTG 2091
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    582 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGTCCCCGTGCTG 641

Qy   2092 GACTCCGACGCGCTCCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db    642 GACTCCGACGGCGCTCCTCCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 701

Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
          |||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Db    702 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCATTACACGCAG 761

Qy   2212 AAGAGCCTCTCCCCTGTCCCCGGGTAAATGA 2241
          |||||||||||||||||||||||||||||||
Db    762 AAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 791
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Search completed: July 18, 2003, 09:26:02
Job time : 3905.3 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   July 18, 2003, 04:14:58 ; Search time 583.029 Seconds
                                     (without alignments)
                                     8686.944 Million cell updates/sec

Title:          US-09-627-896B-23
Perfect score:  2249
Sequence:       1 tctagaccaccatggttgg.........ccgggtaaatgagtgagtgaattc 2249

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:        4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	80.2	2560	13	AAQ30910	pMDR1002 insert; p
2	1761.2	78.3	3223	22	AAS11982	DNA encoding Human
3	1739.4	77.3	2287	13	AAQ25443	Sequence encoding
4	1736.2	77.2	2287	18	AAT60739	IgG1 gene. Homo s
5	1638	72.8	4694	22	AAF5225	Nucleotide sequenc
6	1638	72.8	4694	24	ABK85577	Human IgGgamma4 he
7	1611.8	71.7	4723	18	AAT78802	Gamma heavy chain
8	1611.8	71.7	4723	20	AAZ21997	Nucleotide sequenc
9	1611.8	71.7	4723	22	AAF55224	Nucleotide sequenc
10	1611.8	71.7	4723	24	ABK85576	Human IgGgamma1 he
11	1610.2	71.6	4723	19	AAV39243	Plasmid pCG7-96 nu
12	1609.2	71.6	2029	13	AAQ30909	pBAG101 insert. S
13	1604.4	71.3	9201	15	AA055003	Humanised anti-CD1
14	1584.6	70.5	2482	13	AAQ28089	Encodes CD4-IgG2 c
15	1584.6	70.5	2482	21	AAZ98856	CD4-IgG2 chimeric
16	1584.6	70.5	2482	22	AAF77830	Coding sequence fo
17	1584.6	70.5	2482	22	AAF56396	CD4-IgG2 chimeric
18	1580.4	70.3	1999	21	AAA46891	DNA encoding the h
19	1578.2	70.2	2482	15	AA057751	CD4-IgG2 chimeric
20	1547.2	68.8	2009	24	AAD35054	Human death domain
21	1547.2	68.8	3133	10	AAN03356	Sequence of a gene
22	1547.2	68.8	3133	21	AAA50660	DNA encoding CD4-I
23	1547.2	68.8	3133	21	AAZ44061	Human fusion prote
24	1547.2	68.8	3133	21	AAZ48201	DNA sequence encod
25	1545.6	68.7	2009	17	AAT27385	Human immunoglobul
26	1543.8	68.6	3400	18	AAT62932	2A2 human G2/G4 ch
27	1541.8	68.6	3400	18	AAT62937	3F4 human G2/G4 ch
28	1494.8	66.5	1979	13	AAQ20293	SEQ ID No. 4 that
29	1493.8	66.4	2008	13	AAQ20294	SEQ ID No. 5 that
30	1487.4	66.1	10704	14	AAQ43846	Plasmid pAH425.
31	1465.8	65.2	3108	17	AAT27388	Human IgG CH1-hing
32	1465.8	65.2	3147	17	AAT27389	Human IgG CH1-hing
33	1463.4	65.1	2071	19	AAV70080	Anti-Fas humanised
34	1463.4	65.1	2071	21	AAA72184	DNA encoding human
35	1463.4	65.1	2071	21	AAA11622	Humanised HFE7A de
36	1463.4	65.1	2071	24	ABL46001	Humanised anti-Fas
37	1463.4	65.1	2071	24	ABL48744	Humanised anti-Fas
38	1459.8	64.9	1719	24	ABK40183	Human/rabbit Cgamm
39	1458.6	64.9	2077	19	AAV70079	Anti-Fas humanised
40	1458.6	64.9	2077	21	AAA72159	DNA encoding human
41	1458.6	64.9	2077	21	AAA11597	Humanised HFE7A de
42	1458.6	64.9	2077	24	ABL45976	Humanised anti-Fas
43	1458.6	64.9	2077	24	ABL48719	Humanised anti-Fas
44	1455.4	64.7	2073	21	AAA11644	Humanised anti-Fas
45	1455.4	64.7	2073	21	AAA11645	Humanised anti-Fas

ALIGNMENTS

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RESULT 1
AAQ30910
ID   AAQ30910 standard; DNA; 2560 BP.
XX
AC   AAQ30910;
XX
DT   02-APR-1993  (first entry)
XX
DE   pMDR1002 insert; pre-5A8 humanised heavy chain.
XX
KW   Vector; pMDR1002; NotI; HindIII; pMDR1001; pSAB132; pBAG101; E. coli;
KW   JA221(lq); ampicillin; resistance; immunoglobulin; signal sequence;
KW   humanised; 5A8; heavy chain; variable; region; HV; IgG4; constant;
KW   HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
KW   lymphocytes; helper; inducer; HIV; syncytia; formation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT   sig_peptide     12..68
FT                   /*tag= b
FT                   /note= "Immunoglobulin signal sequence"
FT   mat_peptide     69..2296
FT                   /*tag= c
FT   exon            12..435
FT                   /*tag= d
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FT   intron          436..711
FT                   /*tag= e
FT                   /number= 1
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FT   exon            712..1005
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FT                   /number= 2
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FT                   /*tag= g
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FT                   /*tag= h
FT                   /number= 3
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FT   intron          1432..1549
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FT   exon            1550..1879
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FT                   /*tag= k
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FT   misc_RNA        69..434
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FT                   /note= "AA1-AA122 of humanised 5A8 VH"
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PN   WO9209305-A.
XX
PD   11-JUN-1992.
XX
PF   27-NOV-1991;  91WO-US08843.
XX
PR   27-NOV-1990;  90US-0618542.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Burkly LC,  Chisholm PL,  Rosa JJ,  Rosa MD,  Thomas DW;
XX
DR   WPI; 1992-398399/48.
DR   P-PSDB; AAR28808.
XX
PT   New anti-CD4 antibody homologues - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Claim 27; Page 152-55; 205pp; English.
XX
CC   This sequence represents the insert of the vector pMDR1002.  Three
CC   fragments were used in the construction of pMDR1002; a 443 bp NotI/
CC   HindIII fragment of pMDR1001 (see AAQ30905), the 7913 bp NotI linearised
CC   pSAB112 (see AAQ30906) and a 2109 bp NotI/HindIII fragment of pBAG101
CC   (see AAQ30909).  These fragments were ligated together and the ligation
CC   mixture was used to transform E. coli JA221(Iq) to ampicillin
CC   resistance.  The insert encodes the immunoglobulin signal sequence,
CC   amino acids (AA) 1-122 of the humanised 5A8 heavy chain variable
CC   region (HV) and AA114-AA478 of the human IgG4 heavy chain, ie. the
CC   constant region (HC). The polypeptide encoded by this sequence is
CC   an antibody homolog which was shown to bind to CD4 but did not block
CC   the binding of gp120 to CD4.  CD4 is a cell surface glycoprotein of
CC   CD4+ lymphocytes (helper/inducer cells).  The homolog blocked HIV-
CC   induced syncytia formation.  This homolog can be used in the
CC   detection, prophylaxis and treatment of diseases caused by infective
CC   agents whose primary targets are CD4+ cells.
XX
SQ   Sequence 2560 BP; 544 A; 848 C; 720 G; 448 T; 0 other;

Query Match     80.2%;  Score 1804;  DB 13;  Length 2560;
Best Local Similarity   89.2%;  Pred. No. 0;
Matches 2049;  Conservative   0; Mismatches  185;  Indels  64;  Gaps   7;
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Qy          8 CACCATGGGTTGGAACTGTATCATCTTCTTCTTGGTTACCACAGCTACACAGGTGTGCACTC    67
              ||||||||| ||| ||| ||| ||| |||||| |||| |||||  ||  |||| ||| |||
Db          8 CACCATGGACTGGACCTGGAGGGTCTTCTGCTTCGGGTGAGAGAAGCCTGGGAGCTGCCACTC    67

Qy         68 CCAGGTCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTTGGGAGCTCAGTGAAGGT   127
              |||||||| ||  ||||||||||| | |||||  ||||||  ||||| || ||  |||||||||||
Db         68 CCAGGTCAACTGCAGGGAGTCTGGAGCTGAAGTGAAAAAGCCTGGGGGCTTCAGTGAAGGT   127

Qy        128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGGTGGGTGAGACAGGC   187
              |||||||||| |||| |||| || |  |||  ||| || |||||| ||||||| ||||| 
Db        128 GTCCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATACACTGGGTGAGGCAGGC   187

Qy        188 TCCTGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTACTATGATAATACAAAACTA   247
              |||||||  |||||| ||||| ||||| |||| ||| || || |||| || |||||
Db        188 GCCTGGGCAGGGCCTTGAGTGGATTGGAATATATTAATCCTTACAATGATGGTACTGACTA   247

Qy        248 CAACCAGAAGTTAAGGGCCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA   307
              ||| | |||||||||  || ||||| || |||||| |  || ||| |||| | |||||||
Db        248 CGATGAGAAGTTCAAAGCCACAGTGACTTTAGACACCATCCACCACACAGCCTA   307

Qy        308 TATGGAACTTAGTTCTTTGAGATCTGAAGATACAGGCCGTTATTACTGTGCAAGAG------   363
              ||||  || ||||| |||||| | |||||| || |||  |||||||||||||||||
Db        308 CATGGAGCTCAGCAGCCTGAGGTCTGAGGACACTGCGGTCTATTACTGTGCAAGAGAGAA   367

Qy        364 -------CGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGT   409
                     || ||||| | |||||| ||||||| |||||||  |||| || ||||||
Db        368 GGATAACTACGGCACGGGGCCTGGTTTGCTTACTGGGGCCAAGGGACCCTGGTCACCGT   427

Qy        410 CTCCTCAGGTGAGTCCTTAAA----------------ACCT   434
              |||||||||||||| ||||||
Db        428 CTCCTCAGGTGAGTCCTTAAGCTTGGTACCGGGACCATGTCCAGATCTGCAGCATGCTCGAGCT   487

Qy        435 CTAG-----AGCTTTCTGGGGCGAGCCCGGGCCTGACTTTGGCTTTGGGCAGGGAGTGGG   489
              ||||     |||||| ||||| ||||||||||| |||| ||||||||||
Db        488 CTAGATATCAGCTTTCTGGGGCAGGCCCGGGCCTGACTTTGGCTTTGGGCTG--GGGGCAGGGAGGGGG   546

Qy        490 CTAAGGTGAGGCAGGTGGGCCCAGCCAGTGCACACCCAATGCCCGTGAGCCCAGACACT   549
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        547 CTAAGGTGACGCAGGTGGGCCCAGCCAGTGCACACCCAATGCCCATGAGCCCCAGACACT   606

Qy        550 GGACCCTGCCTGGACCCTCTGGACCATGCGGATAGACAAGAACCGAGGGGCCTCTTGCAGCCTCCAAGGGCC   609
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GGACCCTGCATGGACCCTCTGGACCATGCGGATAGACAAGAACCGAGGGGCCTCTTGCAGCCTTCCAAGGGCC   666

Qy        610 AGCTTGTCCCACACCCGGTCACATGGACCACCTCTTGCAGCTCAGCGGGGAGGGGC   669
              |||| ||  ||||||||||||| ||| ||||||||||||| |||| |||| |||||
Db        667 AGCTCGTCCCACACCCGGTCACATGGACCACCTCTTCTTGCAGCTTCAGCGGGGGGCC   726

Qy        670 CATCCGGTCTTCCCCCTGGCGGCCCTGCTCCAGGAGCACCTCCGAGAGCACCTCCGAGAGCGCGCCCTGG   729
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CATCCGTTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACCTCCGAGAGCGCGCCCTGG   786

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGCGTC   789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGCGCCCC   846

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCCTCAGTCTCACTCCCTCA   849
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCCTCAGGACTCTACTCCCTCA   906

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCTGCAACCTGCAACGTAG   909
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAG   966

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAGGGAG   969
              ||||||| |||||||||||||||| |||||||||||||||||||||| |||||||||||||
Db        967 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCAGCAGGGAG   1026

Qy        970 GGAGGGTGTCTGCTGAAGCCAGCCAGCTCCTCAGCCACCCCGGCTGTGCA   1029
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GGAGGGTGTCTGCTGAAGCCAGCCAGCTCCTCAGCCCTGCGACGCACCCCGGCTGTGCA   1086

Qy       1030 GCCCCAGCCCAGGCAGCAAGGCAGCCCCATCGTGTCCTCACCGGAGGCCTCTGCCC   1089
```

```
Db  2165 TTCTTCCCTACAGCAGGCTAACCGTGGACAAGAGCAGTGGACAAGAGCAGCAGTGGCAGGAGGGGAATGTCTTC 2224
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2167 TCATGCTCCGTGATGCATGAGGGCTTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
              ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  2225 TCATGCTCCGTGATGCATGAGGGCTTCTGCACAACCACTACACAGAAGAGCCTCTCCCTG 2284
Qy  2227 TCCCCGGTAAATGAGTG 2244
              |||| ||||||||||||
Db  2285 TCTCTGGGTAAATGAGTG 2302
```

RESULT 2
AAS11982
ID   AAS11982 standard; DNA; 3223 BP.
XX
AC   AAS11982;
XX
DT   04-DEC-2001 (first entry)
XX
DE   DNA encoding Humanised monoclonal antibody Hu266, heavy chain.
XX
KW   Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW   Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW   heavy chain; ds; gene therapy.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   12..2235
FT   /*tag= a
FT   /product= "Hu266_heavy_chain"
FT   sig_peptide   12..68
FT   /*tag= b
FT   mat_peptide   69..2232
FT   /*tag= c
FT   /label= "Mature_Hu266_heavy_chain"
FT   exon   1..405
FT   /*tag= d
FT   /number= 1
FT   intron   406..637
FT   /*tag= e
FT   /number= 1
FT   exon   638..930
FT   /*tag= f
FT   /number= 2
FT   intron   931..1322
FT   /*tag= g
FT   /number= 2
FT   exon   1323..1365
FT   /*tag= h
FT   /number= 3
FT   intron   1366..1484
FT   /*tag= i
FT   /number= 3
FT   exon   1485..1815
FT   /*tag= j
FT   /number= 4
FT   intron   1816..1912
FT   /*tag= k
FT   /number= 4
FT   exon   1913..2235
FT   /*tag= l
FT   /number= 5
XX
PN   WO200162801-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US06191.
XX
PR   24-FEB-2000; 2000US-0184601.

```
Db  1087 GCCCCAGGCCAGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGGCCTCTGACC 1146
              |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCACCAGGTCCAGGCAGGCA 1149
              ||||||| |||||||||||||||||||||||||||||||||||||||||
Db  1147 ACCCCACTCATGCTCAGGGAGAGGGTCTTCGGATTTTCCACCAGGTCCCGCGCA-CCA 1205
Qy  1150 CAGGCTGGGTGCCCTACCCCCAGGCCCTTCACACACAGGGGCAGGTGCTGTGGCTCAGACC 1209
              |||||||||| ||||||||||||||| |||||||||||||||||||| |||||||||||
Db  1206 CAGGCTGATGCCCCTACCCCCAGGCCCTGCCATACA-GGGCAGGTGCTGCGCTCAGACC 1264
Qy  1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGGCCAAA 1269
              ||||||| ||||||||||||||||||||||||||||||||||||||
Db  1265 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGGCCACCCAAAGGCCAAA 1324
Qy  1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCAGATCCGAGTAACTCCCAATCT 1329
              ||| |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  1325 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCAGATCTGAGTAACTCCCAATCT 1384
Qy  1330 TCTCTCTGCGAGAGCGCAAATGTTGTGTCGAGTGCCACCGTGCCCAGTGAAGCAGCCCA 1389
              |||||||| ||||| |||||| ||||||||| |||||||||||||||||||| ||||||
Db  1385 TCTCTCTGCAGAGTCCAAATATGTGTCCCCATGCCCATCATGCCCAGTGAGCCAACCCA 1444
Qy  1390 GGGCCTGCCCCTCCAGCTCAAGGCCGGACAGGTGCCCTAGAGTAGCCTGATCCAGGGACA 1449
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1445 GGGCCTGCGCCCTCCAGCTCAAGGCCGGACAGGTGCCCTAGAGTAGCCTGATCCAGGGACA 1504
Qy  1450 GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGG 1506
              |||||||| ||| ||||||| |||||||||||||||| ||||||||||    ||||| ||
Db  1505 GGCCCCAGCGCGGGGTGCTGGAGGTGCATCCACCTCCATCTTCCTCCAGCACCTGAGTTCCTGG 1564
Qy  1507 CAGCACCGTCAGTCTTCCGTCTTGTGTCCTCAGCAGTCCATGATCTCCCGGA 1566
              |||| ||||||||||| |||| ||| ||||||||||||||||||||||||||
Db  1565 GGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACACCCTCATGATCTCCCGGA 1624
Qy  1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
              ||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||
Db  1625 CCCCTGAGGTCACGTGCGCCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1684
Qy  1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
              |||||||||||||||| ||||||||||| ||||||||| ||||||||||||||||||||
Db  1685 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1744
Qy  1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
              ||||||||| |||| |||||||||||| |||| ||||||||||||||| |||||||||||
Db  1745 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1804
Qy  1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1806
              ||||||||||||||| ||||||||||| |||||||||| ||||||||| ||||||||||
Db  1805 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCGTCCTCCATCGAGAAAAACCA 1864
Qy  1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCCACATGACCAGAGGCCGGCTC 1866
              ||||||||||| |||| ||||| |||| |||||||||||||||| ||||||||||| ||
Db  1865 TCTCCAAAGCCAAAGGGTCCCACACCCGGGTGCGCACGGCCACAGGCCACAGAGGCCCAGCTC 1924
Qy  1867 GGCCCACCCCTGCCCTGGAGTGACCGCTGTGCCTCCTACAGGGCAGCCC 1926
              |||||| ||||| |||||||| |||| |||||||| ||||||||||||||
Db  1925 GGCCCACCCTGCCCTGGGAGTGACCGCGTGTCCTCCTACAGGGCAGCCC 1984
Qy  1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGATGACCAAGAACCAGGTC 1986
              ||||||||||||||||||||||| ||| ||||||||||||||| ||||||||||||
Db  1985 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 2044
Qy  1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
              |||||||||||||||||||||| |||||||||||| |||||||||||||||||||||||
Db  2045 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2104
Qy  2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  2105 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 2164
Qy  2107 TTCTTCCCTACAGCAGGCTAACCGTGACAAGAGCAGTGGCAGCAGGGGAACGTCTTC 2166
              |||||||||||||||||||| |||||||||  |||||||
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PR   08-DEC-2000; 2000US-0254465.
PR   08-DEC-2000; 2000US-0254498.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI   Vasquez M;
XX
DR   WPI; 2001-550087/61.
DR   P-PSDB; AAU07745.
XX
PT   New humanised antibody for the treatment of Alzheimer's disease.
PT   inhibition and reduction of the formation of amyloid plaques
XX
PS   Example 13; Fig 5; 63pp; English.
XX
CC   The invention relates a humanised antibody comprises the -
CC   an epitope relates a humanised antibody that specifically binds
CC   Abeta. The antibody is contained within positions 13-28 of amyloid beta peptide,
CC   amyloid plaques or the fragments are used the effects of amyloid beta formation of
CC   their fragments are used for the effects of toxic and reduce the formation of
CC   the prolonged expression for the manufacture of recombinant soluble Abeta species in humans
CC   tissues forged expression for the manufacture of a medicant. This includes
CC   Down's syndrome or pre clinical sequences of recombinant This includes
CC   Specifically, the antibody clinical/pre-clinical Alzheimer's disease,
CC   or cerebral, the antibody is used to prevent/reverse cerebral amyloid angiopathy,
CC   peptide within the brain thereby improving cognition of the Abeta
CC   sequence encodes the heavy chain accumulation into plasma, brain
CC   Hu266, based on the mouse antibody 266.
XX
SQ   Sequence 3223 BP; 659 A; 1135 C; 885 G; 544 T; 0 other;

Query Match      78.3%;  Score 1761.2;  DB 22;  Length 3223;
Best Local Similarity   88.1%;  Pred. No.0;
Matches 1984; Conservative  0;  Mismatches  238; Indels  30;  Gaps  5;
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```
Qy       5 GACCACCATGGGTTGGAACTGTATCATCTTCTTCTGGTTACCAGCTGTGCA   64
           ||||||||||||||||||| ||| ||| || |||||||||||||||||||
Db       5 GTCCCACCATGAATTTCGGGCTGCAGTCTGGGGCTGAGAAGCCTACAGTGAA   64

Qy      65 CTCCCAGGTCCAGCTGCAGTCTGGGGCTGCAGTCTGGGGAGTCAGTGAA  124
           || || ||||||||||| |||||||||||||||||||||||||||||||
Db      65 GTGTGAAGTGCAGCTGGTCGTGGGAGTTTAGTGCAGCCCTGGAGGGTCCCTGAG  124

Qy     125 GGTGTCCTGCAAAGCTTCGGCTACACCATTCACTTTTAGTAGGTATTATGCTATC  184
           || || ||||||||||||||||||||||||||||||||||||||||||||||
Db     125 ACTCCTCTGTGCAGCCTCTGAGTTGGAGTTGGAGTGGATTAATATTTACTATGATA  184

Qy     185 GGCTCCTGACACAGGCCCTGAGTGGATTGGAGTTAAATTATTAATTAATTATTACTGGT  244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 GGCTCCAGGCAAGGGCCTGAATTGGTCGCACAAATTAATAGTTGGTAATAGCACCTA  244

Qy     245 CTACACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTGACAGCAGC  304
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 CTATCGAGACACTCTAGAGGCTTTGACATCAGAGACATCTCCAGAGACAACACCCT  304

Qy     305 CTATATGGAACTTAGTTCTTTGAGATCTGAGGTTATTACTTGTGCAAGAGC  364
           ||||||||| |||||||||||||||||||||||||||||||||||| |||
Db     305 GTACCTGCAAATGAACTCCCTGAGGGCTGAGGACACGGCCGTGTATTACTGTGCAAGAGC  364

Qy     365 A-------------------------------GACTACTGGGGTCAAGGAAC  364
           |                               ||||||||||||||||||||
Db     365 CTTAAAACCTCTAGAGCTTTTGCTGTTTGGGGCCAAGGGTCACCGTGAGT  424

Qy     413 CTCACAACCTCTAGAGCTTTGCTTGCTTTGGCTTTGGGGGCCAGGCAGGC  472
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 CTTAAAACCTCTAGAGCTTTGCTTGCTTTGGCTTTGGGGGCCAGGCAGGC  484

Qy     473 GGGGGCTAAGGTGAGGCAGGTTGCCCTTGGGCCCGGTGAGCCCAG  532
           |||||||||||||||||||||||||||||||||||||||||||||
Db     485 GTGGGCTAAGGTGAGGCAGGTTGCCCTTGGGCCCGGTGAGCCCAG  544
```

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Qy     545 ACACTGGACCCTGCCTGGACCTCGTGGATAGACAAGAACCGAGGGGGCTCTGCGCCCTG  604
           ||| ||||||||||||| ||||                 |||||||
Db     533 ACACTGGACCGCT-----------GAACCTGCGGACAGTTAGAACCCAGGGGCCCTGCGCCCTG  587

Qy     605 GGGCCAGCTCTGTCCCACACGGGTCACATGGCACCACCTCTCTTTGCAGCCTCCACAA  664
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     588 GGGCCCAGCTCTGTTCCCACACCACCGCGTCACATGGCACCACCTCTCTTTCGCAGCCTCCACCAA  647

Qy     665 GGGGCCCATCGGTCTTCCCCTGGACCCCTGGCTCCTGGCACCCTCCAGGAGCACCAGCAGCGGC  724
           ||||||||||||||||| || |||||||||||||||||||||||||||||||
Db     648 GGGGCCCATCGGTCTTCCCCGGACCCCTGGCACCCTCCAGGAGCACCAGCAGCGGC  707

Qy     725 CCTGGGCTGCCGGTCAAGGACTACTTCCCCGAACCGGTCACAGCGGTGTGGAACTCAGG  784
           || || ||||||||||||||||||||||||||||||||||||||||||||||||
Db     708 CCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTCGTGACGGTGTCGTGGAACTCAGG  767

Qy     785 CGCTCGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTC  844
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     768 CGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC  827

Qy     845 CCTCAGCAGCGTGGTGACAGCCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAA  904
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     828 CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACACCTGCAA  887

Qy     905 CGTAGATCACAGACCCAGACACACAACAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCA  964
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     888 CGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACA  947

Qy     965 GGGAGGGAGGGTGTCTGCTGGAAGGCAGGCCAGGCTCAGCCCTCCTGCCGTCCTGGAGGGCTC  1024
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     948 GGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCGCACCCGGCT  1007

Qy    1025 GTGACAGCCCCGGGCCAGGGCAGCAAGCAGGGCAGGCCACGGCCCCGGGCTC  1084
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1008 ATGCAGCCCCACTCAGTCCAGCGTTCCTCATGTCTCGCGCCCCTCACCCGGAGGGCTC  1067

Qy    1085 TGCCCGCCCCACTCATGCTCAGGGAGCAGGGTCTTCTGGCTTTTCCACCAGGCTCCAGGC  1144
           |||||||||||||||||||||||||||||||  |||||||||||||||||||
Db    1068 TGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC--CCAGGCTCCGGGC  1126

Qy    1145 AGGCACAGGCTGGGTAGGTGCCCCTAACCCAGGGCCCTGCACCAGGGCCAGTGGGTGTTGGTC  1204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1127 AGGCACAGGCTGGGTAGGTGCCCCTAACCCAGGGGCAGGGCCAGTGGGTGTTGGGTTCGGTC  1186

Qy    1205 AGACCTGCAAAGCCATATCCGGGATGGCCAGTGGGGACACCCCAAAAG  1264
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1187 AGACCTGCCAAGACATATCCGGGGAGGGCAGTGGGGACCCCCAAAGG  1246

Qy    1265 CCAAACTGTCCACTCCCTGGAGCGCAAATGTTGTGTCGA--------GTGCCCACCGTTGCCCA  1324
           ||||||||||||||||||||| |||||||||||          |||||||||||||
Db    1247 CCAAACTCTCCACTCCCTCGGAGCGCAAATCTTGTGTCGACAAAACTCACACATGTGCCCA  1306

Qy    1325 AATCTTCTCTGCGAGAGCCCAGCCGGGGACAGTGCCACCTCCAGTAACTCCC  1375
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1307 AATCTTCTCTGCGAGAGCCCAAATGTTTGTGTCGAAAATCTTGTGACAAAAACTCACACACGTAACTCCA  1366

Qy    1376 GGTAAGCCAGCCAGGCACAGGCGGGGACAGGTGCCCCTAGAGTAGCC  1426
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1367 GGTAAGCCAGCCAGCCCCAGGCCGGGGACAGGTGCCGCCTTAGAGTAGCC  1426

Qy    1436 TGCATCCAGGGACAGGCCCTTCGGTGCTGACAGTGCTGACAGTC  1495
           |||||||||||||||||||||||||||||||||||||||||||
Db    1427 TGCATCCAGGGACAGGGACAGGGACAGTGCCACCTCCATCTCTTCTCAGC  1486

Qy    1496 ACC---ACCTTGCGCACCCTCCGGACTTGCGGCACCCT  1552
           |||      ||||||||||||||||||||||||||||||
Db    1487 ACCTGAACTTCCGGACCTTGCGGCACCTTCCCCCAAAACCCAGGACACCCT  1546

Qy    1553 CATGATCTTCCCCGAGACCCTGAGTCAGTCAGTGCGTGCCTGGTGGTGGTGTGCAGCACCCT  1612
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1547 CATGATCTTCCCCGAGACCCTGAGGTCAGTGCGTGGTGGTGTGGTGCAGGACACCCT  1606

Qy    1613 CGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC  1672
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Db  1607  TGGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC  1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1667  ACGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA  1726
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1673  ACGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTTGTGCACCA  1732
Qy  1727  GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC  1786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1733  GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC  1792
Qy  1787  CATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTATGAGGGCCACATGG  1846
          ||||||||||||||||||||||||||||||||||  ||||||||| |||||||||||
Db  1793  CATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGG  1852
Qy  1847  ACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCC  1906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1853  ACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTACCAACCTCTGTCC  1912
Qy  1907  CTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGA  1966
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1913  CTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA  1972
Qy  1967  CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG  2026
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1973  CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCG  2032
Qy  2027  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGG  2086
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2033  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG  2092
Qy  2087  ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC  2146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2093  ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC  2152
Qy  2147  AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA  2206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2153  AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA  2212
Qy  2207  AGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2238
          |||||||||||||||||||||||||||||||
Db  2213  AGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG  2244
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XX
PF  18-NOV-1991;   91WO-US08605.
XX
PR  23-NOV-1990;   90US-0618314.
XX
PA  (GEHO ) GEN HOSPITAL CORP.
XX
PI  Seed B, Walz G;
XX
DR  WPI; 1992-216789/26.
DR  P-PSDB; AAR24442.
XX
PT  Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PT  - used in treating chronic inflammation, rheumatoid arthritis,
PT  psoriasis, etc.
XX
PS  Disclosure; Fig 1; 46pp; English.
XX
CC  The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC  inventors designed a molecule including several such sites for
CC  attachment of sialyl-Lex side chains (see AAR24442, FT). The
CC  additional N-linked glycosylation sites are introduced at locations
CC  which impair complement fixing and Fc receptor binding ability. They
CC  are preferably located in the CH2 region of the Ig molecule.
CC  Antibodies bearing multiple sialyl-Lex determinants are useful for
CC  disrupting undesirable interactions between cells or proteins.
CC  Disrupting this interaction has therapeutic applications, for
CC  example, in minimising inflammation following tissue injury.
XX
SQ  Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;

Query Match             77.3%;  Score 1739.4;  DB 13;  Length 2287;
Best Local Similarity   89.0%;  Pred. No. 0;
Matches 2036;  Conservative    0;  Mismatches 186;  Indels 65;  Gaps   12;
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Qy     6  ACCACCATGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACAGCTACAGGTGTG   62
          ||||||||||| |||||||      |||||||||| |||||||||||||||||||||
Db     7  ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTGGTGGCAGCAGCTACAGGTGTC   66

Qy    63  CACTCCCAGGTCCAGCTGGTCGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG  122
          |||| ||||||||||||||| ||||||||||||||||||||||||||| |||||||| ||
Db    67  CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG  126

Qy   123  AAGGTGTCCTGCAAAGCTTCCGGCTACACCATTCACTGATTATGCTATACAGTGGGTGAGA  182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   127  AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA  186

Qy   183  CAGGCTCCTGGACAGGGGCTTGAGTGGATGGGATTATTACTATATGATAATACA       242
          ||||| ||||||||| |||||||||||||||||||||    | | | | ||  || ||
Db   187  CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCCTATCTTTGGTACAGCA  246

Qy   243  AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA  302
          ||||||  ||||||||| | ||||| | ||| | |  ||  | ||| |||  ||||||||
Db   247  AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA  306

Qy   303  GCCTATATGGAACTTAGTTCTTGAGATCTGAGGACATACGGCCGTTTATTACTGTGCAAGA  362
          ||||| ||||| || | ||   |||||||||||||| |||||||| |||||||||||| ||
Db   307  GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA  366

Qy   363  GCGG------------------------------CCTGGTATATGGACTACTACCCTGGGT  389
          |  |                              |  | | | ||| |||||| ||||| |
Db   367  GATAATGGAGCTATTGTAGTGGTAGCTGCTCCGGGGTTCGACCCCTGGGGC            426

Qy   390  CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGG   449
          |||||  |||| ||||||||||| || |||||||  |  ||| |||   ||||||||||
Db   427  CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT-----AGCTTTCTGG   481

Qy   450  GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGAGGTGGCTAAGGTGAGGCAGGTGCG   509
          || ||||  |||||||| |||||||||||||||||| | |||||||||||||||||||
Db   482  GCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGAGGGGGCTAAGGTGAGGCAGGTGCG   541

Qy   510  CCAGCCAGGTGCACACCCCAATGCCCGTGGCCCGTGAGCCCGGGCCTGCCTGGACCCTCG  569
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||| ||
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RESULT 3
AAQ25443
ID   AAQ25443 standard; DNA; 2287 BP.
XX
AC   AAQ25443;
XX
DT   02-JAN-1992  (first entry)
XX
DE   Sequence encoding antibody molecule IgG1.
XX
KW   Antibody; immunoglobulin G1; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..453
FT                   /*tag= a
FT   exon            619..972
FT                   /*tag= b
FT   exon            1361..1405
FT                   /*tag= c
FT   exon            1524..1853
FT                   /*tag= d
FT   exon            1950..2273
FT                   /*tag= e
XX
PN   WO9209293-A.
XX
PD   11-JUN-1992.
```

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Db   542  CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT----GAACCTCG  595
Qy   570  TGGATAGACAAGAACCGAGAGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG  629
Db   596  CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCACCACCGCTCTGTCCCACACCGCGG  654
Qy   630  TCACATGGCACCACCCTCTTCTGCAGCCTCCACAGAGACACAGCGCCCCATCGGTCTTCCCCCTGGCG  689
Db   655  TCACATGGCACCACCTCTCTTTGCAGCGTCCACAGAGACACAGCGCCCCATCGGTCTTCCCCCTGGCA  714
Qy   690  CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC  749
Db   715  CCCTCCTCCAGGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC  774
Qy   750  TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC  809
Db   775  TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC  834
Qy   810  TTCCCAGCTGTCCTACAGTCCTCAGCACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  869
Db   835  TTCCCCGGCTGTCCTCCTACAGTCCTCAGCACTCTTCACTCCCTCAGCAGCGTGGTGACCGTGCCC  894
Qy   870  TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC  929
Db   895  TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC  954
Qy   930  AAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC-  989
Db   955  AAGGTGACAAGAAAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGGAGC-  1013
Qy   990  CAGGCTCAGCCCTCCTGCCTGGACGCACCCGGCTGTGCAGCCCCAGCGCAGGGCAGCAA  1049
Db   1014 CAGGCTCAGCCGCTCCTGCCTGGACGCATCCGGCTATGCAGCCCCAGTCCAGGGCAGCAA  1073
Qy   1050 GGCAGGCCCCATCGTCTCGCCCCGGAGGGCCCTGCCCCACTCATGCTCAGGGA  1109
Db   1074 GGCAGGCCCCGTCGTCTGGCTTTTTCCACCAGGGGCCCACTCATGCTCAGGTA  1132
Qy   1110 GAGGGTCTTCTGGCTTTTTTC--CCAGGCTCTGGGCCAGGCACAGGCTGGGTGCCCCTAACC  1169
Db   1133 GAGGGTCTTCTGGCTTTTTTC--CCAGGCTCTGGGCCAGGCACAGGCTGGGTGCCCCTAACC  1190
Qy   1170 CAGGGCCCTTCACACAGGGGGAGGTGCTTGGCTCAGACCTGCCAAAAGCCAATATCCGGG  1229
Db   1191 CAGGGCCCTGCACACAGGGGCAGGTGCTTGGCTCAGACCTGCAGACCTGCCAAAAGCCAATATCCGGG  1250
Qy   1230 AGGACCCTGCCCCTGACCTAAGCCAAAGGCCACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG  1289
Db   1251 AGGACCCTGCCCCTGACCTAAGCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG  1310
Qy   1290 GACACCACCTTCTCTCCTCCCCAGATCCGAGTAACTCCCAAATCTTCTCTTCTCTGCAGAGGCGCAAAT  1349
Db   1311 GACACCACCTTCTCTCCTCCCCAGATTCCAGTAACTCCCAAATCTTCTCTTCTCTGCAGAGGCGCAAAT  1370
Qy   1350 GTTGTGTCGA--------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT  1400
Db   1371 CTTGTGTGACAAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT  1430
Qy   1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG  1460
Db   1431 CCAGCTCAAGGCGGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG  1490
Qy   1461 GGTGCTGACACGTCACCTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCAACCGTCA  1517
Db   1491 GGTGCTGACACGTCACCTCCACCTCCATCTCTTCCTCAGCACCTTCTCAGCACCTGGAACTCGCGGGGACCGTCA  1550
Qy   1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC  1577
Db   1551 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC  1610
Qy   1578 ACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG  1637
Db   1611 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG  1670
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Qy   1638 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACG  1697
Db   1671 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACG  1730
Qy   1698 TTCCCGTGTGGTCAGCGTCCTCACCGTTGTGTCACCAGGACTGGCTGAACGGCAAGGAGTAC  1757
Db   1731 TACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC  1790
Qy   1758 AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACC  1817
Db   1791 AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC  1850
Qy   1818 AAAGGTGGGACCCGTGGGGTATGAGGGCCACATGACAGAGAGGCCGGCTCGGCCCACCCTC  1877
Db   1851 AAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGACAGAGAGGCCGGCTCGGCCCACCCTC  1910
Qy   1878 TGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACA  1937
Db   1911 TGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAACCACA  1969
Qy   1938 GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG  1997
Db   1970 GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG  2029
Qy   1998 CCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  2057
Db   2030 CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  2089
Qy   2058 GGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTA  2117
Db   2090 GGAGAACAACTACAAGACCACACCTCCCGTCCTGGACTCCGACGGCTCCTTCTTCCTCTA  2149
Qy   2118 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGT  2177
Db   2150 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGGACGTGTTCTCATGCTCCGT  2209
Qy   2178 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAA  2237
Db   2210 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA  2269
Qy   2238 ATGAGTG  2244
Db   2270 ATGAGTG  2276
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RESULT 4
AAT60739
ID   AAT60739 standard; DNA; 2287 BP.
XX
AC   AAT60739;
XX
DT   22-APR-1997 (first entry)
XX
DE   IgG1 gene.
XX
KW   IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin;
KW   sialyl-Lewis X; antiinflammatory; inflammation;
KW   extravasation-dependent adverse reaction; organ damage; clotting;
KW   adult respiratory distress syndrome; ischaemic myocardial injury; glomerular nephritis;
KW   septicaemia; therapy; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9700079-A1.
PD   03-JAN-1997.
XX
PF   11-JUN-1996; 96WO-US10043.
XX
PR   14-JUN-1995; 95US-0000213.
XX

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PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Pouyani T, Seed B;
XX
DR   WPI; 1997-077356/07.
DR   P-PSDB; AAW10550.
XX
PT   P-selectin and opt. E-selectin binding organic mol. - having
PT   sialyl-Le(x) and sulphated determinant, useful for protecting
PT   against inflammatory or immune reactions
XX
PS   Disclosure; Page 40-41; 81pp; English.
XX
CC   The gene (AAT60739) encoding IgG1 (AAW10550) can be subjected to site-
CC   directed mutagenesis in order to introduce one or more N-linked
CC   glycan addition sites into the IgG1 molecule (see also AAW10551).
CC   Eukaryotic host cells co-transfected with a vector carrying the
CC   the mutated IgG1 gene and with a vector that expresses an alpha-
CC   (1,3)fucosyltransferase capable of attaching sialyl-Le(x) groups at
CC   the glycosylation sites of the antibody molecule can be used in the
CC   prodn. of sialyl-Le(x)-modified antibody. Such an antibody has
CC   therapeutic applns., e.g. in minimising inflammation and
CC   decreasing extravasation-dependent organ damage and/or clotting.
XX
SQ   Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;

Query Match             77.2%;  Score 1736.2;  DB 18;  Length 2287;
Best Local Similarity   88.9%;  Pred. No. 0;
Matches  2034;  Conservative    0;  Mismatches  188;  Indels   65;  Gaps   12;
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Qy    6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCAGCTACCAGGTGTG   62
         ||||||||| |  || || |||   |||| ||||||| ||||| |||||||||||| |||
Db    7 ACCACCATGACGTGGACCTGGAGGGTTCCCTCTTCTTTGTGGTGGCAGCTACCAGGGTGTC  66

Qy   63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG  122
         ||  || |||||||||| |  | ||||| |||| || ||||||||| |||| |||| |
Db   67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG  126

Qy  123 AAGGTGTCCTGCAAAGTCTTCGGCTACACAGTTCTCGGCTACACATTCACTGATTATGGC  182
         |||||||||||||   | |    ||| || ||   |  | | |  | |||||||||| ||
Db  127 AAGGTCTCCTGCAAGGCTTCTGGCTACACCTTCACCGACTACTATCAGCAGCTGGGTGCGA  186

Qy  183 CAGGCTCCTGGACAGGGGCCTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA  242
         |||| |  |  |||||||  ||||||  | |   | |  || |  ||||||| ||| ||
Db  187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGGGATCATCCCTATCTTTGGTACAGCA  246

Qy  243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTGACGAGCACA  302
         |||| |  |  ||||| || |   ||  | ||| |||||| |    | |  |||||
Db  247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA  306

Qy  303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTATTACTGTGCAAGA  362
         | || |  |   |  |  |   |||||     |||  ||| | |  | |||||| |||
Db  367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTGGGGC  366

Qy  363 GCGG---------CCTGGTATATGGACTACTGGGGT  389
         |||          |  | |  || |  | |||||
Db  367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTGGGGC  426

Qy  390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG  449
         |||| ||  |   || || ||||| |||| |   |   || |   | | |||  | |||
Db  449 CAAGGGACCCTGGTCACCGTCTCCTCAGAGCTTCCTCCAGCTTCCTCTGGAGCTTTCTGGG  481

Qy  450 GCGAGCGCGGCCTGACTTTGGCTTTGGGCAGGTGGGCTAAGGTGAGGCAGGTGCG  509
         | || ||| ||| || |   ||| | ||| || || || |  ||| || ||| |||
Db  482 GCAGGCCAGGCCTGACCTTTGGCTTTGGGTCGGCTTTGGGCTAAGGTGAGGCAGGTGCG  541

Qy  510 CCAGCCAGGTGACACACCCAAATGCCCGGTGAGCCCAGACTGACCCCTGCCTTGACCCCTCG  569
         |  |||||| ||| ||||  | ||| | |||   ||| || |  | | | |   ||| ||
Db  542 CCAG-CAGTGACAGCACACCCAAATGCCCGACACTGGACGCT----GAACCTCG  595

Qy  570 TGGATAGACAAGAACCGGAGGGCCTCTGCGCCTCCCAGCTCTGTCCCACACCGCGG  629
         | ||| |  |||| | || |  |||||| ||   |||||||||| ||||||||||||
Db  596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGGCACCCAGCTCTGTCCCACACCGCGG  654
```

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Qy  630 TCACAATGGCACCACCTTCTTCTGCGAGCCTCTCCTCCAAGAGCACCTCTCCCCCTGGCG  689
         ||||||||||||||||||||||||||||||||| ||  |||||||||| |||||||||
Db  655 TCACAATGGCACCACCTTCTTCTGCGAGCCTCTCCTCCAAGAGCACCTCTCCCCCTGGCA  714

Qy  690 CCCTGCTCCAGGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC  749
         |||| ||||||||||||||||||||||||||||||||||||||||||||
Db  715 CCCTCCTCCAAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC  774

Qy  750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC  809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC  834

Qy  810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  869
         |||| || |||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  894

Qy  870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC  929
         ||||||||| ||||  |||||| ||||||||||||| | ||||||||||||||||||| ||
Db  895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC  954

Qy  930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGCTGCTGGAAGC  989
         |||||||||||||||||| ||||||| ||||| ||| ||||||||||| | ||| |||
Db  955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAA-C 1013

Qy  990 CAGGCTCAGCGCTTCCTGCTTGGCTGACGCACCCTTCTGCGCCCGGAGGCTGAGCAGGGCAGCAA 1049
         |||||||||||| |||||||||||||||||| |||| |||||||| |||||||||||||||||||
Db 1014 CAGGCTCAGCGCTCCCTGCTTGCTGACGCATCCGGCTATGCTCCCGGAGGCTGAGCAGGGCAGCAA 1073

Qy 1050 GGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109
         ||||| ||||||| || | | | |||||||||| |  ||| | |||||||||||||||||
Db 1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGACCGCCCCACTCATGCTCAGGGA 1132

Qy 1110 GAGGGTCTTCTGGCTTTTCCACCAGGTCCAGCCGCACAGCCTGGGCTGCCCTACCC 1169
         ||||||||||| |||||     ||||  |||| | || || ||| || |||  |||
Db 1133 GAGGGTCTTCTGGCTTTTTC--CAGGCTGGGCAGGCACAGCCTGGGTCCTCCGGTC 1190

Qy 1170 CAGGCCCTTCACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
         |||||||| | |||| | ||||||||| |||||||||| |||||||||| || ||||||
Db 1191 CAGGCCCTGCACACAAGAGGGCAGGTGCTTCTGGGCTCAGACCTGCCAAAAGCCATATCCGGG 1250

Qy 1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCCAAAGCCAAACTGTCCACTCCCTCAGTCG 1289
         |||||| || ||||  |  | ||| | ||  |||| |  | |||||| |||||||||||
Db 1251 AGGACCTGCCCTGCCCTGACCTAAGCCCAACCCCAAAGGCCAAACTCTCCACTCCCTCAGTCG 1310

Qy 1290 GACACCTTCTCTCCTCCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGGCCAAAT 1349
         |||||||||| |||| |||||| |  || |||||||||||| ||| ||| ||||| |||
Db 1311 GACACCTTCTCTCCTCCCCAGATTCAGTAACTCCCAATCTTCTCTCTGCAGAGGCCAAAT 1370

Qy 1350 GTTGTGTGA-------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
         | | |||||        ||||||||||||||| ||||||||| || |||||||||||
Db 1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy 1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTCCATCCCAGGACAGGCCCCAGCTG 1460
         ||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||
Db 1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy 1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCAGC---ACCTGCGCGCCAGACCGTCA 1517
         |||||||||||||||||||| |||||| |||||||| |    | || | |  ||||| |||
Db 1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCACTTCCTGAACTCCTGGGGCCGTCA 1550

Qy 1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGGACCCCTGAGGTC 1577
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 1551 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGGACCCCTGAGGTC 1610

Qy 1578 ACGTGGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAGTTCAACTGTACGTG 1637
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1611 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 1670

Qy 1638 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACG 1697
         |||||||||||||||| |||||||||| |  ||| | |||||||||| ||  ||||||||
Db 1671 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 1730
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Qy  1698  TTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTAC  1757
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1731  TACCGGGTGGTCAGCGTCCCTCACCGTCCTGACCAGGACTGGCTGAATGGCAAGGAGTAC  1790

Qy  1758  AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATGCAGAAAACCATCTCCAAAACC  1817
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  1791  AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC  1850

Qy  1818  AAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCCGGCCCACCCTC  1877
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1851  AAAGGTGGGACCCGTGGGGTGCAGGGCCCACATGGACAGGAGCCGGCTCCGGCCCACCCTC  1910

Qy  1878  TGCCCTGGGAGTGACCGCGTGTGCCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACA  1937
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1911  TGCCCTGAGAGTGACCGCGTGTACCAACCTCTGT-CCTTACACGGGCAGCAGCCCCGAGAACCACA  1969

Qy  1938  GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG  1997
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  1970  GGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG  2029

Qy  1998  CCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  2057
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  2030  CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  2089

Qy  2058  GGAGAACAACTACAAGACCACACCCCCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTA  2117
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2090  GGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGGTCCTTCTTCCTCTA  2149

Qy  2118  CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT  2177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2150  CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCCTGTCTCCGT  2209

Qy  2178  GATGCATGAGGGCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA  2237
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  2210  GATGCATGAGGGCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA  2269

Qy  2238  ATGAGTG  2244
          |||||||
Db  2270  ATGAGTG  2276
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RESULT 5

AAF55225

ID   AAF55225   standard; DNA; 4694 BP.

XX

AC   AAF55225;

XX

DT   29-MAY-2001 (first entry).

XX

DE   Nucleotide sequence of pG4HE.

XX

KW   Complementarity determining region; CDR; immune response; antibody;
KW   cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW   autoimmune disease; infectious disease; inflammation; allergy; cancer;
KW   rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   transplant rejection; graft versus host disease; ss.

OS   Unidentified.

XX

PN   WO200114424-A2.

XX

PD   01-MAR-2001.

XX

PF   24-AUG-2000; 2000WO-US23356.

XX

PR   24-AUG-1999; 99US-0150452.

XX

PA   (MEDA-) MEDAREX INC.

XX

PI   Korman AJ, Halk EL, Lonberg N;

XX

DR   WPI; 2001-202933/20.

PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient

XX

PS   Example 10; Page 94-95; 127pp; English.

CC
CC   The present sequence is used in the course of the specification. The
CC   specification describes a human antibodies which specifically bind to
CC   human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC   antibodies are used in methods for inducing, augmenting or prolonging
CC   an immune response to an antigen in a patient, where the antibodies
CC   block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies are used for treating
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions. The polyvalent or polyclonal preparations or allergic
CC   components for the treatment of diseases with inflammatory or allergic
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.

XX

SQ   Sequence 4694 BP; 1068 A; 1396 C; 1248 G; 982 T; 0 other;

Query Match   72.8%; Score 1638; DB 22; Length 4694;
Best Local Similarity   94.6%;
Matches 1719; Conservative   0; Mismatches   95; Indels   4; Gaps   2;

```
Qy  430  AACCTCTAGAGCTTTCTGGGGCCCAGCCGCGGGCCTGACTTTGGCTTTTGGGGCAGGGAGTGG  489
         | ||||||||||||| ||||||||||||||||||||||||||||| |-|||||||||||||||
Db    8  AGCAGCTGAAGCTTTCTGGGGCAGGGCCGGGGCCTGACTTTGGC-TGGGGCAGGGAGGGGGG  66

Qy  490  CTAAGGTGAGGCAGGTGGCGGCCAGCGAGTGCACACCCAATGCCCGTGAGCCCAGACACT  549
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   67  CTAAGGTGACGCAGGTGGCCCCAGCCAGCGTGCACACCCAATGCCCATGCCCAGAGCCAGACACT  126

Qy  550  GGACCCCTGCCTGGACCCCTCGTGGATAGACAAGAACCGAGGGGGCCTCTGCGCCTGGGCCC  609
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  127  GGACCCCATGCGGATAGACAAGAACGAGGGGGCCTCTGCGCCTGGGCCC  186

Qy  610  AGCTCTGTCCCCACCACCGGTCACATGGCCCACCACCTCTCTTGCAGCCTCCAACAAGGCC  669
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  187  AGCTCTGTCCCCACCACCGGTCACATGGCCCACCACCTCTCTTGCAGCTTCCAACAAGGCC  246

Qy  670  CATCGGTCTTCCCCTGGCCTGCCCTGCCCTGCCTCCAGAGAGCCACCTCCAGAGAGCCACC  729
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  247  CATCGTCTTCCCCTGCCCCTGCCCTGCCTCCAGAGAGCCACCTCCAGAGAGCACCAGCGCCCTGG  306

Qy  730  GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC  789
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  307  GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC  366

Qy  790  TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCACTCTACTCCTCA  849
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  367  TGACCAGCGGCGTGCACACCTTCCCGGCTGTCACAGTCCTCAGGACTCTACTCCTCA  426

Qy  850  GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG  909
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  427  GCAGCGTGGTGACCGTGCCCTCCAGCAACTTGGGCACACAGACCTACACCTGCAACGTAG  486

Qy  910  ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAGGGAG  969
         ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  487  ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCAGGGAG  546

Qy  970  GGAGGGTGGTCTGCTGGGAAGCCAGGCTCAGCCCTCCCTCGGCTCCGCTGTGCA  1029
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  547  GGAGGGGTGTCTGCTGGGAAGCCAGGCTCAGCCCCTCCCTCGGCTCCGCTGTGCA  606
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Db   1687 TCTTCCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGCAGGTGGCAGGGGGAATGTCTTC 1746
          |||||||||||||| ||| |||||||| |||||||||||||||||||||||||||||||||||
Qy   2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACCGCGAGAAGAGCCCTCCCCTG 2226
          ||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||
Db   1747 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACCACAGAGAGCCCTCTCCCCTG 1806

Qy   2227 TCCCCGGGTAAATGAGTG 2244
          ||  |||||||||||||||
Db   1807 TCTCTGGGTAAATGAGTG 1824
```

RESULT 6
ABK85577
ID   ABK85577 standard; DNA; 4694 BP.
XX
AC   ABK85577;
XX
DT   03-SEP-2002   (first entry)
XX
DE   Human IgGgamma4 heavy chain plasmid pG4HE.
XX
KW   Transgenic; rodent; immunoglobulin; Ig; transchromosome; B-cell;
KW   human antibody display library; immune-related disorder; mutant;
KW   immunomodulatory; IgGgamma4 heavy chain; pG4HE; cyclic;
KW   circular; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO20243478-A2.
XX
PD   06-JUN-2002.
XX
PF   30-NOV-2001; 2001WO-US45293.
XX
PR   30-NOV-2000; 2000US-250340P.
XX
PA   (MEDA-) MEDAREX INC.
PA   (KIRI) KIRIN BEER KK.
XX
PI   Tomizuka K, Ishida I, Lonberg N, Halk E;
XX
DR   WPI; 2002-500300/53.
XX
PT   New transgenic nonhuman mammal, useful for generating B-cells
PT   expressing human antibody sequences and generating antigen-specific
PT   hybridomas secreting human sequence antibody, comprises two human
PT   immunoglobulin loci -
XX
PS   Disclosure; Page 48-50; 110pp; English.
XX
CC   The present invention relates to novel transgenic nonhuman mammals,
CC   particularly rodents, comprising two human immunoglobulin (Ig) loci,
CC   where one of the two the human immunoglobulin loci is a human heavy chain
CC   locus and the other locus is a human light chain locus, and where
CC   only one of the loci is of a transchromosome. The transgenic animals
CC   are useful for generating a number of B-cell expressing human
CC   antibody sequences. They are also useful for producing rearranged
CC   immunoglobulin sequences, producing human antibody display libraries,
CC   and generating a human sequence antibody that binds to a predetermined
CC   antigen. The produced antibodies are useful for treating immune-related
CC   disorders. The present sequence represents a plasmid used in the
CC   construction of expression vectors for human IgG.
XX
SQ   Sequence 4694 BP; 1068 A; 1396 C; 1248 G; 982 T; 0 other;

Query Match   72.8%; Score 1638; DB 24; Length 4694;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 1719; Conservative 0; Mismatches 95; Indels 4; Gaps 2;

```
Qy    430 AACCTCTAGAGCTTTCTCGGGCGCAGGAGCGCCGGCCCTGACTTTGGGCTTTGGGGCGAGTGGG 489
          | | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy   1030 GCCCAGCCCAGGGCAGCAGGCAGGCCCCATCTGTCTCCTCCACCCGGAGGCCTCTGCCC 1089
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||| ||
Db    607 GCCCCAGCCCAGGGCAGCAGGCAGGCCCATCCCCATCTGTCTCCTCCACCCGGAGGCCTCTGACC 666

Qy   1090 GCCCCACTTCATGCTCAGGGAGAGGGTCTTCTTGGCTTTTTCCACCAGGTTCCAGGCAGGCA 1149
          |||||||||||||||||||||||||||||||||| |||||||||||||||||| |||||| ||
Db    667 ACCCCACTTCATGCTCAGGGAGAGGGTCTTCTTTGGATTTTTCCACCAGGTTCCGGGCAGCCA 726

Qy   1150 CAGGCTGGGTGCCCCTCACACAGGGGCAGGTGCTGGCTCAGACC 1209
          ||||||||| |||||| ||||||||||||||||||||||||||
Db    727 CAGGCTGGATGCCCCTACCCCAGGGCCATACAGGGGCAGGTGCGCTCAGACC 786

Qy   1210 TGCCAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    787 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 846

Qy   1270 CTGTCCACTTCCCTCAGCTCGGACACCTTCTTCCTCCCCAGATCCGAGTAACTCCCAATCT 1329
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    847 CTCTCCACTTCCCTCAGCTCAGACACCTTCTTCCTCCCCAGATCTGAGTAACTCCCAATCT 906

Qy   1330 TCTCTCTGAGAGGCAAATGTTGTGTCGAGTGCCACCGTGCCCAGGTAAGCCAGCCA 1389
          ||||||||||||||  || |||||| ||||||||||||||||||||||||||||||
Db    907 TCTCTCTGAGAGTCCAAATATGGTCCCCCATGCCCATGCCCAGGTAAGCCAACCCA 966

Qy   1390 GGCTCGCCCTCCAGCTCAAGGGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 GGCCTCGCCCTCCAGCTCAAGGGCGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1026

Qy   1450 GGGCCCAGTCGGGTGCTGACACGTCCACCTCACCTCCTCAGCACC---ACCTGCGG 1506
          ||| ||||| ||||||||| |||||||||||| || ||||||||||    ||| |||
Db   1027 GGGCCCAGCCAGGCCGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTG 1086

Qy   1507 CAGACACGGTCAGTCTTCCTCTTCCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGA 1566
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   1087 GGGGACCATCAGTCTTCCTGTTCCCCCCAAAAACCCAAGGACACTCTCATGATCTCCCGA 1146

Qy   1567 CCCCTGAGGTCAGTGCCTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1147 CCCCTGAGGTCAGTGCCTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1206

Qy   1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACACAGCGGAGGAGCAGT 1686
          ||||||||||||| || |||||||||||||||||| |||||||||||||||||||||
Db   1207 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1266

Qy   1687 TCAACAGCACGTTCCGTGCGTGTCAGCGTCCTCCACCGTTGTGCACCAGGACTGGCTGAACG 1746
          ||||||||||| |||||||| || |||||||||||||||||| |||||||||||||||||||
Db   1267 TCAACAGCACGTTCCGTGTCCGTCAGCGTCCTCCACCGTTCCTCGCTGCTGGCTGGCTGAACG 1326

Qy   1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCATCGAGAAAACCA 1806
          ||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||
Db   1327 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCATCGAGAAAACCA 1386

Qy   1807 TCTCCAAAACCAAAGGTGGGACCCCGCGGGGGTATGAGGGCCACATGACGAGAGGCCGGCTC 1866
          |||||||||||||||||||| |||||| |||||||||||||||| |||||||||||||||||
Db   1387 TCTCCAAAAGCCAAAGGTGGGACCCCACCGGGGTGCGGGCCCACATGACACAGAGGTCAGCTC 1446

Qy   1867 GGCCCACCCTGCCCTGGGAGTGACCGGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1926
          |||||||||||||||||||||||| |||||||||||||||| |||||||||||||||
Db   1447 GGCCCACCCTGCCCTGGGAGTGACCGGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1506

Qy   1927 CGAGAACCACAGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
          ||||| ||||||||| |||||||||||||| |||||||||||||| |||||||||||||
Db   1507 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCGGGATGATGACCAAGAACCAGGTC 1566

Qy   1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1567 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 1626

Qy   2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCCTCCGACGCGGCTCC 2106
          |||||||||||||||||||||||||| ||||||||||||||| ||||||||
Db   1627 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 1686

Qy   2107 TTCTTCCTCTACAGCAGGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
          |||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||||
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Query Match   94.6%; DB 24; Length 4694;

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Db
Qy      8 AGCAGCTGAAGCTTTCTGGGCAGGCCGGGCCTGACTTTGGC-TGGGGGCAGGAGGGGG  66
Db

Qy    490 CTAAGGTGAGGCAGGTGCGCCCAGCCAGTGCACACCCAGTGACACACT 549
          |||||||| ||||||||||||||| ||||||||||||||  |  ||||
Db     67 CTAAGGTGACGCAGGTGGCGCCAGCCAGTGCACACCCATGAGCCCAGACACT 126

Qy    550 GGACCCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCCTTCTGCGCCCTGGGCCC 609
          |||||| |||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    127 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCCTTCTGCGCCCTGGGCCC 186

Qy    610 AGCTCTGTCCCACCACCGCGGGTCACATGGCACCACCACCGCGGTCCACCAAGGGGCC 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 AGCTCTGTCCCACCACCGCGGGTCACATGGCACCACCACCGCGGTCCACCAAGGGGCC 246

Qy    670 CATCGGTCTTCCCCCTGGGCGCCCTGCTCCAGGAGCACTTCCGAGAGCACAGCGGCCCTGG 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 CATCCGTCTTCCCCCTGGGCGCCCTGCTCCAGGAGCACTTCCGAGAGCACAGCGGCCCTGG 306

Qy    730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCGCC 366

Qy    790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCCTACACTCCCTCA 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCCTACACTCCCTCA 426

Qy    850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAG 486

Qy    910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAGGGAG 969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 ATCACAAGCCCAGCAACACCAAGGTGTACAAGAGAGTTGGTGAGAGGCCAGCTCAGGGAG 546

Qy    970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCGTGCA 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCACCCCGGCGTGCA 606

Qy   1030 GCCCCAGCCCAGGGCAGCAAGGCAGCAAGGGACATGCAGGGTCTTCTGGCTTTTCTGCCCC 1089
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 GCCCCAGCCCAGGGCAGCAAGGCAGCAAGGGACATGCAGGGAGGAGTCTTCTGGCTTTTCTGCCC 666

Qy   1090 GCCCCACTCATGCTCAGGGGACGGGGTCTTCTGGATTTTCACCAGGCAGGCAGGCA 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 ACCCCACTCATGCTCAGGGGACGGGGTCTTCTGGATTTTCACCAGGCAGGCAGGCCA 726

Qy   1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTGGCTGACC 1209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 CAGGCTGCGATGCCCCTACCCCAGGCCCTGCCATACAGGGGCAGGTGCTGCGCTCAGACC 786

Qy   1210 TGCCAAAAGCCATATCCGGAGGAGCACCCTGCCCTGACCTAAGGCCAAAGGCCAAA 1269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 TGCCAAGAGCCATATCCGGAGGAGCACCCTGCCCTGACCTAAGGCCAAAGGCCAAA 846

Qy   1270 CTGTCCACTCCCTCGAGAGCCCAGCTCGGACACCCTCTCTCCTCCGATCCCAATCT 1329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 CTCTCCACTCCCTCGAGAGCCCAGCTCGGACACCCTCTCTCCTCCGATCCCAATCT 906

Qy   1330 TCTCTCTGCGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCA 1389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 TCTCTCTGCGAGTCCAAATATGTCCCCAACATGTGCCCATGCCCAGGTAAGCCAACCCA 966

Qy   1390 GGGCCCTGCGCCTCCAGTCAAGGCGTCAAGGCGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 GGGCCCGCCGCCTCCAGTCAAGGCGTCAAGGCGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1026

Qy   1450 GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTTCTTCCTCAGCACC---ACCTGCGG 1506
          |||||||||||||||||||||||||||||||||||||||||          ||||||||
Db   1027 GGCCCCAGCTGGGTGCTGACGGTGCTGACGCATCCACCTCCATCTTCTTCCTCAGCACCCTGAGCACCTGCTCCTGG 1086

Qy   1507 CAGCACCGTCAGTCTTCCTCTTCCTGTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 GGGGACCATCAGTCTTCTTCCTGTTCCCCCCAAAAACCCAAGGACACTCTCATGATCTCCCGGA 1146
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```
Qy   1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTCCAGTTCA 1626
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1147 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAGGAGACCCCGAGGTCCAGTTCA 1206

Qy   1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
          ||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||||||
Db   1207 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGGAGGAGCAGT 1266

Qy   1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCGTGCACCAGGACTGGCTGAACG 1326

Qy   1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCA 1386

Qy   1807 TCTCCAAAACCAAAGGTCAGGACCCGGGGTATGAGGGTGCCACATGGACAGGCCGGCTC 1866
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACATGGACAGAGGTCAGCTC 1446

Qy   1867 GGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACAGGGCAGCCC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTACCAACCTCTGTCCCTACAGGGCAGCCC 1506

Qy   1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1566

Qy   1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACACCGCTGTCCCTGGAGAGC 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACACCGCTGTCCCTGGAGAGC 1626

Qy   2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 1686

Qy   2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTC 1746

Qy   2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACAGAGAAGAGCCTCTCCCTG 1806

Qy   2227 TCCCCGGGTAAATGAGTG 2244
          |||||||||||||||||
Db   1807 TCTCTGGGTAAATGAGTG 1824
```

PR   10-OCT-1995;   95US-0544404.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1997-235888/21.
XX
PT   Novel anti-CD4 antibody produced by transgenic mice - used in the
PT   treatment of auto-immune disease etc.
XX
PS   Example 42; Page 262-264; 396pp; English.
XX
CC   A novel composition has been developed which comprises an immunoglobulin
CC   (Ig) having an affinity constant (Ka) of at least 2 multiply
CC   1000000000 M-1 for binding to a predetermined human antigen. The present
CC   sequence represents the kappa light chain plasmid pCK7-96 which includes
CC   the human gamma1 constant region and polyadenylation site. Anti-CD4
CC   antibodies may be used in therapeutic and diagnostic applications,
CC   especially for the treatment of human diseases. These antibodies reduce
CC   activity of CD4 cells and reduce undesirable autoimmune reactions,
CC   inflammatory response and transplant rejection. Transgenic animals are
CC   capable of producing heterologous antibodies of multiple isotypes by
CC   undergoing isotype switching. These animals produce a first Ig type
CC   that is necessary for antigen-stimulated B-cell maturation and can
CC   switch to encode and produce one or more subsequent heterologous
CC   isotypes.
XX
SQ   Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

Query Match   71.7%;   Score 1611.8; DB 18; Length 4723;
Best Local Similarity   94.3%;   Pred. No. 1.7e-313;
Matches 1722;   Conservative   0;   Mismatches   87;   Indels   18;   Gaps   4;

Qy   430 AACCTCTAGAGCTTTCTGGGGCGGAGCCGGGCCTGACTTTGGGGCGCAGGAGTGGG 489
          |||||||||||||||||||||||||| ||||||||||| |||||||||||||||||
Db   8 AGCAGCTGAAGCTTTCTGGGGCGGAGGCCGGGCCAGGCTGACCTTTGGGGCGGGGG 67

Qy   490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy   550 GGACCCTGTGCCTGGACCCCTCGTGATAGACAAGAAACCGAGGGGCCTCTGCGCCTGGGCCC 609
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   128 GGAGCGCT-------GAACCTGCGCGACAGTTAAGAACCCAGGGGCCTCTGCGCCTGGGCCC 182

Qy   610 AGCTCCTGTCCCACCACCGGTCACATGGCACCACCACCTCTCTTGCAGCCTCTTGCAGCGGCC 669
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   183 AGCTCTGTCCCACCACCGGTCACATGGCACCACCACCTCTCTTGCAGCCTCTTGCAGCGGCC 242

Qy   670 CATCGGGTCTTCCCCCTGGCGCCTGCTCCAGGAGCACCTCCAGGAGCACAGCGGCCCCTGG 729
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 CATCGGGTCTTCCCCCTGGCGCCTGCTCCAGGAGCACCTCCAGGAGCACAGCGGCACCCTG 302

Qy   730 GCTGCCTCGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 GCTGCCTCGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCGC 362

Qy   790 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGACTTACTCCCTCA 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGACTTACTCCCTCA 422

Qy   850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 GCAGCGTGGTGACCGTGCCCTCCAGCAACCACAGGTGTGACCACAGGTGTACAACGTGA 482

Qy   910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGTGAGAGGCCACACAGGAG 969
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGTGAGAGGCCACACAGGGAG 542

Qy   970 GGAGGGTGTCTGCTGGAAGCCAGCTCAGCGCTCTGCTCGGACGCACCCCGGCGTCTGCA 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 GGAGGGTGTCTGCTGGAAGCCAGCTCAGCGCTCTGCTCGGACGCATCCCGGCTATGCA 602

Qy   1030 GCCCCAGCCAGGGCAGCAAGGCAGGCCCCATCGTCTCCTCACCCGGAGGCCTCTGCCC 1089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603 GCCCCAGTCCAGGCCAGCAAGGCAGGCCCGTCTCTTCACCCGGAGGCCTCTGCCC 662

Qy   1090 GCCCCACTCATGTCAGGGAGAGGGTCTTCGGCTTTTCCACCAGGCTCCAGGCAGGCA 1149
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   663 GCCCCACTCATGTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTCGGGCAGGCA 721

Qy   1150 CAGGCTGGCTGCCCACCCCAGGCCCTTCACACCAGGGGCAGGTGCTTGGCTGCAGACC 1209
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   722 CAGGCTAGGTGCCCTACCCAGGCCCTGCACACCAAGGGGCAGGTGCTTGGGCTCAGACC 781

Qy   1210 TGCCAAAAGCCATATCCGGGAGACCTGGCCTGACCTAAGCCGACCTAAGGCCAAAGGCCAAA 1269
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   782 TGCCAAGAGCCATATCCGGGAGGACCCCTGCCCCTGACCTAAGCCCACCCAAAGGCCAAA 841

Qy   1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTTCCTCCAGATCCGAGTAACTCCCAATCT 1329
          ||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||||
Db   842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy   1330 TCTCTCCTGCAGAGGCCAAATGTTGTGTCGA--------GTGCCCACGGTGCCCAGGTAA 1380
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   902 TCTCTCCTGCAGAGGCCAAAATCTTGTGACAAAACTCACACATGGCCCACGGTGCCCAGGTAA 961

Qy   1381 GCCAGCCCAGGCCTTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   962 GCCAGCCCAGGCCTTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy   1441 CCAGGGACAGGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTTCCTCAGCACC-- 1498
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1022 CCAGGACAGGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTTCCTCAGCACCTG 1081

Qy   1499 -ACTTGCGGCAGCACCGTCAGTCTTCGTCAGTCTTCCTTCTTCCCCCAAAACCCAAGGACACCCTCATGA 1557
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   1082 AACTCCTGGGGGAGGACCCGTCAGTCCTGTGTCGTGGTGTGGACGTGAGCCACGAGGACCCCGAGG 1141

Qy   1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACACCTGAGG 1617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1142 TCTCCCGGACCCCTGAGGTCACATGCGGTGGTGGTGGACGTGAGCCACGAAGACACCTGAGG 1201

Qy   1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy   1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 AGGAGCAGTTACAACAGCACGTACCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy   1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy   1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGTGTGTGTCGGGGTATGAGGGCCACATGGACAGA 1857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGGTGTGTGCGGGTGCCACATGGACAGA 1441

Qy   1858 GGCCTCGGCCCCGAGAACCCACCAGGTGTACCCCGCCATCCGGGAGGAGATGACCAAG 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 GGCCGCCTCGGCCCCGAGAACCCACCAGGTGTACACCCCGCCATCCGGGAGGAGATGAGCCAAG 1501

Qy   1918 GGGCAGCCCCGAGAACCACACAGGTGTACACCCGCACGACGCACCAGCCTGGAG 1977
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1502 GGGCAGCCCCGAGAACCACACAGGTGTACACCCGCACGACCATCGCCGTCCTGGAG 1561

Qy   1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy   2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCC 1681

```
Qy   2098  GACGGCTCCTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGACAGGTGGCAGCGAGGG  2157
           ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682  GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGACAGGTGGCAGCGAGGG 1741

Qy   2158  AACGTCTTCTCATGCTCCGTGATGCATGAGGGTCTGCACAACCACTACACGCAGAAGAGC  2217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1742  AACGTCTTCTCATGCTCCGTGATGCATGAGGGTCTGCACAACCACTACACGCAGAAGAGC 2217

Qy   2218  CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
           ||||||||||||| |||||||||||||
Db   1802  CTCTCCCCTGTCTCCGGGTAAATGAGTG 1828
```

RESULT 8
AA221997
ID   AA221997 standard; DNA; 4723 BP.
XX
AC   AA221997;
XX
DT   24-NOV-1999 (first entry)
XX
DE   Nucleotide sequence of plasmid pCG7-96.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
KW   human mouse; human heavy chain transgene; transgene; digoxin;
KW   Shinga-like toxin; autoimmune disease; immortalized cell;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Synthetic.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999; 99WO-US05535.
XX
PR   13-MAR-1998; 98US-0042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N, Fishwild DM, Ball WJ;
XX
DR   WPI; 1999-551219/46.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies
XX
PS   Example 42; Page 313-316; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable
CC   amount of an immunoglobulin that specifically binds digoxin or
CC   Shinga-like toxin. B cells from transgenic animals can be used to
CC   generate hybridomas expressing monoclonal high affinity human sequence
CC   antibodies. Antibodies produced from the transgenic animals of the
CC   invention can be used to treat human diseases, e.g. autoimmune
CC   diseases, cancer, infectious disease, transplant rejection, blood
CC   disorders such as coagulation disorders and other diseases. The
CC   present sequence is used in the course of the invention.
XX
SQ   Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

Query Match   71.7%; Score 1611.8; 1253 G; 987 T; 0 other;
Best Local Similarity 94.3%;
Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4;
             Pred. No. 1.7e-313; DB 20; Length 4723;

Qy   430 AACCTCTAGAGCTTTCTGGGGCGAGCCCGGCCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
          |·| |||| ||||||||| || ||||||||||||||||||| ||||||||||||||
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Db     8  AGCAGCTGAAGCTTTCTGGGGCAGGCAGCCAGCCAGGCTGCACACCCAATGCCCATGCCC   67

Qy   490  CTAAGGTGAGGCAGGTGGCGCGCCAGCCAGGTGCACACCCAATGCCCATGCCCGTGAGCCCAGACACT 549
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68  CTAAGGTGAGGCAGGTGGCGCGCCAGCCAGGTGCACACCCAATGCCCATGCCCAGACACT  127

Qy   550  GGACCCTGCCTGACCCTGTTGGATAGACAAGAACCGAGGGCCTCTGCGCCCCTGGGCCC   609
          |||| ||    |||||||||||||
Db   128  GGACGCT----GAACCTCGCGGACCAGTTAAGGACCCGAGGGCCTCTGCGCCCCTGGGCCC  182

Qy   610  AGTCTGTCCCACACCGCGGTCACATGGCACCACCTCTTGGAGCTCCACCAAGGGCC   669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183  AGTCTGTCCCACACCGCGGTCACATGGCACCACCTCTTCTTGCAGCTCCACCAAGGGCC  242

Qy   670  CATCGGTCTCTTCCCCTGGCCCTGCTCCAGGAGCACCTCCGAGAGCACCGGCCCTGG   729
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243  CATCGGTCTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy   730  GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC   789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303  GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC  362

Qy   790  TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCCTACAGACTCTACTCCCTCA   849
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363  TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCCTACAGACTCTACTCCCTCA 422

Qy   850  GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG   909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423  GCAGCGTGGTGACCGTGCCCTCCAGCAACAGCTTGGGCACCCAGACCTACATCTGCAACGTGA  482

Qy   910  ATCACAAGCCCAGCAACACCAAGGTGACAACACAGTTGGTGACAGAAGAGTTGGTGAGGCCGCAGGGAG  969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483  ATCACAAGCCCAGCAACACCAAGGTGACAACACAGTTGGTGACAGAAGAGTTGGTGAGGCCGCAGGGAG  542

Qy   970  GGAGGGGTCTGGAAGCAGCAGGCAAGGCAAGGCAGGCCCTCCTGGCCTCAGGGAGG   1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543  GGAGGGGTCTGGAAGCAGCAGGCAAGGCAAGGCAGGCCCTCCTGGCCTCAGGGAG  602

Qy   1030  GCCCCACCCAGGGCCAGCAAGGCAGGCAGGCCCTCCATCGTGCCTCCTCACCCGGAGGCCTCTGCCC  1089
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603  GCCCCAGTCCAGGGCCAGCAAGGCAGGCAGGCCCCTCATCGTGCCTCCTCACCCGGAGGCCTCTGCCC  662

Qy   1090  GCCCCACTCATGCTCAGGGACAGGGGTCTTCTGCTTTTCCACCAGGCTCCAGGCAGGCA  1149
           |||||||||||||||||||||||||||||||||||||
Db   663  GCCCCACTCATGCTCAGGGACAGGGGTCTTTGCTTTTCC--CCAGGCTCCAGGCAGGCCAGGCCA 721

Qy   1150  CAGGCTGGGTGCCCCTACCCCAGGGGCAGGTTGCTTGGCTCGACCC   1209
           |||||||||||||||||||||||||||||||||||||||||
Db   722  CAGGCTAGGTGCCCCTAACCCCAGGGCCCTGCACACAAAGGGGCAGGCAGGTGCTTGGGCTCGACC  781

Qy   1210  TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGGCAACCCCAAAGGCCAAA  1269
           |||||||||||||||||||||||||||||||||||||||||||||
Db   782  TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGGCAACCCACCCCAAAGGCCAAA  841

Qy   1270  CTGTCCACTCCCTCCGAGCTCTGGCCACCCTGACCTAAGCCCCACTCAAGGCCAATCT   1329
           ||||||||||||||||||||||||||||  ||||||||||||
Db   842  CTCTCCACTCCCTCCGAGCTCTGGCCACCCTGGACTCAAGCCCCACTCCAGTTAACTCCCAATCT  901

Qy   1330  TCTCTTCTGCAGAGCCCAGAGCCCAAATCTTGTGTCGA--------GTGCCCACCGTGCCCCAGGTAA  1380
           |||||||||||||||||||||||   |||||  ||||||||||||
Db   902  TCTCTTCTGCAGAGCCCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy   1381  GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGTGCCCTAGAGTAGCCTGCAT  1440
           ||||||||||||||||||||||||||||||||||||||||||
Db   962  GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACACGTGCCCTAGAGTAGCCTGCAT 1021

Qy   1441  CCAGGGACAGCAGGCCCCAGCTGGGGCTTTGGCTTTGACCTGACCCACCTG  1498
           ||||||||||||||||||||||||||||||||||||||  ||
Db   1022  CCAGGGACGACAGGCCCCAGCTGTGACACGTCCACCTCCACCATCTCTTCTTCCAGCACC-- 1081

Qy   1499  -ACCTGCGGCGACCCAGTCTTGTGACACCTG 1557
            |||  ||||||||  |||||
Db   1082  AACTTCCTGGGGGGACCGTCAGTCTTCCTCTTCTTCCCCCAAAACCAAGGACACCCTCATGA 1141
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Qy   1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1142 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy   1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy   1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
          |||||||| ||||||||||| |||||||||||||||||||||||| ||||||||||||||
Db   1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy   1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
          ||||||| ||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy   1798 AGAAAACCATCTCCAAAACCAAAGGTGGACACCCGCGGGTATGAGGGCCACATGGACAGA 1857
          ||||||||||||||||| |||||||| |||||||||||||| |||||||||||||||||
Db   1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCACCCGGGTGCGAGGGCCACATGGACAGA 1441

Qy   1858 GGCCGGCTCGGCCACCCTCGCCTGGGAGTGACCGCTGCCAACCTCTGTCCCTACA 1917
          |||||||||||||  |||| |||||| |||||||||| |||||||||||||||||
Db   1442 GGCCGGCTCGGCCCACCCCCTCGCCTGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy   1918 GGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   1502 GGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy   1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy   2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
          |||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||
Db   1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

Qy   2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy   2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy   2218 CTCTCCCTGTCTCCGGGTAAATGAGTG 2244
          |||||||||||||||||||||||||||
Db   1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
```

RESULT 9
AAF55224
ID   AAF55224 standard; DNA; 4723 BP.
XX
AC   AAF55224;
XX
DT   29-MAY-2001 (first entry)
XX
DE   Nucleotide sequence of pCG7-96.
XX
KW   Complementarity determining region; CDR; immune response; antibody;
KW   cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW   autoimmune disease; infectious disease; inflammation; allergy;
KW   rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW   multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW   transplant rejection; graft versus host disease; ss.
XX
OS   Unidentified.
XX
PN   WO200114424-A2.
XX
PD   01-MAR-2001.
XX

PF   24-AUG-2000; 2000WO-US23356.
XX
PR   24-AUG-1999; 99US-0150452.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Korman AJ, Halk EL, Lonberg N;
XX
DR   WPI; 2001-202933/20.
DR   P-PSDB;
XX
PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient -
XX
PS   Example 10; Page 93-94; 127pp; English.
XX
CC   The present sequence is used in the course of the specification. The
CC   specification describes a human antibodies which specifically bind to
CC   human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC   antibodies are used in methods for inducing, augmenting or prolonging
CC   an immune response to an antigen in a patient, where the antibodies
CC   block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies of the invention are
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions for the treatment of diseases with inflammatory or allergic
CC   components. The polyvalent or polyclonal preparations are useful for
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.
XX
SQ   Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;
XX

Query Match   71.7%; Score 1611.8; DB 22; Length 4723;
Best Local Similarity   94.3%; Pred. No. 1.7e-313;
Matches 1722; Conservative   0; Mismatches 87; Indels 18; Gaps   4;

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Qy   430 AACCTCTAGAGTTTCTGGGGCGAGCCGGCCTGACTTTGGCTTTGGGCAGGGAGTGG 489
         | ||| ||||| ||||||||||| ||||||||||| ||||| |||||||||||| || 
Db     8 AGCAGCTGAAGCTTTCTGGGGCAGGCCGGCCTGACCTTGGGCTTTGGGCAGGGAGGGGG 67

Qy   490 CTAAGGTGAGGCAGGTGGCGCGCCAATGCCGTGCACACCCCAGTGCACCCCAGAGCCCAGAGACT 549
         |||||||||||||||||||||| |||  ||||| ||||||||||||||||||||||  ||||||| ||||||
Db    68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCCAGTGCACCCCATGAGCCCAGACACT 127

Qy   550 GGACCCTGCCTGGACCCTGGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTCGGCCC 609
         |||| |||    ||||| |||||| ||||||||| ||||||||| | ||||||||||| 
Db   128 GGACGCT----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCCTCGCGCCCTCGGCCC 182

Qy   610 AGTCTGTCCCAAGCCGGTCACATGCACCACTCTCTTCACCAAGGGC 669
         |||||||||||  || |||||||||||||||||||| |||||||||
Db   183 AGTCTGTCCCACCACGCGGTCACATGCACCACTCTCTTCAACCAAGGGC 242

Qy   670 CATCGGTCGTCTCCCCTGCGCCCTGCTCCAGGAGCACCCAGAGCAGCGGCCGTGG 729
         ||||||| ||| ||||||| ||||| |  ||||| ||| | |||||||||||| || 
Db   243 CATCGGTCTTCCCCCTGGCACCCTCCCCAAGAGCAGCACCTCTGGGGCACAGCGGCCCTGG 302

Qy   730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy   790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy   850 GCAGCGTGGTGACCGTGCCCTCCCAGCAACTTCGGCACCCAGACCTACATCTGCAACGTAG 909
         |||||||||||| |||||||||||||||||| |||  ||||||
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Db
Qy   423 GCAGCGTGGTGACCGTGCCCTCCCAGCAGCTTGGGCACCCAGACCTTACATCTGCAACGTGA 482
Db
Qy   910 ATCACAAGCCCAGCAACACCAGCAGTTGGTGAGGAGGCAGCTCAGGGAG 482
Db   483 ATCACAAGCCCAGCAACACCAGCAGTTGGTGAGGAGGCAGCACAGGGAG
Qy   970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCGCTTCTCCTGGACGCACCCGGTGTGCA 1029
Db   543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCGCTCCTGGACGCATCCGGGCTATGCA 542
Qy 1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCAGGCAGGGCCCCGTGCTGCCTCTGCCC 1089
Db   603 GCCCCAGTCCAGGGCAGCAAGGCAGGCAGGGCCCGTGCTGCCTCTTCACCCGGAGGCCTCTGCCC
Qy 1090 GCCCCACTCATGCTTCAGGGAGAGGGTCTTCTTGGCGTTTTCCACCAGGCTCCAGGCAGGCA 1149
Db   663 GCCCCACTCATGCTCAGGGAGGAGGGTCTTCTTGGCGTTTTCC--CCAGGCTCTGGGCAGGCA 721
Qy 1150 CAGGCTGGGGTGCCCCTCACCCCAGGGCCTTCACACACAGGGGCAGGTCTGTTGGCTGCAGACC 1209
Db   722 CAGGCTAGTGCCCCTAACCCAGGCCCTGCACAACAAGGGGCAGGTGCTGGCTGCAGACC 781
Qy 1210 TGCCAAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAGGCCGACACCCCAAAAGGCCAAA 1269
Db   782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCCAAAAGGCCAAA 841
Qy 1270 CTTGTCCACTCCCTCAGCTCGGGACACCCTTCTCTCTCCTCCCAGATCTCCCAATCT 1329
Db   842 CTCTCCACTCCCTCAGCTCGGGACACCCTTCTCTCTCCTCCCAGATTCCCAGTTAACTCCCAATCT 901
Qy 1330 TCTCTCTGCGAGACGGCCAAATGTTCGTGTCGA--------GTGCCCACCGTGCCCAGGTAA 1380
Db   902 TCTCTCTGCGAGACGGCCCAAAATCTTTGTGACAAAACTTCACACACACGTGCCCAGGTAA 961
Qy 1381 GCCAGCCCAGGGCTCGCCCTCGGCGTCAAGGCGGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
Db   962 GCCAGCCCAGGCCTCCGCCTCCAGCTCAAGGCGGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021
Qy 1441 CCAGGGACAGGCCCCAGCCCCCAGCTGGGTCGTGACACGTCCCACCTCATCTCTTCCTCAGCACC-- 1498
Db 1022 CCAGGGACAGGCCCCAGCCGCGGGTCTGACACGTCCCACCTCATCTCTTCCTCAGCACCTG 1081
Qy 1499 -ACCTCGCGACGACCACCGTCAGTCTTCTCCCCAAAAACCCAAGGACACCCTCATGA 1557
Db 1082 AACTCCTCGGGGGACCACCGTCAGTCTTCTCCTCTTCTCCCCCAAAAACCCAAGGACACCCTCATGA
Qy 1558 TCTCCCGGACCCCCTGAGGTCACGTGCGTGTGGTGTGGACGTGGAGCCAGGACCCCGAGG 1617
Db 1142 TCTCCCGGACCCCCTGAGGTCACATGCGTGGTGGTGGACGTGGAGCGTGGAGCCACGAGGACCCCGAGG
Qy 1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
Db 1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG
Qy 1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTTGTGCACCAGGACT 1737
Db 1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321
Qy 1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
Db 1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381
Qy 1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCCACATGGACAGA 1857
Db 1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441
Qy 1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGTGCCCAACCTTGTCCTACA 1917
Db 1442 GGCCGGCTCGGCCCACCCACCCTCTGCCCTGAGAGTGACCGTGCCCTTCCCAACCTTACCCTACA 1501
Qy 1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGACGAGAGGACCAAG 1977
Db 1502 GGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy 1978 AACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
Db 1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621
Qy 2038 TGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
Db 1622 TGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCC 1681
Qy 2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
Db 1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741
Qy 2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
Db 1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801
Qy 2218 CTCTCCCTGTCTCCGGGTAAATGAGTG 2244
Db 1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828

RESULT 10
ABK85576
ID   ABK85576 standard; DNA; 4723 BP.
XX
AC   ABK85576;
XX
DT   03-SEP-2002 (first entry)
XX
DE   Human IgGgammal heavy chain plasmid pCG7-96.
XX
KW   Transgenic; rodent; immunoglobulin; Ig; transchromosome; B-cell;
KW   human antibody display library; immune-related disorder; mutant;
KW   immunomodulatory; IgGgammal heavy chain; pCG7-96; cyclic; ds.
KW   circular; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200243478-A2.
XX
PD   06-JUN-2002.
XX
PF   30-NOV-2001; 2001WO-US45293.
XX
PR   30-NOV-2000; 2000US-250340P.
XX
PA   (MEDA-) MEDAREX INC.
PA   (KIRI) KIRIN BEER KK.
XX
PI   Tomizuka K, Ishida I, Lonberg N, Halk E;
XX
DR   WPI; 2002-500300/53.
XX
PT   New transgenic nonhuman mammal, useful for generating B-cells
PT   expressing human antibody sequences and generating antigen-specific
PT   hybridomas secreting human sequence antibody, comprises two human
PT   immunoglobulin loci
XX
PS   Disclosure; Page 47-48; 110pp; English.
XX
CC   The present invention relates to novel transgenic nonhuman mammals,
CC   particularly rodents, comprising two human immunoglobulin (Ig) loci,
CC   where one of two the human immunoglobulin loci is a human heavy chain
CC   locus and the other locus is a human light chain locus, and where
CC   only one of the loci is of a transchromosome. The transgenic animals
CC   are useful for generating a number of B-cell expressing human
CC   antibody sequences. They are also useful for producing human
CC   immunoglobulin sequences. They are also useful for producing rearranged
CC   and generating a human sequence antibody display libraries,
CC   antigen. The produced antibodies are useful for treating immune-related
CC   disorders. The present sequence represents a plasmid used in the

CC   construction of expression vectors for human IgG.
XX
SQ   Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

Query Match   71.7%; Score 1611.8; DB 24; Length 4723;
Best Local Similarity   94.3%; Pred. No. 1.7e-313;
Matches 1722; Mismatches 87; Conservative 0; Indels 18; Gaps 4;

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Qy    430 AACCTTCTAGAGCTTTCTGGGCGAGCCGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG  489
          |||| ||||||||||||||||||| || |||||| ||||||||||||||||||
Db      8 AGCAGCTGAAGCTTTCTGGGCGAGCCAGGCCTGGCTTTGGGGCAGGGAGGGGGG       67

Qy    490 CTAAGGTGAGGCAGGTGGCGCGACCCAGCAGTGCACCAGCCCGTGAGCCCAGACACT    549
          ||||| ||||||||||||||||||||| |||||||||| |||||||||||||||
Db     68 CTAAGGTGAGGCAGGTGGCGCGACCCAGCAGCCCCAATGCCCCAATGCCCAGACACT   127

Qy    550 GGACCCTGCCTGGACCCTCGTGATAGACAAGAACGAGGGCCTCTGCCCGTGGGCCC    609
          ||||||| |||||||||||||||||||||||||||||||||||||||
Db    128 GGACGCT------GAACCTCGGGACAGTTAAGAACCCAGGGGCCTCTGCGCGTGGGCCCC   182

Qy    610 AGCTCTGTCCACACCGCGGTCACATGGACCACCTTCTTGCAGCCTTCCACCAAGGGCC    669
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    183 AGCTCTGTCCACACCGCGGTCACATGGACCACCTTCTTGCAGCCTCTTCCACCAAGGGCC   242

Qy    670 CATCGGCTTCTCCCCTGGCGCCGCTTCCCAGGAGCACTTCGGAGAGCACAGGGCCCTGG    729
          ||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db    243 CATGGGTCTTCCCCCTGGCACCCTCTGGGGCACACCTTCCCGGCTGTCCTACAGTCCTCA   302

Qy    730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC    789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC   362

Qy    790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTTCTACTCCCTCA    849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA   422

Qy    850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG    909
          |||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db    423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCACATCTGCAACGTGA         482

Qy    910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGTCAGGGAG    969
          |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db    483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG   542

Qy    970 GGAGGGTGTCTGGAAGCCAGTCAGCTCCCTGCCTCCAGCCCCATCTGTCCTCCGGCTGTCGA  1029
          |||||||||||||||||||||||||||| |||||||||||||||||||| ||| ||||||
Db    543 GGAGGGTGTCTGGAAGCCAGTCAGCTCCCTGCCTGCCGCTCCGGAGGGCCTGCTATGCA     602

Qy   1030 GCCCCAGCCAGGGCAGCAGGGCAGGGAGAGGTCTTCAGGGAGGCGTCCACCGGGCAGCA   1089
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GCCCCAGTCAGGGCAGCAGGGCAGGGAGGTGTCCAGCCTGCCCTCCACGGGCAGCA       662

Qy   1090 GCCCCACTCAGGGCTCAGGGGAGAGGTCTTCCACCAAGGCTCTCAGGCGGCAGCA    1149
          ||||||||||||||||||||||| |||||||||  ||||||||
Db    663 GCCCCACTCAGGGCTCAGGGGAGAGGTCTTTTTCC--CCAGGCTCTGGGCAGGCA       721

Qy   1150 CAGGCTGGGGTGCCCCCAGCCCTGCCCCACACAGAGGGGCAGGTGCTTGGCTCAGACC  1209
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 CAGGCTGTAGGTGCCCCTAACCCAGGCCCTGCCCCACACAGAGGGGCAGGTGCTGGGGTCAGACC  781

Qy   1210 TGCCAAAGCCAATATCCGGGGACACCTCCTCTCTCCCAGATCCCGAGTAACTCCCAAA  1269
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    782 TGCCAAGAGCCAATATCCGGGGACACCTCCTCTCTCCCAGATCCCGAGTAACTCCCAA    841

Qy   1270 CTGTCCACTCCCTCGGACACCTTCTCTCCCAGATCCCGAGTAACTCCCAATCT    1329
          |||| |||||||||||| |||||||||||||||||||||||||||||||||||
Db    842 CTCTCCACTCCCTCGGACACCTTCTCTCCCAGATTCCAGATTCCAGTAACTCCCAATCT   901

Qy   1330 TCTCTTCGCAGAGGCCAAATGTTGTGTCGA-------GTGCCCACCGTGCCCAGGTAA  1380
          |||||||||||||||||||||||||||||||            |||||||||||||||
Db    902 TCTCTTCTGCGAGAGCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA  961

Qy   1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT
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Db    962 GCCAGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGCCTGCCTAGAGTAGCCTGCAT 1021
          ||  |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Qy   1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC--        1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1022 CCAGGGACAGGCCCCAGCTGGGTGCTGACAGTCCACCTCCATCTCTTCCTCAGCACCTG       1081

Qy   1499 -ACCTGCGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA     1557
           ||||||||||||||||||||||||||| || |||||||||||||||||||||||||||
Db   1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA    1141

Qy   1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGG  1617
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGG    1201

Qy   1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG  1677
          |||||||||||||||||||||||||| |||||||||||||||||| |||||| |||||||
Db   1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG    1261

Qy   1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT  1737
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT   1321

Qy   1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGGCCTCAACAAAGCCCTCCC  1797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG   1381

Qy   1798 AGAAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGGACAGAGATGACCAAG 1857
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||
Db   1382 AGAAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA    1441

Qy   1858 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTGTCCCTACA    1917
          |||||||||||||||||||||||||||||||||| ||||||||||||
Db   1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA   1501

Qy   1918 GGGCAGCCCCGAGAACCAGGTGTACACCCTGCCCCCATCCCGGGAGATGACCAAG  1977
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   1502 GGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG  1561

Qy   1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG  2037
          ||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db   1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG   1621

Qy   2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC  2097
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC   1681

Qy   2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG  2157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG   1741

Qy   2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  2217
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC   1801

Qy   2218 CTCTCCCTGTCTCCGGGTAAAATGAGTG    2244
          ||||||||||||||||||||||||||||
Db   1802 CTCTCCCTGTCTCCGGGTAAAATGAGTG    1828
```

RESULT 11
AAV39243
ID   AAV39243 standard; DNA; 4723 BP.
XX
AC   AAV39243;
XX
DT   18-DEC-1998 (first entry)
XX
DE   Plasmid pCG7-96 nucleotide sequence.
XX
KW   Transgenic animal; human heterologous antibody; transgene;
KW   isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW   autoimmune reaction; inflammatory response; transplant rejection;

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KW   acid induced lung injury; acute adult respiratory distress syndrome;
KW   ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW   cystic fibrosis; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO924884-A1.
XX
PD   11-JUN-1998.
XX
PF   01-DEC-1997;  97WO-US21803.
XX
PR   02-DEC-1996;  96US-0758417.
XX
PA   (GENP-) GENPHARM INT.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1998-333306/29.
XX
PT   Hybridoma producing antibody specific for interleukin-8 - used to
PT   prevent efflux of neutrophils from vasculature, and treat
PT   reperfusion injury
XX
PS   Example 42; Pages 312-315; 452pp; English.
XX
CC   The present sequence represents the gammal heavy chain plasmid, pCG7-96,
CC   which includes the human gammal constant region and polyadenylation site.
CC   The plasmid is used in the construction of minigenes for expression of
CC   IgGkappa anti-CD4 antibodies, in the transgenic mouse of the invention.
CC   The specification describes transgenic non-human animals, especially a
CC   mouse, which are capable of producing a human heterologous antibodies of
CC   multiple isotypes by undergoing isotype switching. The transgenic animals
CC   have human heavy and light chain transgenes. The transgenes are capable
CC   of functionally rearranging a heterologous diversity (D) gene in a
CC   variable-diversity-junction (V-D-J) recombination. The transgenes include
CC   a heavy chain transgene comprising at least one V, D and J gene segment,
CC   and one constant region gene segment. The immunoglobulin (Ig) light chain
CC   transgene comprises at least one V and J gene segment and one constant
CC   region gene segment. The gene segments are heterologous to the transgenic
CC   animal. The antibody can be used to prevent efflux of neutrophils from
CC   vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC   antibodies are used to reduce undesirable autoimmune reactions,
CC   inflammatory responses and rejection of transplanted organs. The
CC   anti-IL-8 antibodies can reduce tissue damage and prolong survival in
CC   animal models of acute adult respiratory distress syndrome (ARDS) and
CC   acid induced lung injury. The anti-IL-8 antibodies can also be used for
CC   the treatment of vasculitis, septic shock, allergic reactions
CC   (e.g. asthma) and cystic fibrosis.
XX
SQ   Sequence 4723 BP; 1072 A; 1410 C; 1253 G; 988 T; 0 other;
```

Query Match   71.6%; Score 1610.2; DB 19; Length 4723;
Best Local Similarity 94.2%; Pred. No. 3.6e-313;
Matches 1721; Conservative   0; Mismatches 88; Indels 18; Gaps 4;

```
Qy    430 AACCTCTAGAGCTTTCTGGGGCGCCAGGCCTGACTTTGGCTTTGGGGCGCAGGGAGTGGG  489
              ||| ||||||||||||||||| ||  || | ||||||||||||||||  |||||| |||
Db      8 AGCAGCTGAAGCTTTCTGGGGCAGGCAGGCCTGCACCTTGGCTTTGGGGCGCAGGGAGGGGG   67

Qy    490 CTAAGGTGAGGCAGGTGGCGCCAGCCTGTGATAGACAAGAACCGAGGGGCCTCTGCCGCC  549
              ||||||||||||||||||||||||||| |||||||||||| |||||||||||||||
Db     68 CTAAGGTGAGGCAGGTGGCGCCAGCCTGCACCAAGGTGCACACCCATGAGCCCAGACACT  127

Qy    550 GGACCCTGCCTGGACCCTCTGACCCTCCGTGATAGACAAGAGTTAAGAACCCAGGGGCCC  609
              ||  |||||||||||            |||||||||||||||||| |||||||||||
Db    128 GGACGCT----GAACCTCGCGACCAGGTAAGAACCCAGGGGCCCTGCCCCTGGGGTC  182

Qy    610 AGCTCTGTCCCACACCGCGTCACATGCACCACCTCTTCGCAGCCTCCACCAAGGGCC  669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 AGCTCTGTCCCACACCGCGTCACATGCACCACCTCTTCGCAGCCTCCACCAAGGGCC  242
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Qy    670 CATGCGGTCTTCCCCCTGGCGGCCCTGCTCCTCCAGGAGCACCTTCCAGAGGAGCACAGGCGGGGCCCTGG  729
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    243 CATGCGGTCTTCCCCCTGGCGGCCCTGCTCCTCCAAGAGCACCTTCCGGGGGCACAGGCGGCGGCCCCTGG  302

Qy    730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGTCGTGGAACTCAGGCGCTC  789
              |||||||||||||||||||||||||||| || ||||||||||||||||||||
Db    303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC  362

Qy    790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA  849
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA  422

Qy    850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG  909
              |||||||||||||||||||||||||||||| ||||||| |||||||||||||||||
Db    423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA  482

Qy    910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG  969
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG  542

Qy    970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTTCCTGCCTGGACGGACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTTCCTGCCTGGACGGACCCCGGCATGCA  602

Qy   1030 GCCCCAGCCAGGGCAGGAGCAAGGCAGGCAGGCCCCATCTGTCCTCCTCACCCGGAGGCCTCTGCCC 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GCCCCAGTCCAGGACAGGAGCAAGGCAGGCCCCGTGTCCTCCTCACCCGGAGGCCTCTGCCC  662

Qy   1090 GCCCCACTCATGCTCAGGGAGGAGGGTCTTCGGCCTTTTCACCAGGCTGCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||| || |||  ||||||||||||
Db    663 GCCCCACTCATGCTCAGGGAGGAGGGGTCTTCTGCCTTTTTCC--CCAGGCTGCAGGCAGGCA  721

Qy   1150 CAGGCTGGGTGCCCCTACCCCAGGCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||||||||||||||| ||||||||||||||||||||| |||||||||||||||||
Db    722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACACAAAGGGGCAGGTGCTGGGCTCAGACC  781

Qy   1210 TGCCAAAAGCCATATCCGGAGGAGACCCTGCCCCTGACCTAAGGCCGACCCCAAAGGCCAAA 1269
              ||||||||| |||||||||||||||||||||||||||||||||||||| |||||||||||
Db    782 TGCCAAGAGCCATATCCGGAGGAGACCCTGACCTAAGCCCACCCCAAAGGCCAAA  841

Qy   1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCCCAGATCCGAGTAACTCCCAATCT 1329
              ||||||||||||||||||||||||||||||||||||||||| ||| |||||| ||| |
Db    842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCCCAGATTCCAGTAACTCCCAATCT  901

Qy   1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA-------GTGCCACGTGCCCAGTAA 1380
              |||||| |||||||||||||||||| ||||       |||||||||||||||||
Db    902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA  961

Qy   1381 GCCAGCCCAGGCCTCCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy   1441 CCAGGGACAGGCCCAGCTGGGTGCTGACACGTCCACCTCACTCTCCTCAGCACC-- 1498
              |||||| ||||||||||||||||||||||||| |||||||||||||||||||||
Db   1022 CCAGGGACAGGCCCAGCCGGGTGCTGACACGTCCACCTCCCCCAAAACCAAGGACACCCTG  1081

Qy   1499 -ACCTGCGGCAGCCAGCACCTCAGTGTTCCTCCTCCCCCAAAACCAAGGACACCCCTCATGA 1557
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1082 AACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGACACCCTCATGA 1141

Qy   1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1201

Qy   1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy   1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy   1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
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CC   pBAG101 was designed to carry genomic DNA encoding the human IgG4
CC   heavy chain constant region. The IgG4 DNA was isolated by polymerase
CC   chain reaction from human placental DNA using the primer sequences given
CC   in AAQ30907-08.  The amplification product of this reaction was approx.
CC   2109 bp. This fragment was inserted into EcoR5 linearised pNN03 (see
CC   also AAQ30566) to give the intermediate plasmid pBAG101.
XX
SQ   Sequence 2029 BP; 423 A; 710 C; 564 G; 331 T; 1 other;

Query Match             71.6%;  Score 1609.2;  DB 13;  Length 2029;
Best Local Similarity   94.5%;  Pred. No. 5.1e-313;
Matches 1711;  Mismatches  0;  Conservative  0;  Indels  93;  Gaps  4;

Qy    438 GAGCTTTCTGGGGGCGAGCCGGCCTGACTTGGCTTGGGGCAGGAGAGTGGGCTTAAGGTG 497
          |||||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||
Db      2 GAGCTTTCTGGGGGCGAGCCGGCCTGACTTGGC-TGGGGCAGGGGAGGGGCTTAAGGTG 60

Qy    498 AGGCAGGTGCGCCAGCCAGGTGCACAACCAATGCCGGCCCTGAGCCCCAGACACTGGACCCCTG 557
          | |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     61 ACGCAGGTGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCCAGACACTGGACCCCTG 120

Qy    558 CCTGACACCCTGTCGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCCAGCTCTGT 617
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    121 CATGACCACCATCGCGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCCAGCTCTGT 180

Qy    618 CCCACACCGGTCACATGGCCACCACCTCTTCTTGCGAGAGCACCTCCAGAGAGCACAGCGGGTC 677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCACACCGGTCACATGGCCACCACCTCTTCTTGCGAGTTCACCTCCAGAGAGCACAGCCGTC 240

Qy    678 TTTCCCCCTGCGCCCTGCTTCCCGGGAACCCGTGACCGTGTCGTGGAACTCAGCGGCCTCTG 737
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    241 TTTCCCCCTGCGCCCTGCTTCCCGGGAACCCGTGACCGTGTCGTGGAACTCAGCGGCCTCTG 300

Qy    738 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    301 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC 360

Qy    798 GGGTGCACACCTTCCCAGCTCGTCGTCCTACAGTCCTCAGACTCTACTCCCTCAGCAGCGTG 857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGTGCACACCTTCCCCGCTGTGTCCTACAGTCCTCAGACTCTACTCCCTCAGCAGCGTG 420

Qy    858 GTGACCGTGCCCTGCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAG 917
          |||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||| 
Db    421 GTGACCGTGCCCTGCAGCAGCGTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAG 480

Qy    918 CCCAGCAACACCAAGGTGGACAAGACAGAGTTGGTGACAGAGTTCAGGTGCAGGCCAGGAGGGTG 977
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    481 CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGGAGGTCAGGCACAGGGAGGGGTG 540

Qy    978 TCTGCTGAAGCAGCTCAGCCCCGGCTGCACCCGGCTGTGCAGCCCCCAGC 1037
          |||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    541 TCTGCTGAAGCAGCTCAGCCCCGGCTGCACCCGGCTGTGCAGCCCCCAGC 600

Qy   1038 CCAGGCAGCAAGGCAGCAGGCATGCCCCATCGCCCATCGTGTCCTCTGTCCTCCACCCCACCCACT 1097
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    601 CCAGGCAGCAAGGCAGCATGCCCCATCGCCCATCGTGTCCTCCTCTGTCCTCCTCGACCACCCCACT 660

Qy   1098 CATGCTCAGGGAGGAGGGGTCTTCTGGCTTTTCCACCAGGCTCAGGCAGGCAGACAGGCTGG 1157
          |||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||| 
Db    661 CATGCTCAGGGAGGAGGGGTCTTCTGGATTTTTCCACCAGGCTCCGGCA-CCAACGGCTGG 719

Qy   1158 GTGCCCTACCCCAGGCCCCTTCACACACAGGGCAGGTGCTTGGCTCAGACCTGCCAAAA 1217
          ||||||||||||||||| |||||||||||| |||||||||||||||||||||| 
Db    720 ATGCCCTACCCCAGGCCCTGCCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAGA 778

Qy   1218 GCCATATCGGGAGGAGACCCTGCCCCTGACCTAAGCCCAAAGGCCAAATGTCCAC 1277
          ||||||||||||||||||||||||||||||| |||||||| ||||||| ||||| 
Db    779 GCCATATCGGGAGGAGACCCTGCCCCTGACCTAAHCCCCAAAGGCCAAATCTCCAC 838

Qy   1278 TCCCTCAGCTCGGACACCTTCTCTCCCCAGATCCGAGTAACTCCCAATCTTCTCTCTG 1337
          ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    839 TCCCTCAGCTCAGACACCTTCTCTCCCTCCCCAGATCTGAGTAACTCCCCAATCTTCTCTCTG 898
```

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Db   1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGGCCACATGGACAGA 1857
          ||||||||||||||||| |||||||| ||||||||| || ||||||||||||||||||||
Db   1382 AGAAAACCATCTCCAAAGCCAAAGGCCAAAGGGACCCGTGGGGTGCGAGGGGCCACATGGACAGA 1441

Qy   1858 GGCCGGCTCGGCCCACCCTCTGCCTGCCGTGTCGCCAACCTTCTGTCCCTACA 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 GGCCGGCTCGGCCCACCCTCTGCCTGCCGTGTCGCCAACCTTCTGTCCCTACA 1501

Qy   1918 GGGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGGAGGATGACCAAG 1977
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1502 GGGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy   1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCCAGCGACATCGCCGTGGAG 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy   2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 1681

Qy   2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy   2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1742 AACGTCTTCTCATGTTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy   2218 CTCTCCCTGTCTCCGGGTAAATGAGTG 2244
          |||||||||||||||||||||||||||
Db   1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
```

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RESULT 12
AAQ30909
ID   AAQ30909 standard; DNA; 2029 BP.
XX
AC   AAQ30909;
XX
DT   02-APR-1993 (first entry)
XX
DE   pBAG101 insert.
XX
KW   Primer; polymerase chain reaction; amplify; IgG4; heavy chain;
KW   constant region; human; placenta; EcoR5; pNN03; pBAG101; HIV;
KW   antibody; anti-CD4; gp120; ss.
XX
OS   Synthetic.
XX
PN   WO9209305-A.
XX
PD   11-JUN-1992.
XX
PF   27-NOV-1991; 91WO-US08843.
XX
PR   27-NOV-1990; 90US-0618542.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
XX
DR   WPI; 1992-398399/48.
XX
PT   New anti-CD4 antibody homologues - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Disclosure; Page 149-50; 205pp; English.
XX
CC   The sequence given is the insert from the intermediate plasmid pBAG101.
```

```
Qy    1338  CAGAGCGCAAAATGTTGTGTCGAGTGCCACCGTGCCCAGGCTCGC  1397
            ||||||||| |||||| ||||||||||||||||||||||||||||
Db     899  CAGAGTCCAAAATATGGTCCCCATGCCCAGGTAAGCCAGCCCAGGCCTCGC  958

Qy    1398  CCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTTCCTCAGCCCCAG  1457
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db     959  CCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTTCCTCAGCCCCAG  1018

Qy    1458  CTGGGGTGCTGACACGTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCG  1514
            |||||||||||||||||||||||||||||||||||   |||||||||||||
Db    1019  CCGGGGTGCTGACGCATCCATCTCCATCTCCTCAGCACCTGAGTTCCTGGGGGACCA  1078

Qy    1515  TCAGTCTTCTCTTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  1574
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1079  TCAGTCTTCTCTTGTCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAG  1138

Qy    1575  GTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTAC  1634
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1139  GTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTAC  1198

Qy    1635  GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGC  1694
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1199  GTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGC  1258

Qy    1695  ACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAG  1754
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1259  ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAG  1318

Qy    1755  TACAAGTGCAAGGTCTCCAACAAAGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  1814
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1319  TACAAGTGCAAGGTCTCCAACAAAGCCTCCCATCCCCGTCCTCCATCGAGAAAACCATCTCCAAA  1378

Qy    1815  ACCAAAGGTGGACCCCGGGGTGATGAGGGCCACCACGGGTGCGAGGGCCAGCCCGCCCACC  1874
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1379  GCCAAAGGTGGACCCCGGGGTGCGAGGGCCAGCCCGCCCACC  1438

Qy    1875  CTCTGCCCTGGAGTGACCGCGTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACC  1934
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1439  CTCTGCCCTGGGAGTGACCGCGTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACC  1498

Qy    1935  ACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC  1994
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1499  ACAGGTGTACACCCCTGCCCCCATCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC  1558

Qy    1995  CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA  2054
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1559  CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA  1618

Qy    2055  GCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT  2114
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1619  GCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT  1678

Qy    2115  CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTC  2174
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1679  CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC  1738

Qy    2175  CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGG  2234
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1739  CGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGG  1798

Qy    2235  TAAAATGAGTG  2244
            |||||||||||
Db    1799  TAAAATGAGTG  1808
```

RESULT 13

AAQ55003
ID   AAQ55003 standard; DNA; 9201 BP.
XX
AC   AAQ55003;
XX
DT   06-JUL-1994 (first entry)
XX

CC
CC   A humanised monoclonal antibody corresponding to the murine anti-CD18
CC   antibody 60.3 was prepared. The variable (V) region sequences from
CC   both the heavy (H) and light (L) chains were determined from cDNA
CC   (amplified by PCR) and spliced onto human constant (C) regions,
CC   resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC   expressed in tissue culture (Ag8.653 mouse myeloma cells, detected
CC   by ELISA), and examined in binding assays showed that the results from
CC   competition and inhibition assays showed that the results from
CC   as effective as the murine 60.3 MAb. The deduced murine VH was
CC   protein sequences were compared to the protein sequence data base,
CC   and two human Ig protein sequences were selected to be used as
CC   templates. A murine 60.3 Fv was modeled according to the deduced
CC   VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC   human template sequences selected from the protein data base, a
CC   humanised Fv was modeled. Construction of the humanised 60.3 was
CC   done by piecing 5 pairs of complementary oligonucleotides 60.3 was
CC   (spanning the entire V region) to form the VH and VL. These were
CC   then attached onto vectors containing genes for appropriate C regions
CC   to form humanised Ab (IgG, kappa). The humanised proteins were again
CC   expressed in Ag8.653 cells, and binding assays were done. FACS analyses
CC   indicated a dozen of the humanised Ab recognised cells expressing CD18.
CC   About a dozen of the humanised 60.3 Ab master wells were transferred
XX   and assayed for Ig.
SQ   Sequence 9201 BP; 2280 A; 2558 C; 2319 G; 2044 T; 0 other;

Query Match
Best Local Similarity 71.3%; Score 1604.4; DB 15; Length 9201;
Matches 1714; Conservative 94.3%; Pred No. 5.8e-312;
Matches 1714 Conservative 0; Mismatches 86; Indels 18; Gaps 4;

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Qy   439  AGCTTTCTGGGGCGGGCGGAGCCGGGCCTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGA  498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2  AGCTTTCTGGGGCGGGCGGCCAGGCCTGCACACCCCACACCCATCCCTGGGGCGTGGGCTAAGGTGA  61

Qy   499  GGCAGGTGGGGCCAGCCAGGTGCACACCCCAATGCCCATGAGCCCAGACACTGAGACCCTGC  558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    62  GGCAGGTGGGGCCAGCCAGGTGCACACCCCAATGCCCATGAGCCCAGACACTGAGACCCTGC  119

Qy   559  CTTGGACCCCGTGGATAGACAAGAACCGAGGGGGCCCGTCGCGCCCCCGGGCCCAGCTCTGTC  618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120  ---GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCGCGCCCCCGGGCCCCAGCTCTGTC  176

Qy   619  CCACACCGCGGTCACATGGCACCACCTCTTCAGCCCGCTCCACCAGGCCCATGCGGTCT  678
```

The page consists of dense nucleotide sequence alignments (Qy query vs Db database) with flanking position numbers, followed by a database record block.

```
RESULT 14
AAQ28089
ID   AAQ28089 standard; cDNA; 2482 BP.
XX
AC   AAQ28089;
XX
DT   06-FEB-1993  (first entry)
XX
DE   Encodes CD4-IgG2 chimeric heavy chain.
XX
KW   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW   chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS   Homo sapiens chimeric.
XX
FH   Key          Location/Qualifiers
FT   CDS          76..980
FT                /*tag= a
FT                /label= CD4 domain
FT   CDS          1374..1408
FT                /*tag= b
FT                /label= hinge domain
FT   CDS          1528..1854
FT                /*tag= c
FT                /label= CH2 domain
FT   CDS          1976..2275
FT                /*tag= d
FT                /label= CH3 domain
FT   CDS          688..981
FT                /*tag= e
FT                /label= CH1 domain
XX
PN   WO9213947-A.
XX
PD   20-AUG-1992.
```

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XX
PF    10-FEB-1992;    92WO-US01143.
PR
PR    08-FEB-1991;    91US-0653684.
XX
PA    (PROG-) PROGENICS PHARM INC.
PI
XX
DR    WPI; 1992-300034/36.
DR    P-PSDB; AAR26783.
XX
PT    CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT    treatment, prevention and diagnosis of HIV infection
XX
PS    Claim 13; Fig 4; 90pp; English.
XX
CC    This sequence encodes a CD4-gamma2 chimeric heavy chain homodimer.
CC    Human CD4 cDNA was excised from plasmid pSP6T4 as an EcoRI/StuI
CC    0.7 kb fragment, and cloned into M13mp18 forming M13mp18(CD4). This
CC    was linearised with PstI, and the SacII(flush)/PstI fragment from pBr
CC    gamma2 containing human gamma2 heavy chain (CH1 exon) isolated and
CC    ligated to the M13mp18(CD4) vector. Resulting recombinants were then
CC    screened by restriction analysis for the presence of both CD4 and
CC    CH1 which occur in tandem CD4(EcoRI/StuI)-CH1(SacI(flush)/PstI).
CC    Site directed mutagenesis was performed to juxtapose the CD4 and
CC    CH1 heavy chain sequences in frame. The resulting chimeric DNA
CC    molecule encodes a protein containing the V1V2 domains of CD4 fused
CC    to the CH1 domain of heavy chain. Plaques containing the chimeric gene
CC    with the correct sequence were then grown in TG1 cells and Rf DNA
CC    isolated from the cells.
XX
SQ    Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 other;

Query Match             70.5%;  Score 1584.6;  DB 13;  Length 2482;
Best Local Similarity   99.7%;  Pred. No. 4.4e-308;
Matches 1587;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    654  GCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG  713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688  GCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG  747

Qy    714  AGGACAGCGCCCGGCCCTGGGCTGCCTGGTCAAGGACTATACTTCCCCGAACCGGTGTTCG  773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748  AGGACAGCGCCCGGCCCTGGGCTGCCTGGTCAAGGACTATACTTCCCCGAACCGGTGTTCG  807

Qy    774  TGGAACTTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA  833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808  TGGAACTTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA  867

Qy    834  GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868  GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  927

Qy    894  TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928  TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  987

Qy    954  AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAC  1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    988  AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAC  1047

Qy   1014  GCACCCCCGGCTGTGCAGCCCCAGGGCAGCAAGGCAGCCCCATCTGTCTCCTCAC  1073
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1048  GCACCCCCGGCTGTGCAGCCCCAGGGCAGCAAGGCAGCCCCATCTGTCTCCTCAC  1107

Qy   1074  CCGGGAGGCCTCGGCCGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCCC  1133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1108  CCGGGAGGCCTCGGCCGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCCC  1167

Qy   1134  AGGCTCCAGGGAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG  1193
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1168  AGGCTCCAGGGAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG  1227

Qy   1194  GTGCTTGGCTCAGACCTTGC  1253
           ||||||||||||||||||||
Db   1228  GTGCTTGGCTCAGACCTTGC  1287

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Db   1288  GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCTCCAGATCC  1347

Qy   1314  GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGCGAGTGCCCACCGTGCC  1373
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Qy   1554  ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  1613
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Db   2248  GAGCCTCTCCCTGTCCCGGGTAAATGAGTG  2278
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RESULT 15

AA298856

ID   AA298856 standard; cDNA; 2482 BP.
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AC   AA298856;
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DT   19-JUN-2000 (first entry)
XX
DE   CD4-IgG2 chimeric heterotetramer heavy chain nucleotide sequence.
XX
KW   CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment;
KW   cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW   cellular immune response interaction mediator; HIV interaction;
KW   staging; prognosis; envelope glycoprotein burden; human; ds.
XX
OS   Homo sapiens.
XX
PN   US034223-A.
XX
PD   07-MAR-2000.
XX
PF   07-JUN-1995;   95US-0477460.
XX
PR   07-AUG-1992;   92US-0927931.
PR   06-AUG-1993;   93WO-US07422.
PR   03-FEB-1995;   95US-0379516.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Allaway GP, Maddon PJ;
XX
DR   WPI; 2000-269502/23.
DR   P-PSDB; AAY85080.
XX
PT   New immunoconjugate, used to treat, prevent or image human immune
PT   deficiency virus infection, comprises radionuclide attached to
PT   heterotetramer of CD4-immunoglobulin chimeras -
XX
PS   Disclosure; Fig 4; 58pp; English.
XX
CC   This sequence represents the CD4-IgG2 chimeric heavy chain nucleotide
CC   sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates
CC   to an immunoconjugate comprising a cytotoxic radionuclide and a
CC   heterotetramer of two heavy chains and two light chains. The cytotoxic
CC   radionuclide is linked to either the heavy chains or the light chains, or
CC   to all four chains, directly or through a bifunctional chelator. Both
CC   heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by
CC   vector CD4-IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric
CC   CD4-kappa chains encoded by vector CD4-kLc-pRcCMV (ATCC 75194). CD4 is a
CC   non-polymorphic cell surface glycoprotein that is expressed on the
CC   surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
CC   and dendritic cells. CD4 associates with major histocompatibility complex
CC   (MHC) class II molecules on the surface of antigen presenting cells to
CC   mediate efficient cellular immune response interactions. In humans CD4 is
CC   the target of interaction with the human immunodeficiency virus HIV. The
CC   immunoconjugate is used to kill cells infected with HIV, and for treating
CC   or preventing infection. It is also used for imaging HIV-infected tissues
CC   (for staging or prognosis of infection, and for assessing efficacy of
CC   treatments). The immunoconjugate is also used to determine the HIV
CC   envelope glycoprotein burden, once determined, this information is used
CC   in the staging and prognosis of HIV infected patients. The
CC   immunoconjugate should be active against all strains of HIV (since the
CC   CD4-gp120 interaction is essential for infection). The heterotetramers
CC   are assembled intracellularly and secreted efficiently from mammalian
CC   cells, allowing high recovery and purification from the culture medium.
CC   They have longer half-life in serum and greater avidity than heavy chain
CC   dimers.
XX
SQ   Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 other;

Query Match   70.5%;   Score 1584.6; DB 21; Length 2482;
Best Local Similarity 99.7%;   Pred. No. 4.4e-308;

Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy         714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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1	2249	100.0	2249	11	US-09-249-011A-23	Sequence 23, Appl
2	1787.6	79.5	2009	15	US-10-047-542-55	Sequence 55, Appl
3	1638	72.8	4694	15	US-10-000-433-3	Sequence 3, Appli
4	1613	71.7	2028	15	US-10-047-542-57	Sequence 57, Appl
5	1611.8	71.7	4723	15	US-10-000-433-2	Sequence 2, Appli
6	1584.6	70.5	2482	8	US-08-485-163-2	Sequence 4, Appli
7	1584.6	70.5	2482	10	US-09-766-995-3	Sequence 3, Appli
8	1580.4	70.3	1999	15	US-10-153-382-2	Sequence 2, Appli
9	1548	68.8	2770	15	US-10-027-075-29	Sequence 29, Appl
10	1547.2	68.8	2009	15	US-10-047-542-54	Sequence 54, Appl
11	1463.4	65.1	2071	15	US-10-216-484-116	Sequence 116, App
12	1458.6	64.9	2077	15	US-10-216-484-88	Sequence 88, Appl
13	1455.4	64.7	2073	15	US-10-216-484-142	Sequence 142, App
14	1455.4	64.7	2073	15	US-10-216-484-144	Sequence 144, App
15	1455.4	64.7	2077	15	US-10-216-484-156	Sequence 156, App
16	1453.8	64.6	2073	15	US-10-216-484-146	Sequence 146, App
17	1426.4	63.4	2399	15	US-10-267-286A-1	Sequence 1, Appli
18	1093.8	48.6	11265	15	US-10-185-318-1	Sequence 1, Appli
19	1093.8	48.6	11265	15	US-10-185-799-1	Sequence 1, Appli
20	1086.4	48.3	1494	12	US-09-822-851B-4	Sequence 4, Appli
21	1086.4	48.3	1494	15	US-10-119-637A-4	Sequence 4, Appli
22	1042.4	46.3	2590	15	US-10-047-542-56	Sequence 56, Appl
23	901.8	40.1	1796	10	US-09-766-995-1	Sequence 1, Appli
24	898.6	40.0	1796	8	US-08-485-163-2	Sequence 2, Appli
25	815.2	36.2	1394	15	US-10-176-266-1	Sequence 1, Appli
26	807.2	35.9	1747	15	US-10-027-075-27	Sequence 27, Appl
27	806.4	35.7	1705	15	US-10-027-075-23	Sequence 23, Appl
28	804	35.7	1747	15	US-10-027-075-25	Sequence 25, Appl
29	545.4	24.3	1616	11	US-09-859-053-27	Sequence 27, Appl
30	545.4	24.3	1673	11	US-09-859-053-35	Sequence 35, Appl
31	545.4	24.3	1708	11	US-09-859-053-31	Sequence 31, Appl
32	542.4	24.1	1392	15	US-10-153-382-1	Sequence 1, Appli
33	542.4	24.1	1392	15	US-10-153-382-12	Sequence 12, Appl
34	542.4	24.1	1395	15	US-10-153-382-8	Sequence 8, Appli
35	542.4	24.1	1413	15	US-10-153-382-16	Sequence 16, Appl
36	541.8	24.1	1332	12	US-09-932-812-17	Sequence 17, Appl
37	541.8	24.1	1368	12	US-09-968-362-17	Sequence 17, Appl
38 c	540.6	24.0	571	10	US-09-864-761-8612	Sequence 8612, Ap
39	539.4	24.0	978	15	US-10-047-542-21	Sequence 21, Appl
40	539.2	24.0	1392	15	US-10-153-382-4	Sequence 4, Appli
41	539	24.0	1344	10	US-09-822-849A-33	Sequence 33, Appl
42	539	24.0	1539	10	US-09-822-849A-87	Sequence 87, Appl
43	539	24.0	1574	10	US-09-822-849A-82	Sequence 82, Appl
44 c	534.4	23.8	2732	10	US-09-822-849A-154	Sequence 154, App
45	514	22.9	1426	15	US-10-264-634-28	Sequence 28, Appl

ALIGNMENTS

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RESULT 1
US-09-249-011A-23
; Sequence 23, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT: VASQUEZ, MAXIMILIANO
;  APPLICANT: CARRENO, BEATRIZ
;  APPLICANT: CELNIKER, ABBIE CHERYL
;  APPLICANT: COLLINS, MARY
;  APPLICANT: GOLDMAN, SAMUEL
;  APPLICANT: GRAY, GARY S.
;  APPLICANT: KNIGHT, ANDREA
;  APPLICANT: O'HARA, DENISE
;  APPLICANT: RUP, BONITA
;  APPLICANT: VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;  TITLE OF INVENTION: OF TREATMENT THEREWITH
;  FILE REFERENCE: 08702.0081-00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 23
;  LENGTH: 2249
;  TYPE: DNA
;  ORGANISM: Mus sp.
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (12)..(417)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (655)..(948)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1341)..(1376)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1495)..(1821)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1919)..(2238)
US-09-249-011A-23

Query Match      100.0%;  Score 2249;  DB 11;  Length 2249;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2249;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      1 TCTAGACCACCATGGGTTGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTG    60
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Db      1 TCTAGACCACCATGGGTTGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTG    60

Qy     61 TGCACTCCCAGTCCAGTCGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTGCTTG   120
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Db     61 TGCACTCCCAGTCCAGTCGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTGCTTG   120

Qy    121 TGAAGGTGTCCTGCAAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGA   180
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Db    121 TGAAGGTGTCCTGCAAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGA   180

Qy    181 GACAGGCTCCTGGACAGGGGCCTGAGTGGATTGGAGTTATTAATATTACTATGATAATA   240
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Db    181 GACAGGCTCCTGGACAGGGGCCTGAGTGGATTGGAGTTATTAATATTACTATGATAATA   240

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Qy    301 CAGCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAA   360
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Qy    361 GAGCCGGCCTGTATATGGACTACTGGGGTCAAGGTACCCTGGTCACCGTCTCCTCAGGTG   420
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Qy    421 AGTCCTTAAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGGCGGGGCCTTTGGCTTTGGGGCA   480
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Qy    481 GGGAGTTGGGCTAAGGTGAGGCAGGCAGGTGAGCGGTGCCCTGGGCGCGGTGAGGTCC   540
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Qy    541 CCAGACACTGACCCCTGCCTGGACCCTGTGATAGACAAGAACCGAGGGGGCCTCTGCGC   600
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Qy    601 CCTGGGCCCAGCTCTGTCTCCCACACCGCGTCACATGGACCACCTCTCTTCTTGCAGCCTCCA   660
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Db    601 CCTGGGCCCAGCTCTGTCTCCCACACCGCGTCACATGGACCACCTCTCTTCTTGCAGCCTCCA   660

Qy    661 CCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTTCCCGGAGCACCTCGAGAGCACACAG   720
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Db    661 CCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTTCCCGGAGCACCTCGAGAGCACACAG   720

Qy    721 CGGCCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT   780
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Db    721 CGGCCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT   780

Qy    781 CAGGCGCTGTCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCT   840
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Qy    841 ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT   900
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Db    841 ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT   900

Qy    901 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGGACGAGGCCAG   960
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Db    901 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGGACGAGGCCAG   960

Qy    961 CTCAGGGAGGGAGGGTGTGCTGCTGGAAGCCAGGCTCAGCCTCCTGCTGGACGCACCCCC   1020
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Db    961 CTCAGGGAGGGAGGGTGTGCTGCTGGAAGCCAGGCTCAGCCTCCTGCTGGACGCACCCCC   1020

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Qy   1081 CCTCTGCCCGCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCACCAGGCTCC   1140
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Db   1081 CCTCTGCCCGCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCACCAGGCTCC   1140

Qy   1141 AGGAGGCACAGGTGGGTGCCCCTACCCCAGCCCCTCACACACAGGGCCAGGTGCTTG   1200
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Db   1141 AGGAGGCACAGGTGGGTGCCCCTACCCCAGCCCCTCACACACAGGGCCAGGTGCTTG   1200

Qy   1201 GCTCAGACTTGCCAAAAGCCATATCCGGGAGGACCCCTGCCCCTGACCTAAGCCGACCCCA   1260
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Db   1201 GCTCAGACTTGCCAAAAGCCATATCCGGGAGGACCCCTGCCCCTGACCTAAGCCGACCCCA   1260

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Db   1261 AAGGCCAAACTGTCCACTCCCAGCTCGGACACCTTCTCTCCCCCAGATCCGAGTAAC   1320

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Qy   1981 CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG   2040
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Db   1981 CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG   2040

Qy   2041 GAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGAC   2100
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Db  2041 GAGAGCAATGGCAGCCCGGAGACAACTACACAAGACGACCACACCTCCCATGCTGGACTCCGAC 2100
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RESULT 2
US-10-047-542-55
; Sequence 55, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 2009
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-047-542-55

  Query Match             79.5%;  Score 1787.6;  DB 15;  Length 2009;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1801;  Conservative  0;  Mismatches  4;  Indels  1;  Gaps  1;
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Db  1500 GTGTACACCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCAGGTCAGCTCAGCTGACCTGC 1559    Db   247 CATCCGTCTTCCCCCCTGGCCGCCCTGCTCCGAGGAGCACCACCTCCGAGAGCACAGCCGCCCTGG 306
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Qy  1999 CTGGTCAAAGGCTTCACCCCAGCGACATCCGTGGAGTGGGAGGCAATGGGCAGCCG 2058     Qy   730 GCTGCCTGGTCAAGGACTACTTCCCGGAACGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
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Db  1560 CTGGTCAAAGGCTTCACCCCCAGCGACATCCGCGTGGAGTGGGAGGCAATGGGCAGCCG 1619    Db   307 GCTGCCTGGTCAAGGACTACTTCCCGGAACGGTGACGGTGTCGTGGAACTCAGGCGCCC 366

Qy  2059 GAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTAC 2118    Qy   790 TGACCAGCGGCGTGCACACCTGCTCCAGTGTCCTACAGTCCTCCTCAGACTCTACTCCCTCA 849
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Qy  2119 AGCAAGGTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG 2178    Qy   850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
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Qy  2179 ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAA 2238    Qy   910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTGGTGAGACAGAGGCCAGCTCAGGGAG 969
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Qy  2239 TGAGTG 2244                                                         Qy   970 GGAGGGTGTCTGCTGGAGCAGGCAGGCAGCCCCATCGTCTCCTCACCCGGAGGCCCTGTGCA 1029
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RESULT 3                                                                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-000-433-3                                                          Db   607 GCCCCAGCCCAGGGCAGGCAGCATGGCCCAAGCATGCCCCCATCTGTCTCCTCGTCTCCTCACCCGGAGGCCCTGACC 666
; Sequence 3, Application US/10000433
; Publication No. US20020199213A1                                       Qy  1090 GCCCCACTCATGCTCAGGGAGGAGGGTCTTCTGGCTTTTTCCACCAGGGTCCAGGCAGGCA 1149
; GENERAL INFORMATION:                                                              ||||||||||||||||||||||||||||||||||||||||||||||||||||
; APPLICANT: Tomizuka, Kazuma                                           Db   667 ACCCCACTCATGCTCAGGGAGGAGGGTCTTCTGGATTTTTCCACCAGGGTCCAGGCAGCCA 726
; APPLICANT: Ishida, Isao
; APPLICANT: Lonberg, Nils                                              Qy  1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTGCACACACAGGGGCAGTGCTTGGCTCAGACC 1209
; APPLICANT: Halk, Ed                                                               ||||||||||||||||||||||||||||||||||||||||||||||||||||
; TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN  Db   727 CAGGCTGGATGCCCCTACCCCAGGCCCTGCACACACAGGGGCAGTGCTTGGCTCAGACC 786
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 014643-012110US                                       Qy  1210 TGCCAAAGCCATATCCGGAGGACCCTGCCCTAAGCCCACACCCCAAAGGCCAAA 1269
; CURRENT APPLICATION NUMBER: US/10/000,433                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||
; CURRENT FILING DATE: 2001-11-30                                       Db   787 TGCCAAGAGCCATATCCGGAGGACCCTGCCCTGACCTAAGCCCACACCCCAAAGGCCAAA 846
; PRIOR APPLICATION NUMBER: US 60/250,340
; PRIOR FILING DATE: 2000-11-30                                         Qy  1270 CTGTCCACTCCCTCAGCTCAGCACACCTTCTTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
; NUMBER OF SEQ ID NOS: 10                                                          |||||||||||||||||||||||||||||||||||||||||||||||||
; SOFTWARE: PatentIn Ver. 2.1                                           Db   847 CTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCT 906
SEQ ID NO 3
; LENGTH: 4694                                                          Qy  1330 TCTCTCTGCAGAGCGCAAATGTTGTGTGAGTGCCACCGTGCCCACCGTAAGCCAGCCCA 1389
; TYPE: DNA                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||
; ORGANISM: Artificial Sequence                                         Db   907 TCTCTCTGCAGAGTCCAAATATGTCCCCATGCCCATCATGCCCCAGGTAAGCCAACCCA 966
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gamma4 heavy    Qy  1390 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
; OTHER INFORMATION: chain plasmid                                                  |||||||||||||||||||||||||||||||||||||||||||||||||
; OTHER INFORMATION: pG4HE                                              Db   967 GGCCTCGCCCTCCAGCTCAAGGCGGACAGGTGCGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1026
US-10-000-433-3
                                                                        Qy  1450 GGCCCCAGCTGGTGCTGCACAGTCACACCTCCATCTTCTTCCTCAGCACC---ACCTGCGG 1506
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Query Match        72.8%;  Score 1638;  DB 15;  Length 4694;             Db  1027 GGCCCCAGCCAGGCGGGTGCTGCACGCATCCATCCACCTCCATCTTCTTCCTCAGCACCTGAGTTCCTGG 1086
Best Local Similarity  94.6%;  Pred. No. 0;
Matches 1719;  Conservative  0;  Mismatches  95;  Indels  4;  Gaps  2;   Qy  1507 CAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
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Qy  430 AACCTCTAGAGCTTTCTGGGGGGCCGAGCCGGGGCCGGCCCTGACTTTGGCTTTTGGGGCTTGGGGCAGGGAGTGGG 489    Db  1087 GGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGA 1146
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Db    8 AGCAGCTGAAGCTTTCTGGGGCAGGTGGCGCGCAGCAGGCCCTGACTTTGGC-TGGGGGCAGGGAGGGGGG 66   Qy  1567 CCCCTGAGGTGCACGTGCGTGGTGGTGGAGGTGCACGAGAACCCCGAGGTCCAGTTCA 1626
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Qy  550 GGACCCTGCCTGGACCCTCGTGATGGATAGACAAGAACCGAGGGCCTTCTGCCCCCTGGGCC 609    Db  1207 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1266
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Db  187 AGCTCTGTCCCCACACCGCGGTCACACCGGTCACATGCACCACCTCCTTCTCTGCAGCCTTCCACCAAGGGC 246    Qy  1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
                                                                                   ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGCGCCCTG 729    Db  1327 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCA 1386
             |||| ||||||||
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```
Qy  1807 TCTCCAAAACCAAAGGTGGACCCGCGGGGTATGAGGGCCACATGACGAGAGGCCGGCTC 1866
         ||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||||
Db  1387 TCTCCAAAGCCAAAGGTGGGACCCGCGGGGTGCCAACCTGTCGAGGCCACAGGGCAGGTCAGCTC 1446

Qy  1867 GGCCCACCCTGCCGGAGTGACCGGTGACCGTGTGCCAACCTGTCCCGGAGGCAGGGCCAGCCC 1926
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1447 GGCCCACCCTGCCGGAGTGACCGGTGACCGTGTGCCAACCTGTCCCGGAGGCAGGGCCAGCCC 1506

Qy  1927 CGAGAACCACAGTGTACACCCTGCCCCATCCCGGAGGAGATGACCAAGAACCAGAGTC 1986
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1507 CGAGAGCCACAGGTGTACACCCTGCCCCATCCCGGAGGAGGAGATGACCAAGAACCAGAGGTC 1566

Qy  1987 AGCCTGACCTGGCTCCGTGGTCAAAGGCTTCTACCCCGACCTCCGTGGAGTGGGAGAGC 2046
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1567 AGCCTGACCTGCTCCGTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 1626

Qy  2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACTCCCATGCTGGACTCCGACGCGCTCC 2106
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1627 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 1686

Qy  2107 TTTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1687 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTC 1746

Qy  2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1747 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTG 1806

Qy  2227 TCCCCGGGTAAATGAGTG 2244
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Db  1807 TCTCTGGGTAAATGAGTG 1824
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RESULT 4
US-10-047-542-57
; Sequence 57, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-047-542-57

Query Match   71.7%;   Score 1613;   DB 15;   Length 2028;
Best Local Similarity 94.7%;   Pred. No. 0;
Matches 1713;   Conservative 0;   Mismatches 90;   Indels 6;   Gaps 4;

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Qy   439 AGCTTTCTGGGGCGCAGCCGGGGCCTGACTTTGGCTTTGGGCAGGGAGTGGGCTAAGGTGA 498
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Db     1 AGCTTTCTGGGGCGCAGCCGGGGCCTGACTTTGGC--TGGGGGCAGGGGCAGCACTGGCTTAAGGTGA 59

Qy   499 GGCAGGTGCGCGCCAGCCAGGTGCACACCCGGTGAGCCCAGCACTGGACCCTGC 558
         |||||||||||||   ||||||||||||||| ||||||||||||||||
Db    60 CGCAGGTGCGCGCCCAGCCAGGTGCACACCCAATGCCAATGCCAGAGCCCGACCACTGGACCCCTGC 119

Qy   559 CTGGACCCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 618
         |||||| |||   ||||||||||||||||||||||||||||||||||||||||
Db   120 ATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 179
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Qy   430 AACCTCTAGAGCTTTCTGGGGCAGGCCGGAGGCGGCGGCCGCGGCCGTCGACTTGGCTTTGGGGCAGGGAGGAGTGGG 489
         ||||||||| ||||||||||||||||||||||||       ||  |||||||| ||||||||||||||||||||| |||
Db     8 AGCAGCTGAAGCTTTCTGGGGCAGGCCGGAGGCAGCCAGCCAGCCGTCGACCTGGCTTTGGGGCAGGGAGGAGGGGG 67

Qy   490 CTAAGGTGAGGCAGTGCGCGCAGGTGCGCCCATCGAGAAAACCATCTCCAAAA 549
         ||||||||||||||||||||||||||||||| |||||||||||||||||| || |
Db    68 CTAAGGTGAGGCAGTGCGCGCAGGTGCACCATCGAGAAAACCATCTCCAAAG 127

Qy   550 GGACCCTGCCTGGACCTGTCGTCGATAGACAGCAGCGGCCTGGGCCTGGGCCC 609
         ||    ||     |||| |     |||||||||||   ||   ||  ||  |||
Db   128 GGACGCT----GAACCTCGCGGACAGTTAAGAACCAGGGGCCTCGGCCCCTGGGCCC 182

Qy   610 AGCTCTGTCCCACACCGCGGTCACATGCACCACTCTTGCAGCCTCCAGCAAGGGCC 669
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 AGCTCTGTCCCACACCGCGGTCACATGCACCACTCTTGCAGCCTCCAGCAAGGGCCA 242

Qy   670 CATCGCGCTCTTCCCCTGGCGCCCTGCTCCGAGGAGACCACCTCCGAGCACGGGCCCTGG 729
         |||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   243 CATCGGCTCTTCCCCCTGCCACCCCTGGGGGGCACCCTCGGGGCACCCTGGGGGCGCCCTGG 302

Qy   730 GCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
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Db   303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCAG 362

Qy   790 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCCTCACTCCCTCA 849
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   363 CGGACCGGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCCTCACTCTCCTCA 422

Qy   850 GCAGCGTGGTGACCGTGCCCTGCAGCAACTTCGGCACCCAGACCTACACCGCCAACGTAG 909
         |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACACTTGTGCAACGTGA 482

Qy   910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy   970 GGAGGGTGTCTGTGAAGCCAGGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
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Db   543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy  1030 GCCCCAGCCCAGGGCAGCAAGGCAGCCCCATCCTGTCTCCTCTGTCTCGCCTTCTCACCCGGAGGCCTCTGCCC 1089
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||| |||||||||||||||
Db   603 GCCCCAGTCCAGGGCAGCAAGGCAGCCCCGTCCTGTCTCCTCTTTCCGCCTTTTTCCACCCGGAGGCCTCTGCCC 662

Qy  1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCCACCAGGCTCCAGGCAGGCA 1149
         |||||||||||||||||||||||||||||| |||||||||     |||||||||||||||||
Db   663 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC--CCAGGCTCTGGGCAGGCA 721

Qy  1150 CAGGCTGGGTGCCCCTACCCCAGGCCCCTTCACACACAGGGGCAGGTGCTTGGCTCGACC 1209
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Db   722 CAGGCTAGTGCCCCTAACCCCAGGCCCTCGACACAAGGGGCAGGTGCTGGGCTCGGACC 781

Qy  1210 TGCCAAAGCCATATCCGGAGGACCCTGCCCTGACCTAAGCGACCCCAAAGGCCAAA 1269
         ||||||| ||||||||||||||||||||| |||||||||||| ||||||||||||||
Db   782 TGCCAAGAGCCATATCCGGAGGACCCTGCCCTGACCTAAGCGACCTAAGCCCCAAAGGCCAAA 841

Qy  1270 CTGTCCACTCCCTCGGACACCTTCTCCTCCCCGAGATCCGAGTAACTCCCAATCT 1329
         || ||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db   842 CTCTCCACTCCCTCGGACACCTTCTCTCTCCCCAGATTCCGAGATTCCAGTAACTAACTCCCAATCT 901

Qy  1330 TCTCTCTGCAGAGCGCAAATGTTGTCTGA------GTGCCCACGTGCCCAGTAA 1380
         |||||||||||||||||||||||||||||      ||||||||||||||||||||
Db   902 TCTCTCTGCAGAGCCCAAATCTGTGACAAAATCTGTGACAAAACTCACACATGCCCACCGTGCCCAGTAA 961

Qy  1381 GCCAGCCCAGGCCTCGCCCTCCAGTCAAGGGCAGGTAGCAGTTGCCTAGAGTAGCCTGCAT 1440
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Db   962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGGCAGGTAGCAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy  1441 CCAGGGACAGGCCCCAGCTGGCCCAGCCGCTCCACTCCTGTGCTGCTGACACCTCCTGACC--1498
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Db  1022 CCAGGGACAGGCCCCAGCCCAGGCCGGGCTGACGTCTCCCATCCTCTTCCTCAGCACCTG 1081

Qy  1499 ACCTGCGCGAGCAGCCAGGCCACCGTCAGTTCCTTCTCCCCCCAAAACCCAAGGCACCCTCATGA 1557
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Qy  1696 CGTTCCGTGTGGTCAGGCTCTCCACCGTTGTGCACCAGGACTGGCTGACACGGCAAGGAGT 1755
         |||| |||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db  1258 CGTACCGTGTGGTCAGGCTCTCCACCGTTGTCCACCAGGACTGGCTGACACGGCAAGGAGT 1317

Qy  1756 ACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAA 1815
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1318 ACAAGTGCAAGGTCTCCAACAAAGGCCTCCCATCGAGAAAACCATCTCCAAAG 1377

Qy  1816 CCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCTCACCC 1875
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Db  1378 CCAAAGGTGGGACCCACGGGGTGCGAGGGCCACACGGACAGAGGCCAGCTCGGCCCACCACCC 1437

Qy  1876 TCTGCCCTGGGAGTGACCGCGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCA 1935
         ||||||   |||||||||||||| |||||||||||||||||||||||||||| ||||||||
Db  1438 TCTGCCCTGGGAGTGACCGTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCA 1497

Qy  1936 CAGGTGTACACCCTGCCCCCATCCCGGGAGGATGACCAAGAACCAGGTCAGCCTGACC 1995
         |||||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||
Db  1498 CAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACC 1557

Qy  1996 TGCCTGGTCAAGGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 2055
         ||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Db  1558 TGCCTGGTCAAGGCTTCTACCCCGCGCTGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1617

Qy  2056 CCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTC 2115
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Db  1618 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1677

Qy  2116 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 2175
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Db  1678 TACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCC 1737

Qy  2176 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 2235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  1738 GTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGT 1797

Qy  2236 AAATGAGTG 2244
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Db  1798 AAATGAGTG 1806
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RESULT 5
US-10-000-433-2
; Sequence 2, Application US/10000433
; Publication No. US20020199213A1
; GENERAL INFORMATION:
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Ishida, Isao
; APPLICANT: Lonberg, Nils
; APPLICANT: Halk, Ed
; TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 014643-012110US
; CURRENT APPLICATION NUMBER: US/10/000,433
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,340
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gamma1 heavy
; OTHER INFORMATION: chain plasmid
; OTHER INFORMATION: pCG7-96
US-10-000-433-2

Query Match   71.7%; Score 1611.8; DB 15; Length 4723;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4;

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/485,163
  FILING DATE: 07-JUN-1995
  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
  NAME: White, John P.
  REGISTRATION NUMBER: 28,678
  REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 278-0400
  TELEFAX: (212) 391-0525
  TELEX:
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 2482 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: unknown
  MOLECULE TYPE: cDNA
  ORIGINAL SOURCE:
  ORGANISM: homo sapien
  CELL TYPE: lymphocyte
US-08-485-163-4

Query Match 70.5%;   Score 1584.6;   DB 8;   Length 2482;
Best Local Similarity 99.7%;   Pred. No. 0;
Matches 1587;   Conservative 0;   Mismatches 0;   Indels 4;   Gaps 0;

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Qy   654  GCCTCCACCAAGGGCCATCGGTCTTCCCCTGCCCCTGCCCCTGCTTCCCCGAGCACCTCCGAG   713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   688  GCCTCCACCAAGGGCCATCGGTCTTCCCCTGCCCCTGCCCCTGCTTCCCCGAGCACCTCCGAG   747

Qy   714  AGCACAGCCGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG   773
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   748  AGCACAGCCGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG   807

Qy   774  TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA   833
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   808  TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA   867

Qy   834  GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC   893
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   868  GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC   927

Qy   894  TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG   953
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Db   928  TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG   987

Qy   954  AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAC   1013
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Db   988  AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAC   1047

Qy  1014  GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCATGGGAGGCCAAGGCAG   1073
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Db  1048  GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCATGGGAGGAGGTCTTCAC   1107

Qy  1074  CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGACGGGTCTTCGGCTTTTTCCACC   1133
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Db  1108  CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGACGGGTCTTCGGCTTTTTCCACC   1167

Qy  1134  AGGCTCCAGGCAGGCACAGCAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG   1193
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Db  1168  AGGCTCCAGGCAGGCACAGCAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG   1227

Qy  1194  GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC   1253
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Db  1228  GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC   1287

Qy  1254  GACCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC   1313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1288  GACCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC   1347

Qy  1314  GAGTAACTCCCAATCTTCTCTGCGAGAGCGCAAATGTTGTCGAGTGCCCACCGTGCC   1373
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Db  1082  AACTTCCTGCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCAAGGACACCCTCATGA   1141
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Qy  1558  TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCGACCCCGAGG   1617
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Db  1142  TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAGACCCTGAGG   1201

Qy  1618  TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG   1677
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Db  1202  TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG   1261

Qy  1678  AGGAGCAGTTCAACAGCACAGTTCCGTGTGTCTCCACCGTGTGCACCAGGACT   1737
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Db  1262  AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT   1321

Qy  1738  GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG   1797
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Db  1322  GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCCAGCCCCCATCG   1381

Qy  1798  AGAAAACCATCTCCAAAACCAAAGGGCACCCGCGGGGTATGAGGGCCACATGGACAGA   1857
          ||||||||||||||||  |||||||||||||| || |||||||||||||||||||||||
Db  1382  AGAAAACCATCTCAAAGCCAAAGGGCACCCGGGAGCCACAGGTGTGCACCCTGCCCCCATCCCGGGACAGA   1441

Qy  1858  GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCTACA   1917
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Db  1442  GGCCGGCTCGGCCCACCCTCCGCCCTGAGAGTGACCGCTGTGCCACCTCTGTCCCTACA   1501

Qy  1918  GGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG   1977
          |||||||||||||||||||||||||| || |||||||||||||||| || |||||||||
Db  1502  GGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGACCAAG   1561

Qy  1978  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG   2037
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  1562  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG   1621

Qy  2038  TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC   2097
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  1622  TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC   1681

Qy  2098  GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG   2157
          |||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||||
Db  1682  GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG   1741

Qy  2158  AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC   2217
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Db  1742  AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC   1801

Qy  2218  CTCTCCCTGTCCCCGGGTAAATGAGTG   2244
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Db  1802  CTCTCCCTGTCTCCGGGTAAATGAGTG   1828
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; CURRENT APPLICATION NUMBER: US/09/766,995
; CURRENT FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
;
SEQ ID NO 3
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-766-995-3

Query Match        70.5%;    Score 1584.6;    DB 10;   Length 2482;
Best Local Similarity  99.7%;   Pred. No. 0;
Matches 1587;   Conservative  0;   Mismatches  0;   Indels  4;   Gaps  0;
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Qy   654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
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Db   688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy   714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
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Db   748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy   774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy   834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy   894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGACAGTTGGTGAG 953
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGACAGTTGGTGAG 987

Qy   954 AGGCCAGCTCAGGGAGGAGGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCGCTGCTGGAC 1013
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   988 AGGCCAGCTCAGGGAGGAGGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCGCTGCTGGAC 1047

Qy  1014 GCACCCCGGCTGTGCAGCCCCAGGGCAGCCAGGCAAGGCAGCAGGGCCCATCGTCTCCTCAC 1073
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Db  1048 GCACCCCGGCTGTGCAGCCCCAGGGCAGCCAGGCAAGGCAGCAGGGCCCATCGTCTCCTCAC 1107

Qy  1074 CCGGAGAGGCCCTGCGCCGCCCACTCATGCTCAGGGAGAGGGTCTTCGGCTTTTTCCACC 1133
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1134 AGGCTCCAGGCAGGCAGGCAATGTTGTGTGCAAATGTTGTGTGCGGGACAGGGGCAG 1193
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1194 GTGCTTGGCTCAGACCTGCCAAAGCCATATCCGGGAGACCCTGCCCCTGACCTAAGCC 1253
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1228 GTGCTTGGCTCAGACCTGCCAAAGCCATATCCGGGAGACCCTGCCCCTGACCTAAGCC 1287

Qy  1254 GACCCCAAAGCCAAACTGTCCACTCCCTCCAGCTCGGCACACCTTCCCTCCCCCAGATCC 1313
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1288 GACCCCAAAGCCAAACTGTCCACTCCCTCCAGCTCGGCACACCTTCCCTCCCCCAGATCC 1347

Qy  1314 GAGTAACTCCCAATCTTCTCTCTGCGAGCGCAAATGTTGTGTCGAGTGCGCCACCGTGCC 1373
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Db  1348 GAGTAACTCCCAATCTTCTCTCTGCGAGCGCAAATGTTGTGTCGAGTGCGCCACCGTGCC 1407

Qy  1374 CAGGTAAGCCAGCCAGCCCAGGCCTCGCCCTCCCAGCTCCAGCTCCAGCGTGCCCTAGAGTAG 1433
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Db  1408 CAGGTAAGCCAGCCAGCCCAGGCCTCGCCCTCCCAGCTCCAGCTCCAGCGTGCCCTAGAGTAG 1467

Qy  1434 CCTGCATCCAGGGACAGCAGGCCCAGCTGGTGTGCACGTCGACACGTCCACCTCTTCCTCA 1493
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1494 GCACCACCTGCGCGACACCGTCAGTTCTTCCTTCCCCCAAAACCCAAGGACACCCTC 1553
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Db  1348 GAGTAACTCCCAATCTTCTCTCTGCGAGAGCGCAAATGTTGTCGAGTGCGCCACCGTGCC 1407

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Qy  1434 CCTGCATCCAGGGACAGCAGGCCCAGCTGGTGTGCTGACACGTCCACCTCTTCCTCA 1493
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Db  1348 GAGTAACTCCCAATCTTCTCTCTGCGAGAGCGCAAATGTTGTGTCGAGTGCGCCACCGTGCC 1407

Qy  1374 CAGGTAAGCCAGCCAGCCCAGGCCTCGCCCTCCCAGCTCCAGCGTGCCCTAGAGTG 1433
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Db  1408 CAGGTAAGCCAGCCAGCCCAGGCCTCGCCCTCCCAGCTCCAGCGTGCCCTAGAGTG 1467
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Db  1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613

Qy  1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613

Db  1588 ATGATCTCCCGGACCCCTGAGGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1647

Qy  1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
Db  1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy  1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733
Db  1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1767

Qy  1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
Db  1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827

Qy  1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1853
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Qy  1854 CAGAGGCCGGCTCGGCCCACCCTCTGCGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913
Db  1888 CAGAGGCCGGCTCGGCCCACCCTCTGCGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy  1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
Db  1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy  1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
Db  2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

Qy  2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093
Db  2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2127

Qy  2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153
Db  2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy  2154 GGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
Db  2188 GGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy  2214 GAGCCTCTCCCCGTCTCCCGGGTAAATGAGTG 2244
Db  2248 GAGCCTCTCCCCGTCTCCCGGGTAAATGAGTG 2278
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RESULT 7
US-09-766-995-3
; Sequence 3, Application US/09766995
; Patent No. US2002005248lA1
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway et al.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 2048/41215-CB/JPW/SHS
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Sat Jul 19 10:01:52 2003

us-09-627-896b-23.rnpb

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Qy    652 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCGCCCTGCTCCAGGAGCACCTCCG  711
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Db    410 CAGCTAGGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCTGCTCCAGGAGCACCTCCG  469

Qy    712 AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT  771
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Db    470 AGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGT  529

Qy    772 CGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCT  831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    530 CGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCT  589

Qy    832 CAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGA  891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    590 CAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGA  649

Qy    892 CCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTG  951
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Db    650 CCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTG  709

Qy    952 AGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTCCGTCT  1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    710 AGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTCCGTC   769

Qy   1012 ACGCACCCCCGGGTGTGCAGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCA  1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    770 ACGCACCCCCGGGTGTGCAGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCA  829

Qy   1072 ACCCGGAGGCCTTGCCCTGCCCCCAGCCCTACCCCAGCCCCTGCCCCTGACCTAAG  1131
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Db    830 ACCCGGAGGCCTTGCCCTGCCCCCAGCCCTACCCCAGCCCCTGCCCCTGACCTAAG   889

Qy   1132 CCAGGCTCAGGACTCAGACTGGGCCAAAAGCCAAATCTTCCACTCCTCTGCGAGAGCC  1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 CCAGGCTCAGGACTCAGACTGGGCCAAAAGCCAAATCTTCCACTCCTCTGCGAGAGCC   949

Qy   1192 AGTGCTTGGGCTCAGACCTGCCAAGAGCCATATCCCGGAGGACCCGGACCCTGACCTAAG  1251
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Db    950 AGTGCTTGGGCTCAGACCTGCCAAGAGCCATATCCCGGAGGACCCGGACCCTGACCTAAG  1009

Qy   1252 CCGACCCCAAAGGCCAAACTGTCCACTCCTCTGCGAGAGCCCAAGTTGTGTGACCGTG  1311
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Db   1010 CCGACCCCAAAGGCCAAACTGTCCACTCCTCTGCGAGAGCCCAAGTTGTGTGACCGTG  1069

Qy   1312 CCGAGTAACTCCCATCTTCTTCCTCAGCAGGGACAGGTGCCCTAGAGT  1371
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Db   1070 CCGAGTAACTCCCATCTTCTTCCTCAGCAGGGACAGGTGCCCTAGAGT  1129

Qy   1372 CCGAGTAAGCACCAGCCAGGGAGGCGTCCACCTCCATCCTCTTCCT  1431
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CCGAGTAAGCACCAGCCAGGGAGGCGTCCACCTCCATCCTCTTCCT  1189

Qy   1432 AGCCTGCATCCAGGGACAGGCCCCAGCTGGGCTGTGCTGACACGTCCCCAAAACCCAGGAC  1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 AGCCTGCATCCAGGGACAGGCCCCAGCTGGGCTGTGCTGACACGTCCCCAAAACCCAGGAC  1249

Qy   1492 CAGCACCACCTGCGGCAGACCCCTGAGGTCACGTGGTTGGGAGTGGTTGGGAGTGGACGAAGAGACC  1551
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Db   1250 CAGCACCACCTGTGGCAGACCCCTGAGGTCACGTGGTTGGGAGTGGTTGGGAGTGGACGAAGAGACC  1309

Qy   1552 TCATGATCTCCCGAGGTCACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TCATGATCTCCCGAGGTCACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  1369

Qy   1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1370 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC  1429

Qy   1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTCACC  1731
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Db   1430 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTCACC  1489
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Qy   1554 ATGATCTCCCGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGAGACCC  1613
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Db   1588 ATGATCTCCCGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCGCATAATGCCAAGACAAAGCCA  1647

Qy   1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA  1673
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Db   1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA  1707

Qy   1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG  1733
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Db   1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG  1767

Qy   1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1827

Qy   1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGTATGGGCCACATGGA  1853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGTATGGGCCACATGGA  1887

Qy   1854 CAGAGGCCCCGGCTGTGGGCTCGGGCCCCAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGATGAC  1913
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1888 CAGAGGCCCCGGCTGTGGGCTCGGGCCCCAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGATGAC  1947

Qy   1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGCGACGACCGGT  1973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGCGACGACCGGT  2007

Qy   1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT  2033
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Db   2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT  2067

Qy   2008 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA  2093
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Db   2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA  2127

Qy   2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA  2153
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Db   2088 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA  2187

Qy   2068 CTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA  2187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 CTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA  2213

Qy   2094 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA  2213
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Db   2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA  2247

Qy   2128 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA  2247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   2154 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2244
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Db   2188 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2278

Qy   2188 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2244

Qy   2214 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2278

Qy   2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG
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SEQUENCE CHARACTERISTICS:
     LENGTH: 2770 base pairs
     TYPE: nucleic acid
     STRANDEDNESS: single
     TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-027-075-29

Query Match
Best Local Similarity  68.8%;   Score 1548;  DB 15;  Length 2770;
Matches 1716;  Conservative  93.8%;  Pred. No. 0;  Indels  24;  Gaps  9,
        Mismatches  90;

Qy    427 TAAAACCTCTAGAGCTTTCTGGGGCGGCCGCCTGCACTTTGGCTTTGGGGCAGGGAGT  486
          ||||||| || |||||||||   ||| || |||  |||||||||||||||||||||||
Db    750 TAGAGGATCCCCAGCTTTCTCGGGGAGCCAGCTTGACCCTTGGCTTTGGGGCAGGGAGG  809

Qy    487 GGGCTAAGGTGAGGCAGGTGGCGCAGCCAGCCAGCCTGAGCCCCAGAC  546
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Db    810 GGGCTAAGGTGAGGCAGGTGGCGCGGCCAG-CAGGTGCACACCAATGCCCATGAGCCCCAGAC  868

Qy    547 ACTGGACCCTGCCTGGACACCTGTGATGACAAGAACAGGGGCCTTGCTCGCGCCTGGG  606
          ||||||||||       ||||  | | || ||| |||||||||||| |||||   |||
Db    869 ACTGGACGCT-----GAACCTGCGGACAGTTAAGAACCCAGCACCCTCTGCG-CCTGGG  922

Qy    607 CCAGCTCTGTCCCACCGCGGTCCTGCCTCCACCGCTGCTCCAGCGCTCCACCAAGG  666
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Db    923 CCAGCTCTGTCCCACCGCGGTCACATGGCCCTGCTCCTCAGGAGCACCTCCACCAAGG  982

Qy    667 GCCCATCGGTCTTCTCCCCTGCTCCAGGACGGCCGCCC  726
          || ||||| ||||  ||||| |||||||||| ||||||
Db    983 GCCCATCGGTCTTCCCCCCTGCACCCTCCTCAAAGAGCACCTCTGGGGGCACAGCGGCCCC  1042

Qy    727 TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCG  786
          |||||||||||||||||||||||| ||||||||||||||||||| ||||||||||||||
Db   1043 TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCG  1102

Qy    787 CTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCC  846
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1103 CCCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCC  1162

Qy    847 TCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACG  906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1163 TCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG  1222

Qy    907 TAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAG  966
          |  |||  ||  ||||||||||||||||||||| ||||   ||||||| ||||||||||
Db   1223 TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGG  1282

Qy    967 GAGGGAGGGTGTCTGCTGGAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGGCTGT  1026
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Db   1283 GAGGGAGGGTGTCTGCTGGAAG-CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTGT  1341

Qy   1027 GCAGCCCCAGTCCAGGCAGCAAGGCAGGCCCCGTCTTCTGGGAGGCCCTG  1086
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Db   1342 GCAGCCCCACTCCAGGCAGCAAGGCAGGCCCCGTCTTCTGGGAGGGCCTG  1400

Qy   1087 CCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAG  1146
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Db   1401 CCCGCCCCACTCATCGTGCTCAGGGAGAGGGTTCTGGCTTTTTC---CCAGGCTCCAGGCAG  1458

Qy   1147 GCACAGCTGGGTGCCCCTAACCCAGGCCCTGCACCTCCTGACCTAAGCGACCCCAAAGGCC  1206
          |||||||||||  ||| ||| |||| |||||| | ||||||||||||||||||||||||
Db   1459 GCACAGCTAGGTGCCCATATCCGGGAGGCACCTTCACACAACCCAGGCCCTGACCTAAGCCTAAGCCCAAAGGCC  1518

Qy   1207 ACCTGCCGAGAGCAATATCCGGGAGGACACCTTCTCCTCCCAGATTCCAGTAACTCCCA  1266
          ||||||| || ||||||||||||||||||||||||||||||||| |||| || |||||
Db   1519 ACCTGCCGAGAGCAATATCGGGGAGGACACCTTCGGACACCTTCTCCTCCCAGATTCCAGTAATCCCCAA  1578

Qy   1267 AAACTGTCCACTCCCCTCACCCTTCTCCTCCCAGATCCCGGGAGACACCTTC  1326
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Db   1579 AAACTCTCCACTCCCCTCACCCTTCTCCTCCCAGATTCCAGTAACTCCCA  1638
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Qy   1732 AGGACTGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC  1791
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Db   1490 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCC  1549

Qy   1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG  1851
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1550 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGTATGAGGGCCACATG  1609

Qy   1852 GACAGAGAGGCCGGCTCGGGCCACCCTCCGCCCTCTGGGAGTGACCGCTGTGCCAACCTCTGTC  1911
          ||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Db   1610 GACAGAGAGGCCGGCTCGGGCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC  1669

Qy   1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG  1971
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG  1729

Qy   1972 ACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC  2031
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1730 ACCAAGAACCAGGTCAGCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC  1789

Qy   2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG  2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG  1849

Qy   2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  1909

Qy   2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG  2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG  1969

Qy   2212 AAGAGCCTCTCCCTGTCTCCGGGTAAATGA  2241
          ||||||||||||||||||||||||||||||
Db   1970 AAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1999
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RESULT 9
US-10-027-075-29
Sequence 29, Application US/10027075
Publication No. US20020114814A1
GENERAL INFORMATION:
APPLICANT: Gray, Gary S. et al.
TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
Having Modified Effector Functions and Uses Therefor
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,075
FILING DATE: 20-Dec-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/227,595
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION: <Unknown>
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 29:

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;   TITLE OF INVENTION:   AND BACTERIAL DISEASES
;   FILE REFERENCE: 030905.0004.CIP1
;   CURRENT APPLICATION NUMBER: US/10/047,542
;   CURRENT FILING DATE:   2001-10-26
;   PRIOR APPLICATION NUMBER: PCT/US01/13932
;   PRIOR FILING DATE: 2001-04-28
;   PRIOR APPLICATION NUMBER: 60/200,298
;   PRIOR FILING DATE: 2000-04-28
;   NUMBER OF SEQ ID NOS: 101
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 54
;   LENGTH: 2009
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-047-542-54

Query Match     68.8%;    Score 1547.2;    DB 15;   Length 2009;
Best Local Similarity   94.1%;    Pred. No. 0;
Matches 1711;   Conservative   0;   Mismatches   83;   Indels   24;   Gaps   9;

Qy    439 AGCTTTCTGGGCGCAGCCGCGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGA 498
          ||||||||||  ||||  |||||||||||||||||||| ||||||||| |||||||||||
Db      1   AGCTTTCTGGGCAGGCCGCAGGCCTGACCTTTGGGCAGGGAGGGGGCTAAGGTGA 60

Qy    499 GGCAGGTGCGCGCCAGCCAGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCCTGC 558
          |||||||||||||| | ||||| |  |||||||||| |||||||||||||  ||||||
Db     61   GGCAGGTGGGCCCAG-CAGTGCACCCCATGCCCATGAGCCCAGACACTGGACGCT-- 117

Qy    559 CTGGACCCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGGGCCCTGGGCCCAGTCTGTC 618
          ||||||||||||||||  |||||||||||  |||||||||||||||||||| |||||||||
Db    118   --GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGGG-CCTGGGCCCAGTCTGTC 173

Qy    619 CCACACCGCGGTCACATGGACCACCACCTCTTGCAGCCTCCACCAAGGGCCCATGGTCT 678
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    174   CCACACCGGCGGTCACATGGACCACCACCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 233

Qy    679 TCCCCCTGCGCGCCCTGCTCCAGGAGCACCTCCAGGAGGCGTGTCGTGGAACGGTGCCTGG 738
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    234   TCCCCCTGGCGACCCCTCCTCAAGAGCACCTCTGGGGCGCAGCGGCCCTGGGCTGCCTGG 293

Qy    739 TCAAGGACTACTTCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGCTCTGACCAGCG 798
          |||||||||||||||||||||||  |||||||||||||||||| ||||||||||||||
Db    294   TCAAGGACTACTTCCCGAACCGGTGTCGTGGAACTCAGGGCGCGCCCTGACCAGCG 353

Qy    799 GCGGTGCACACTTCCCAGCTGTCTCTACAGTCCCTACGGCGACATCGCGTG 858
          |||||||||||||||||||||||  ||||||||||||||||||| |||||||
Db    354   GCGTGCACACTTCCCGGCTGTCTCCAGGACTTCCTCAGTCCCTACAGTCCCGTG 413

Qy    859 TGACCGTGCCCTGCAGCAACTTCGGCGCACCCCAGACCACCTCCATGCTCTGGAC 918
          |||||||||||||||||||||||||||||||||||| |||||| |||||||||||
Db    414   TGACCGTGCCCTGCAGCAGCTTCGGCGCACCCCACGCCTGCCGTCCCGTGCTGGAC 473

Qy    919 CCAGCAACAACAGGTGACAAGAGACAGTTGGTGAGGAGCCAGCTCAGGGAGGAGGGTGT 978
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    474   CCAGCAACAACAGGTGACAAGAGACAGTTGGTGAGGAGCCAGCTCAGGGAGGAGGGTGT 533

Qy    979 CTGCTGGAAGCAGGCTCAGCCGCTCCATGCTGGAGGCCGCGCCCCGGCGTGTGCAGCCAGCC 1038
          ||||||||||||||||||||||  | ||||| |||||||||||||||||||||||||||||
Db    534   CTGCTGGAAG-CAGGCTCAGCCGCTCAGCCTCAGCCTCATGCGCTATGCAGCCCCAGTC 592

Qy   1039 CAGGGCAGCAAGGCAGGCCCCGTCCTCCATCTGTCTCCTGCCGCCGCCCCACTC 1098
          |||||||||||||||||||||||||| |||||||||||||||| | |||||||||
Db    593   CAGGGCAGCAAGGCAGGCCCCGTCCTGCTGCCTGCCCTTCACCCGGA-GCCTGCCGCCCCCACTC 651

Qy   1099 ATGCTCAGGGAGAGGGTCTTCTCTGGCTTTTTCCACCAGGCTTCGTCCAGGCACAGGCTGGG 1158
          ||||||||||||||| |||||||||||||||||||||||| ||||||
Db    652   ATGCTCAGGGAGAGGGTCTTCTGCCTTTTTC--CCAGGCTCTGGGGCAGCACAGGCTAGG 709

Qy   1159 TGCCCCTACCCCAGGCCCTTCACACAGGGGGCAGGTGCTGGCTGCCAAAAG 1218
          ||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    710   TGCCCCTAACCCAGGCCCTTGCACACAAAGGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAG 769

Qy   1219 CCATATCCCGGAGGACCCCTGCCCTGACCTAAGCCCAGGACCCCAAAGGCCAAACTGTCCACT 1278
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Qy   1327 TCTTCTCTGCAGAGCGCAAATGTGTCGA-------GTGCCCACCGTGCCCAGG 1377
          |||||||||||||||||||||||||||||              |||||||||||||
Db   1639   TCTTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCACCGTGCCCAGG 1698

Qy   1378 TAAGCCAGCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGTGCCTCAGTAGTAGCCTG 1437
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1699   TAAGCCAGCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGTGCCTCAGTAGTAGCCTG 1758

Qy   1438 CATCCAGGGACAGGCCCCAGTGGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCAC 1497
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1759   CATCCAGGGACAGGCCCCAGCGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCAC 1818

Qy   1498 C--ACCTGCGGCAGCACGTCAGTCTTCTCTCTCCCCCAAAACCCAAGGACACCCTCA 1554
          |     ||||| |||||||||||| ||||||||||||||||||||||||||||||||||
Db   1819   CTGAACTCCTGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAAGGACACCCTCA 1878

Qy   1555 TGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCG 1614
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879   TGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTG 1938

Qy   1615 AGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCAC 1674
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   1939   AGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC 1998

Qy   1675 GGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTGTGCACCAGG 1734
          ||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1999   GGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGG 2058

Qy   1735 ACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCA 1794
          ||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||||
Db   2059   ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA 2118

Qy   1795 TCGAGAAAACCATCTCCAAAACCAAAGGTGGACCCGCGGGGTATGAGGGCCACATGGAC 1854
          ||||||||||||||||||||||||||| |||||||||||||  ||||| |||||||||||
Db   2119   TCGAGAAAACCATCTCCAAAGCCAAAGGTGCAGCCCGAGAACCACAGGTGTGCACCCTG 2178

Qy   1855 AGAGGCCGGCTCGGCCCACCCTGTGCCCGGATGACCGTGTGCCAACCTCTGTCCT 1914
          |||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db   2179   AGAGGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGTGTACCAACCTCTGT-CCT 2237

Qy   1915 ACAGGGGCAGCCCCGAGAACCACAGTGTACACCCGGGAGGAGATGACC 1974
          |||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2238   ACAGGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 2297

Qy   1975 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG 2034
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   2298   AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 2357

Qy   2035 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGAC 2094
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358   GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 2417

Qy   2095 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 2154
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2418   TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 2477

Qy   2155 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 2214
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2478   GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 2537

Qy   2215 AGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2244
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Db   2538   AGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2567
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RESULT 10
US-10-047-542-54
; Sequence 54, Application US/10047542
; Publication No. US2002016836 7A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

US-10-216-484-116
: Sequence 116, Application US/10216484
: Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 116
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
; OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
; OTHER INFORMATION: antibody
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (21)..(77).
; FEATURE:
; NAME/KEY: intron
; LOCATION: (735)..(1125)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1171)..(1288)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1619)..(1715)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (21)..(734)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1126)..(1170)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1289)..(1618)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1716)..(2036)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (78)..(734)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (1126)..(1170)
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; LOCATION: (1289)..(1618)
; FEATURE:
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; LOCATION: (1716)..(2036)
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; LOCATION: (1126)..(1170)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1289)..(1618)
; FEATURE
; NAME/KEY: CDS

Db   770 CCCATATCCGGGAGGAGACCCTGCCCCTGACCTAAGCCACCCAAACCTCTCCACT 829
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||
Qy   1279 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGGAGTAACTCCCAATCTTCTCTCTGC 1338

Db   830 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGC 889
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Qy   1339 AGAGCGCAAATGTGTGTCGAG------TGCCCACCCGTGCCCAGGTAAGCCAGCCCA 1389

Db   890 AGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCCGTGCCCAGGTAAGCCAGCCCA 949
              ||| ||||||||| | |||||||||||||||||||||||||||||||||||||||||||
Qy   1390 GGCCTCCGCCCTCCAGCTCAAGGCGGGAACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449

Db   950 GGCCTCCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1009
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy   1450 GGCCCCAGCTGGGTGCTGACACGTCCACTTCACTCTTCCTCAGACACC---ACCTGCCG 1506

Db   1010 GGCCCCAGCCGCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGACACCTCGAACTCCTGG 1069
              |||||||||||||||||||||||| ||||||||| |||||||||||||| |||||
Qy   1507 CAGCACCGTCAGTCTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566

Db   1070 GGGGACCGTCAGTCTTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGGA 1129
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626

Db   1130 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1189
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1686

Db   1190 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1249
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Qy   1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746

Db   1250 ACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCGTGCACCAGGACTGGCTGAATG 1309
              |||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Qy   1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806

Db   1310 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1369
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Qy   1807 TCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA 1866

Db   1370 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA 1429
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Qy   1867 GGCCCACCCCTCTGCCCTGGGAGTGACCGCTGTGTGCCAACCTCTGTCCCTACAGGGCAGCCCC 1926

Db   1430 GGCCCACCCCTTGCCCCTCTCGCCCTGAGAGTGACCGCTGTACCAGGCGCAGCCC 1488
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy   1927 CGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986

Db   1489 CGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTC 1548
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy   1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCGGTGGAGTGGGACGAGC 2046

Db   1549 AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGACGAGC 1608
              |||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||
Qy   2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106

Db   1609 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 1668
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Qy   2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166

Db   1669 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 1728
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226

Db   1729 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 1788

Qy   2227 TCCCCGGGTAAATGAGTG 2244
              ||||||||||||||||||
Db   1789 TCTCCGGGTAAATGAGTG 1806

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;  LOCATION: (1716)..(2036)
US-10-216-484-116

Query Match           65.1%;   Score 1463.4;   DB 15;   Length 2071;
Best Local Similarity 82.2%;   Pred. No. 0;
Matches 1848;   Conservative   0;   Mismatches 166;   Indels 235;   Gaps   5;

Qy      8 CACCATGGTTGGAACTGTATCATCTTCTTTCTCGTTACCACAGCTACAGGTGTCACTC 67
          ||||||||||||  | |||||| | ||||| ||| ||||| |||||||||| ||||||
Db     17 CACCATGGATGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTC 76

Qy     68 CCAGTCCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAGCCTGGAGTCAGTGAAGT 127
          | |||||||| |||||| |||||||||||||| |||||||||| | ||||| ||
Db     77 TCAGTCCAACTGGTGCAGTCTGGGCTGAGGTCAAGAAGAGCCTTCAGTGAAGT 136

Qy    128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGTGAGACAGGC 187
          |||||||||||||||||||||||||||| | |||||||||||  | ||| | | |  ||
Db    137 GTCCTGCAAGGCTTCGGCTACACCTTCACCGATTATGCTATACAGTGGGTAAAACAGGC 196

Qy    188 TCCTGGACAGGGCCTGAGTGGATTGGAGTTATTAATATTACTGATGATAATACAAACTA 247
          |||||||||||||||||||||||| |||| |   |  |||  | ||||||||||||||
Db    197 CCCTGGACAGGGCCTGAGTGGGATTGGAGAGATTGATCCTTCTGATAGCTATACTAACTA 256

Qy    248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACAGCACAGCCTA 307
          ||| |  |||||||| |||||||||||| |  || ||||||||| ||| ||||| ||||
Db    257 CAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCACCAGCACCAGCCTA 316

Qy    308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC 367
          |||||||| ||  ||| ||| |||||||||| | | ||||| |||||||| |||| | |
Db    317 CATGGAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCAAGAAATAG 376

Qy    368 CTGGTATATGGACTACTGGGGTCAAGGTACCCTGTCCTGTCTCCTCAGTGAGTCTT 427
          ||| |||| | ||||||||||| ||||  | |  | || |  ||
Db    377 GGACTATAGTAACAACTGG-------------------------------------- 395

Qy    428 AAAACCTCTAGAGTTTCTGGGGCGAGCCGGGCTGACTTTGGCTTTGGGCAGGGAGTG 487
          | || || |    |  |||||||||||||||| |  | | |  ||
Db    396 ------TACTTCGATGTGTGGGGCGAAGGGACCCTGG------------------- 426

Qy    488 GGCTAAGGTGAGGCAGGTGGCGCGCAACCAGTGCACACCCAATGCCCGTGAGCCCAGACA 547
          |||| |||||||  |  ||| | || |  | |||||||||||| |||||||||| |||
Db    427 -------------------------------------------------------------- 426

Qy    548 CTGGACCCTGCCTCTGGACCCTCGTGGATAGACAAGAAACCGAGGGCGCCTCTGCCGCCCTGGGC 607
          ||||||||||||||||| ||   | || ||||| || || ||| | || ||||||||| |||||
Db    427 CTGGACCCTGCCTCTGAACCTCCCCAAGACGCCTCTGCCGCCTCTGCCGCCCCTGGGC 607

Qy    608 CCAGCTCTGTCCCACACCGCGGGTCACATGGCACACCTCTTGCAGCCTCCACACGGG 667
          ||||||||||||||||  ||  || | || || |||||||| |||||| | | |||
Db    427 -----------TCACCGGTCGATGTGACACCTTCCCAGGACCTCTACTCCCT 454

Qy    668 CCCATGCGGTCTTCCCCGCGCCCTGCCGTCCAGGAGCACAGCGGCGGCCCT 727
          |||| | |||||||||||  ||||||| | |||||| |||||| |||||||
Db    455 CCCATGCGGTCTTCCCCGCGACACCTTCCCAAGACACCCTGGGCGGCGGCCCT 514

Qy    728 GGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGGC 787
          ||||||||||||||||||||||||||||||||||||||||| | ||| ||| || ||||| |
Db    515 GGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGACA 574

Qy    788 TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCCTCAGGACTCTACTCCCT 847
          |||||||||||||||||||||||||||||| |||||||||||||||| |||||||||| ||
Db    575 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCCTCAGGACTCTACTCCCT 634

Qy    848 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 907
          ||||||||| |||| ||||  | ||| | || |||| | | ||||||||||| ||||| |
Db    635 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT 694

Qy    908 AGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAGGG 967
          ||| |||||||||||| | |||||||||| | |||| ||||| |||||||||||| ||||
Db    695 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGG 754

Qy    968 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCCACCCCGGCGTGTG 1027
          |||||||  |||||||||||||||||||||||| |||||||
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Qy   2096  CCGACGGCGCCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG  2155
                  ||||||||||||||||||| ||||||||  |||||||||||||||||||||||||||||
Db   1894  CCGACGGCGCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG  1953

Qy   2156  GGAACGTCTTCTTCATGCTCCGTGATGCATGCAGGCTCTGACGAGCTCGCACAACCACTACACGCAGAAGA  2215
                  ||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1954  GGAACGTCTTCTTCATGCTCCGTGATGCATGCAGGCTCTGACGAGCTCGCACAACCACTACACGCAGAAGA  2013

Qy   2216  GCCTCTCCCTGTCCCCGGGTAAATGAGTG  2244
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Db   2014  GCCTCTCCCTGTCCCCGGGTAAATGAGTG  2042
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RESULT 12
US-10-216-484-88

; Sequence 88, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;   APPLICANT: Serizawa, No. US20030103976Alufusa
;   APPLICANT: Haruyama, Hideyuki
;   APPLICANT: Nakahara, Kaori
;   APPLICANT: Tamaki, Ikuko
;   APPLICANT: Takahashi, Tohru
;   TITLE OF INVENTION: Anti-Fas Antibodies
;   FILE REFERENCE: 980126CIP/HG
;   CURRENT APPLICATION NUMBER: US/10/216,484
;   CURRENT FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: US/09/499,662
;   PRIOR FILING DATE: 2000-02-09
;   PRIOR APPLICATION NUMBER: US 09/053,583
;   PRIOR FILING DATE: 1998-04-01
;   NUMBER OF SEQ ID NOS: 165
;   SEQ ID NO 88
;   LENGTH: 2077
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;   OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
;   OTHER INFORMATION: antibody
;   FEATURE:
;   NAME/KEY: sig peptide
;   LOCATION: (27)..(83)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (741)..(1131)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1177)..(1294)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1625)..(1721)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (27)..(740)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1132)..(1176)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1295)..(1624)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1722)..(2042)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (84)..(740)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (1132)..(1176)
;   FEATURE:
;   NAME/KEY: mat peptide

;   LOCATION: (1295)..(1624)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (1722)..(2042)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (27)..(740)
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1295)..(1624)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1722)..(2042)
US-10-216-484-88

Query Match   64.9%;   Score 1458.6;   DB 15;   Length 2077;
Best Local Similarity   82.0%;   Pred. No. 0;
Matches 1845; Conservative   0; Mismatches   169; Indels 235; Gaps   5;

Qy   8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACCAGCTACAGGTGTGCACTC   67
              |||||| | ||||||||||||||| ||||| |||| ||| |||||||||||||||||
Db   23 CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTC   82

Qy   68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
              ||||||||| |||||| ||||||||||| || |||| || ||||||||| ||||||||
Db   83 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTCAAGAAGGTTCAGTGAAGGT 142

Qy   128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
              |||||| |||||||||||||| ||||||| || ||| |||||||||||||| ||||||
Db   143 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGGC 202

Qy   188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATAATTACTATGATAATACAAACTA 247
              ||| ||||||| || |||||| |||||| || ||||||||| ||| ||||||||||||
Db   203 CCCTGGACAGAGGCTTGAGTGGATGGGAGAGATTGATCCTTCTGATAGCTATACTAACTA 262

Qy   248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACAGCACAGCCTA 307
              ||||| ||||||| ||||||||||| ||||| |||||||| | ||||| ||||| ||||
Db   263 CAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCGCTAGCACAGCCTA 322

Qy   308 TATGGAACTGAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC 367
              ||||||| || |||| |||||||||||| | ||||||||||||||||||| |||||
Db   323 CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAAGAAATAG 382

Qy   368 CTGGTATATGGACTACTGGGGTCAAGGTACCCCTGTCACCGTCTCCTCAGGTGAGTCTT 427
              ||| |||| | |||| |||||||||| ||||||||||||||||||| ||||||
Db   383 GGACTATAGTAACAACTGG--- 401

Qy   428 AAAACCTCTAGAGCTTTCTCGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGACTG 487

Db   402 ------TACTTCGATGTCTGGGGCGCAAGGGACCCCTGG---------------------- 432

Qy   488 GGCTAAGGTGAGGCAGGTGGCGCGCCAGCCAATGCCCGTGAGCCCCAGACA 547
                                                              |||||
Db   433 -- 432

Qy   548 CTGGACCCTGCCTGGACCCCTCGTGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC 607

Db   433 -- 432

Qy   608 CCAGCTCTGTCTCCACACCGCGGTCACATGGACCACCTCTCTTGCAGCCTTCCACCAAGGG 667

Db   433 ----------------------------------TCACCGTCTCCTCCACCAAGGG 460

Qy   668 CCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCT 727
              |||||||||||||||||||||||||| |||| |||||| |||||||| ||| | |||||
Db   461 CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT 520

Qy   728 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 787
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   521 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 580
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LOCATION: (1295)..(1624)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (1722)..(2042)
FEATURE:
NAME/KEY: CDS
LOCATION: (27)..(740)
FEATURE:
NAME/KEY: CDS
LOCATION: (1132)..(1176)
FEATURE:
NAME/KEY: CDS
LOCATION: (1295)..(1624)
FEATURE:
NAME/KEY: CDS
LOCATION: (1722)..(2042)
US-10-216-484-88
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Qy   788  TCTGACCAGCGGCGGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT  847
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   581  CCTGACCAGCGGCGGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT  640

Qy   848  CAGCAGGCGGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT  907
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||| |
Db   641  CAGCAGGCGGTGGTGACCGTGCCCTCCCTCCAGCAGCTTGGGCACCCAGACCTACACATCTGCAACGT  700

Qy   908  AGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGCAGTTGGTGAGAGGCCAGCTCAGGG  967
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   701  GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGG  760

Qy   968  AGGGAGGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTCGCTGCTGGCCACCCCGGCTGTG  1027
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   761  AGGGAGGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACCGCATCCCCGGCTATG  820

Qy  1028  CAGCCCCAGCCAGGGAGCAAGGCAGGCCCCATCGTCTCCTCCACCCGGAGGGCCTCTGC  1087
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   821  CAGTCCCCAGTCCAGGGCAGCAGGCAGGCCCCGTCTCTGCGTCTCCACCCGGAGGGCCTCTGC  880

Qy  1088  CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG  1147
          ||||||||||||||||||||||| |||||||||||||||||    |||||||||||||
Db   881  CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC--CCAGGCTCTGGGCAGG  939

Qy  1148  CACAGGCTGGGTGCCCTACCCCAGGCCCTCACACAGGGGGCAGTGTGCTTGGCTCAGA  1207
          |||||||||||||||||||||||||||  ||||||||||   |||||||||||||||
Db   940  CACAGGCTAGGTGCCCTTAACCCAGGCCCTGACACAGGGGGCAGTGTGGCAGTGGCTCAGA  999

Qy  1208  CCTGCCAAAAGCCATATCCGGAGGAGACCCGCCCCTGACCTAAGCCGACCCAAAGGCCA  1267
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1000  CCTGCCAAGAGCCAATATCCGGAGGAGACCCGCCCCTGACCTAAGCCGACCCCAAAGGCCA  1059

Qy  1268  AACTGTCCACTCCCTCAGCTCGACACCTTCTCTCTCCTCCGAGTAACTCCCCAAT  1327
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1060  AACTTCCCACTCCCTCAGCTCGACACCTTCTCTCTCCCAGATTCCAGTAACTCCCCAAT  1119

Qy  1328  CTTCTCCTGCAGAGCGGCAAAATGTTGTGTCGA-------GTGCCACCGTGCCCAGGT  1378
          ||||||||||||||||      ||||||||||   ||||||||||||||||||||
Db  1120  CTTCTCCTGCAGAGCCCAAATCTTGTGACAAAATCTCACACACTGCCACCGTGCCCAGGT  1179

Qy  1379  AAGCCAGCCCAGGCCTCGCCTCCAGCTCAAGGCGGGGACAGGTGCCCTAGAGTAGCCTGC  1438
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1180  AAGCCAGCCCAGGCCTCGCCTCCAGCTCAAGGCGGGGACAGGTGCCCTAGAGTAGCCTGC  1239

Qy  1439  ATCCAGGGACAGGCGCCCAGCTGGGTGCTGACAGTGCCACCTCCATCTCTTCCTCAGCACC  1498
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1240  ATCCAGGGACAGGCGCCCAGCCGGGTGCTGACAGTGCCACCTCCATCTCTTCCTCAGCACC  1299

Qy  1499  ---ACCTGCGCAGCACCCAGTCTGCCTTCTTCCCCCCAAAACCCAAGGACACACCCTCAT  1555
             ||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db  1300  TGAACTCCTGGGGGGACCCCAGTCTCAGTCTTCTTCCTCCCCCCAAAACCCAAGGACACCCTCAT  1359

Qy  1556  GATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGA  1615
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  1360  GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGA  1419

Qy  1616  GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG  1675
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Db  1420  GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG  1479

Qy  1676  GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGA  1735
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  1480  GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA  1539

Qy  1736  CTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCAT  1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1540  CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT  1599

Qy  1796  CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACA  1855
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  1600  CGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACA  1659
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Qy  1856  GAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGTGCCCAGTGCCTGTCCCCTA  1915
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  1660  GAGGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCGTACCAACCTCTGTCCCCTA  1719

Qy  1916  CAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA  1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1720  CAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA  1779

Qy  1976  AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG  2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1780  AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG  1839

Qy  2036  AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACT  2095
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  1840  AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT  1899

Qy  2096  CCGACGGCTCCTTCTTCCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG  2155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1900  CCGACGGCTCCTTCTTCCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG  1959

Qy  2156  GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA  2215
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Db  1960  GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA  2019

Qy  2216  GCCTCTCCCTGTCCCCGGGTAAATGAGTG  2244
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Db  2020  GCCTCTCCCTGTCCCCGGGTAAATGAGTG  2048
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RESULT 13
US-10-216-484-142
; Sequence 142, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 142
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
; OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
; OTHER INFORMATION: antibody
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (23)..(79)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (737)..(1127)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1173)..(1290)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1621)..(1717)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (23)..(736)
; FEATURE:
; NAME/KEY: exon

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;  LOCATION: (1128)..(1172)
;  FEATURE:
;  NAME/KEY: exon
;  LOCATION: (1291)..(1620)
;  FEATURE:
;  NAME/KEY: exon
;  LOCATION: (1718)..(2038)
;  FEATURE:
;  NAME/KEY: mat peptide
;  LOCATION: (80)..(736)
;  FEATURE:
;  NAME/KEY: mat peptide
;  LOCATION: (1128)..(1172)
;  FEATURE:
;  NAME/KEY: mat peptide
;  LOCATION: (1291)..(1620)
;  FEATURE:
;  NAME/KEY: mat peptide
;  LOCATION: (1718)..(2038)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (23)..(736)
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;  NAME/KEY: CDS
;  LOCATION: (1128)..(1172)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1291)..(1620)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1718)..(2038)

US-10-216-484-142

Query Match       64.7%;  Score 1455.4;  DB 15;  Length 2073;
Best Local Similarity 81.9%;  Pred. No. 0;
Matches 1843;  Conservative 0;  Mismatches 171;  Indels 235;  Gaps 5;
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Qy    548  CTGGACCCTGCCTGGACCCTCGTCGGTGGATAGACAAGAAGACCGAGGGGCCTCTGCGCCCTGGGC  607
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Db    407  -------------------------------------------------------GTCTGGGGCCAAGGT  421

Qy    608  CCAGCTCGTCTGCCACACCGCGGTCACATGGCACCACCTCTTGCAGCCTCCACCAAGGG  667
                 |                            |    ||||||||||||||||||
Db    422  ACACTGGTCACCGTCTCC-----------------------TCAGCCTCCACCAAGGG  456

Qy    668  CCCATCGGTCTTCCCCCTGGCGCCCTGTCTGGCTCCTCCCAAGAGCAGCACCTCCGAGGAGCACAGCGCGGGCCCT  727
                 |||||||||||||||| |||| |  ||||    |  |||||||||||| |||||
Db    457  CCCATCGGTCTTCCCCCTGGCACCCTGGCACCCTCTGGGGGCACAGCACCTCGGGGCACAGCGCGGGGCCCT  516

Qy    728  GGGCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCGTGGAACTCAGGCGC  787
                 ||||||||||||||||||||||| |||||||||| ||||||||||||||||||||||
Db    517  GGGCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCGTGGAACTCAGGCGC  576

Qy    788  TCTGACCAGCGGCGGGTGCACACCTTCCCAGCTGTCCTACAGTCTCAGGACTCTACTCCCT  847
                 ||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||
Db    577  CCTGACCAGCGGCGGGTGCACACCTTCCCGGCTGTCCTACAGTCTCAGGACTCTACTCCCT  636

Qy    848  CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT  907
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Db    637  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT  696

Qy    908  AGATCACAAGCCCAGCAACACCAAGGTGACAAGACAGTTGGTGAGAGGCCAGCTCAGGG  967
                 |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    697  GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGG  756

Qy    968  AGGGAGGGTGTCTGCTGAGGAGCCAGGTCAGGCTGAGGCCCTGCTCCTGGACCCACCCGGCTGTG  1027
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Db    757  AGGGAGGGTGTCTGCTGAGGAGCCAGGTCAGGCTCAGGCTCAGGCCCTGCTCCTGGACCCACCCGGCTATG  816

Qy   1028  CAGCCCCAGCCCAGGGAGCAAGGCAGGCAGCAGCCCCCATCGTCTCCTCACCCGGAGGCCCTCTGC  1087
                 ||||||||  |||||||||||||||||||||||  ||||||||| ||||||||||||||||
Db    817  CAGTCCCAGTCAGGGAGCAAGGCAGGCAGCAGCCCCGCTCCTCTTCACCCGGAGGCCCTCGC  876

Qy   1088  CCGCCCCACTCATGTCCAGGGAGAGGGTCTTCTGGCTTTTCCCACCAGGCGTCTCCAGGCAGG  1147
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Db    877  CCGCCCCACTCATGCTCCAGGGAGAGGGTCTTCTGGCTTTTCC--CCAGGCTCTGGGCAGG  935

Qy   1148  CACAGGCTGGGTGCCCTCACCCCGGGCCCTCACAGCACAGGGCAGGTGCTTGGCTCAGA  1207
                 |||||| ||| ||||||||  ||||||||||| ||||  ||||||||||||||||||||
Db    936  CACAGGCTAGGTGCAGTCCCTAAACCCAGGCCCTGACACACAAAGGGGCAGGTGCTGGGCTCAGA  995

Qy   1208  CCTGCCAAAGCCATATCCGGGAGGACCCGCCCTGACCTAAGCCGACCCAAAGGCCA  1267
                 |||||||| |||| ||| |||||||| |||||||||||||||||||  ||||||||||
Db    996  CCTGCCAAGAGCCATATCCGGGAGGACCCGCCCTGACCTAAGCCCACCCCAAAGGCCA  1055

Qy   1268  AACTGTCCACTCCCAGCTGGAGTCTATTAATAATTACTACTGATAATACAAACTA  1327
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Db   1056  AACTTCCACTCCCAGCTCCCAGATTCTCTCCCAGATTCCCAGTTCCAGTAGCTATAACTAACTA  1115

Qy   1328  CTTCTCTCTGCGAGAGCCAAATGTTGTGTCGA--------GTGCCCACCGTGCCCAGGT  1378
                 ||||||||||| |||| |||||| ||||||||        |||||||| |||||||||
Db   1116  CTTCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACACATGCCCACCGTGCCCAGT  1175

Qy   1379  AAGCCAGCCCAGGCCTCGGCCTGCCTCCATCCCTCCTAGAGTAGCCTGC  1438
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Db   1176  AAGCCAGCCCAGGCCTCGCCCTGCCTCCAGCTCAAGGCGGACAGCAGTGTCCCTAGAGTAGCCTGC  1235

Qy   1439  ATCCAGGGACAGGCCCAGGTGCTGGGTGCTGCACGTCACCTCCATCTTCCTCAGCACC  1498
                 ||||||||||||||||||||||  |||||| ||||||||||||||| |||||||||||||
Db   1236  ATCCAGGGACAGGCCCAGGTGCTGGGTGCTGCACGTCACCTCCATCTTCCTCAGCACC  1295

Qy   1499  ---ACCTGCGCACAGCCCTCAGTCTCCCCCCCCAAAACCCAAGGACACCCTTCAT  1555
                       || ||  |||  ||| ||||  |||||||| ||||| || |||||||||
Db   1296  TGAACTCCTGGGGGACCCGTCAGTCTCAGTCTTTTGGGGTTTGGGGGGCAGGGAGTG  1355

Qy   1556  GATCTCCGGACCCCTGAGGTCACGTGGTGGTGAGGACCCCGA  1615
                 ||||  || ||||  |||||||| ||||||||  |||||||||
Db   1356  GATCTCCGGACCCCTGAGGTCACATGGTGGTGAGGACCCCAGACA  1415

Qy   1616  GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG  1675
           --------------------------------------------------------------
Db   1416  ------------------------------------------------------------
```

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Qy      8  CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACACAGGTGTGCACTC  67
                 |||||||| |||||||||||  ||||||| |||||| |  ||||||||| ||||||
Db     19  CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTC  78

Qy     68  CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT  127
                 |||||||||||| |||||||||||||||| |    ||||||  ||||||||||||||
Db     79  TCAGGTCCAACTGGTCGGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT  138

Qy    128  GTCCTGCAAAGTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC  187
                 ||  ||| |||||  || ||||||| |  || | ||| ||| |||||||||| || ||||
Db    139  GTCCTGCAAGGCTTCGGCTACACCTTCACCAGCTACTATATGCACTGGGTGAGACAGGC  198

Qy    188  TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATCCTAATGATAATACAAAACTA  247
                 |||||||| ||||| | || ||| ||  || |||| |||| ||||||||| |||||||||
Db    199  CCCTGGACAGGGACTTGAGTGGATGGGATATCCTTCTGATAGCGGTAGTAGCTATAACCTA  258

Qy    248  CAACCAGAAGTTTAAGGCCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA  307
                 ||| || ||||| |||||||||| |||| | |||  ||| | || || ||||||||||||
Db    259  CAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCACCAGCACAGCCTA  318

Qy    308  TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC  367
                 |||||||| ||| | ||| || ||||| || ||  ||||||||||||||||||| ||| ||
Db    319  CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAGAAATAG  378

Qy    368  CTGGTATATGGACTACTGGGGTCAAGGTACCCCTGTCACCGTCTCCTCAGGTGAGTCCTT  427
                 ||||| ||  |||||||| ||
Db    379  GGACTATAGTAACAACTGGTACTTCGAT-----------------------------  406

Qy    428  AAAACCTCTAGAGCTTTCTGGGGCAGCCGGCCTGGGGCTTTGGCTTTGGGGGCAGGGAGTG  487
           -------------------------------------------------------------
Db    407  ------------------------------------------------------------  406

Qy    488  GGCTAAGGTGAGGCAGGTGGCCCAGCCCAGCCAGGTGCACACCCAAATGCCCGTGAGCCCCAGACA  547
           -------------------------------------------------------------
Db    407  ------------------------------------------------------------  406
```

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```
Db   1416 GGTCAAGTTCAACAGCACGTTCCGTGTCGTGTCGGAGCGTGCATAATGCCAAGACAAAGCCGCG 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1676 GGAGGAGCAGTTCAACAGCACGTTACCGTGTCGGTCGTCAGCGTCCTCACCGTTGTCCACCAGA 1735

Db   1476 GGAGGAGCAGTAGTACAACAGCAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCCAT 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1736 CTGGCTGAACGGCAAGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCAT 1595

Db   1536 CTGGCTGAATGGCAAGGAGTACAAGTTGCAAGGTCTCCAACAAAGGCCCACATGGACA 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1796 CGAGAAAACCATTCTCCAAAACCAAAGGTGGGACCCGGCCGGCCCACATGGACA 1915

Db   1596 CGAGAAAACCATTCTCCAAAGCCAAAGGTGGGACCCGTGCCAACCTCTGTCCCTA 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1856 GAGGCCGGCCTCGGCCCACCCTCTGCCCGTGCCCCCATCCCGGAGGATGACCA 1975

Db   1656 GAGGCCGGCCTCGGCCCCACCCTCTGCCCGTGCCCCCATCCCGGAGGAGAGTGACCA 1775
          ||||||||||||||||||||||||||||||||||||||||||||||
Qy   1916 CAGGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGCTGGACT 2035

Db   1716 CAGGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGTGCTGGACT 1835
          ||||||||||||||||||||||||||||||||||||||||||||
Qy   1976 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG 2095

Db   1776 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG 1895
          ||||||||||||||||||||||||||||||||||||||||||
Qy   2036 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACAGG 2155

Db   1836 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACAGG 1955
          ||||||||||||||||||||||||||||||||||||||||
Qy   2096 CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 2215

Db   1896 CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGATGAGCATGGAGCCTGGACAGG 2015
          |||||||||||||||||||||||||||||||||||||||
Qy   2156 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2244

Db   1956 GGAACGTCTTCTTCCTCTTCATGCTCCGGGTAAATGAGTG 2044

Qy   2216 GCCTCTCCCCTGTCCCCGGGTAAATGAGTG 2015

Db   2016 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2044
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RESULT 14
US-10-216-484-144, Application US/10216484
; Sequence 144, Application US2003010397GA1ufusa
; Publication No. US20030103976A1ufusa
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Hideyuki
; APPLICANT: Naruhara, Kaori
; APPLICANT: Nakahara, Ikuko
; APPLICANT: Tamaki, Tohru
; APPLICANT: Takahashi, Tohru Antibodies
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/499,662
; PRIOR APPLICATION DATE: 2000-02-09
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: US 09/053,583
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 144
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;   encoding the heavy chain of a humanized anti-Fas
;   antibody
; OTHER INFORMATION: antibody
; FEATURE:
; NAME/KEY: sig peptide

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LOCATION:        (23)..(79)
FEATURE:
NAME/KEY:  intron (1127)
LOCATION:        (737)..(1127)
FEATURE:
NAME/KEY:  intron (1290)
LOCATION:        (1173)..(1290)
FEATURE:
NAME/KEY:  intron (1717)
LOCATION:        (1621)..(1717)
FEATURE:
NAME/KEY:  exon
LOCATION:        (23)..(736)
FEATURE:
NAME/KEY:  exon (1172)
LOCATION:        (1128)..(1172)
FEATURE:
NAME/KEY:  exon (1620)
LOCATION:        (1291)..(1620)
FEATURE:
NAME/KEY:  exon (2038)
LOCATION:        (1718)..(2038)
FEATURE:
NAME/KEY:  mat peptide
LOCATION:        (80)..(736)
FEATURE:
NAME/KEY:  mat peptide (1172)
LOCATION:        (1128)..(1172)
FEATURE:
NAME/KEY:  mat peptide (1620)
LOCATION:        (1291)..(1620)
FEATURE:
NAME/KEY:  mat peptide (2038)
LOCATION:        (1718)..(2038)
FEATURE:
NAME/KEY:  CDS
LOCATION:        (23)..(736)
FEATURE:
NAME/KEY:  CDS (1172)
LOCATION:        (1128)..(1172)
FEATURE:
NAME/KEY:  CDS (1620)
LOCATION:        (1291)..(1620)
FEATURE:
NAME/KEY:  CDS (2038)
LOCATION:        (1718)..(2038)

US-10-216-484-144
Query Match             64.7%;  Score 1455.4;  DB 15;  Length 2073;
Best Local Similarity   81.9%;  Pred. No. 0;  Mismatches 171;  Indels 235;  Gaps 5;
Matches 1843;  Conservative 0;  Mismatches 0;

Qy      8 CACCATGGGTTGGAACTGTATCATCTTCTTTCCTTCTTGGTTACCACTACAGTGTCCACTC 67
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||| |||||
Db     19 CACCATGGGATGGAGCTGTGTCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTTCAGTGAAGGT 127

Db     68 CCAGTCCAACTCGTCGAGTCGTCGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAGACAGGCC 187

Qy     79 TCAGGTCCAACTCGTCGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTTCAGTGAAGGT 198

Db    128 GTCCTGCAAAGCTTCCGGCTACAACATTCACTGATTATGGTCAGTGGGTAAAACAGCAT 247

Qy    139 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGCGACAGGCC 307

Db    188 TCCTGGACAGGGGCCTCGAGTGGATTGGATGGGAGAGAGTTGATCCTTCTGATAGTGACA 307

Qy    199 CCCTGGACAGGGACTTGAGTGGATGGGACGAGGCCAATGACTGTAGACAAGTCGAGAGCA 318

Db    248 CAACCAGAAGTTCAAGGGCAGGGCCACAATACTGTAGACAATCGTGAGACATCCACTAGCA 367

Qy    259 CAATCAAAAGTTCAAGGGCAGGGCCACAATACTCGAGGATACGCCGTTATTACTGTGCAAGAGCGGC 367

Db    308 TATGGAACTTAGTTCTTTGAGATCTGAGAGGGA
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Left column alignment:

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Db  319  CATGGAGCTCAGCAGCC...||||||...
Qy       ||||||  |||
Db  368  CTGGTATATGTGGGACTACTGGGGTCAAGGTCATTACTGTGCAAGAAATAG 378
Qy       ||   ||   ||||||
Db  379  GGACTATAGTAACAACTGTACTTCGAT
Qy       ||||| |
Db  428  AAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTG 487
Qy       |||  ||||||
Db  407  ----------
Qy  488  GGCTAAGGTGAGGCAGGTGGCGCCGCCAGCAGTCGCACACCCAATGCCCTGAGCCCAGACA 547
Db  407  ----------
Qy  608  CCAGCTCTCGTGTCCCACACGGCCGTCGTCGCCCTGGGC 607
Db  422  ACACTGGTCACCGTCTCC----
Qy       GTCTGGGGCCAAGGT 421
Db  668  CCCATGGTCTTCCCCGTGTCCCGCTCCAGGAGCACCTCCGAGGAGCACAGCCGCGGCCCT 727
Qy  457  CCCATCGGTCTTCCCCGTGTCCCTGCAGCTCCTGAGGACTCTGCTTCAGGACTTCACTCCT 516
Db  728  GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 787
Qy  517  GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGTCGTGGAACTCAGGCGC 576
Db  788  TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 847
Qy  577  CCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 636
Db  848  CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 907
Qy  637  CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 696
Db  908  AGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCACAGGG 967
Qy  697  GGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCACAGGG 756
Db  968  AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCGCACCCCGGCTGTG 1027
Qy  757  AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCGCCTGGCTATG 816
Db  1028 CAGCCCCAGCCCAGGGCAGCAAGGCAGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGC 1087
Jy  817  CAGTCCCAGCCCAGGGCAGCAAGGCAGCCCCATCTGTCTCCTCTTCACCCGGAGGCCTCTGC 876
Db  1088 CCGCCCCACTCATGGTGCCCTCCAGCCCTTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG 1147
b    877 CCGCCCCACTCATGGTGCCCTCCAGCCCTTTCTGGCTTTTTCC--CCAGGCTCCAGGCAGG 935
Db  1148 CACAGGGCTGGGTGGCCCCTACCCCGGTGCCCCTTCACACAGGGCCAGTGCTTGGCTCAGGA 1207
Qy  936  CACAGGGCTAGGTGGCCCCTTACCCGGTGCCCCTTCACACAGGGCCAGTGCTTGGCTCAGA 995
Db  1208 CCTGCCAAAAGCCATATCCGGGAGGACCCCGTGCCCCTGACCTTAAGCCCACCCAAAGGCCA 1267
Qy  996  CCTGCCAAGAGCCATATCCGGGAGGACCAGGTGCCCGTCCTGGCTCGA 1055
Db  1268 AACTGTTCCACTCCCTGCAGAGCGCCAGGCCTCCGCCCTCCTCCCTCTCTT... 1327
Db  1056 AACTCTTCCACTCCCTGCAGAGCGCCAGGCCTCCGCCCTCCTCCCTCTCT--- 
Db  1328 CTTTCTTCTCTGCAGAGCGCCAAAATGTTGTGTCGA------GTGCCCACCGTGCCCCAGG 1378
      1116 CTTCTCTCTGCAGAGCGCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCCAGG
Db  1379 AAGCCAGGCCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC 1438
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Right column alignment:

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Db  1176 AAGCCAGGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC 1235
Qy
Db  1439 ATCAGGGACAGGCCCAGCTGGGTGCTGCACGTGACACCTCCATCTTCCTCCAGCACC 1498
Qy  1236 ATCCAGGGACAGGCCCAGCTGGGTGCTGCACGTGACACCTCCATCTTCCTCCAGCACC 1295
Db  1499 ---ACCTGCGGCGAGACCGTCAGTTTCCTCTTCCCCCAAAACCCAAGGACACCCTCAT 1555
Qy  1296 TGAACTCCTGGGGGGACCGTCAGTTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCAT 1355
Db  1356 GATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCTCAT 1355
Qy
Db  1616 GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGA 1675
Qy  1416 GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG 1475
Db  1676 GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGA 1735
Qy  1476 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA 1535
Db  1736 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1795
Qy  1536 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1595
Db  1796 CGAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 1855
Qy  1596 CGAGAAAACCATCTCCAAAGCCAAAGGTGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 1655
Db  1856 GGAGGGCCGGCTCGGCCCACCTCTCCGCCCGAGAACCACAGGTGTACACCGTGTACACCCTGCCCTA 1915
Qy  1656 GGAGGGCCGGCTCGGCCCACCTCTCCGCCCGAGAGTGTACACCGTGTACACCCTGCCCTA 1715
Db  1916 CAGGGACGCAGCCCCAGGCCTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACACCGGAGGAGTGATGACCA 1975
Qy  1716 CAGGGACGCAGCCCCAGGCCTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG 1775
Db  1976 AGTGTGGGAGGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACCGGG 2035
Qy  1776 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG 1835
Db  2096 CCGACGGCTCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 2095
Qy  1896 CCGACGGCTCTTCTTCCTCTATAGCAAGCTCATATGATGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTGTCCCCGG 1895
Db  2156 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2155
Qy  1956 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAGG 1955
Db  2216 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
Db  2016 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2015
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; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 156
; LENGTH: 2077
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (27)..(83)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (741)..(1131)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1177)..(1294)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1625)..(1725)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (27)..(740)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1295)..(1624)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1722)..(2042)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (84)..(740)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (1132)..(1176)
; FEATURE:
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; LOCATION: (1722)..(2042)
; FEATURE:
; NAME/KEY: CDS
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; FEATURE:
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; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1295)..(1624)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1722)..(2042)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
; OTHER INFORMATION: encoding the heavy chain of humanized anti-Fas
; OTHER INFORMATION: antibody
US-10-216-484-156
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Query Match       64.7%;   Score 1455.4;   DB 15;   Length 2077;
Best Local Similarity  81.9%;   Pred. No. 0;
Matches 1843;   Conservative  0;   Mismatches 171;   Indels 235;   Gaps 5;
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Qy     8  CACCATGGGTTGGAACTGTATCATCTTTCTTCTTGGTTACCACAGTACAGGTGTGCACTC     67
          ||||||||||| ||||||| ||||||||  ||| ||||| |||||||||||||||||||
Db    23  CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTC     82

Qy    68  CCAGCTCCAGCTGTGCAGTCTCGGGCTGAGGTCAAGAAGCCTCGGGGCTTCAGTGAAGGT    127
          |||||||||||||||||||| |||||||||||
Db    83  TCAGTCCAACTGGTGCAGTCTCGGGCTGAGGTCAAGAAGCCTCGGGGCTTCAGTGAAGGT    142

Qy   128  GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGTGAGACAGGC     187
          |||||||||  |||||  ||||| ||  |||||||||      |    | |||
Db   143  GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACAGTGGTGACGACAGGC         202

Qy   188  TCCTGGACAGGGCCTGAGTGGATTGGAGTTATTAATATTACTAGTGAGTAATAATACAAACTA    247
          |||| |||  ||||||||||||||  ||||   ||  ||   |   || ||||
Db   203  CCCTGACAGGGCCTGAGTGGATGGGAGATGATTGATCCTGATAGTAGCTATTAACTA      262

Qy   248  CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCACGAGCACAGCCTA     307
          ||||  |||||  || |  |||||  ||  ||| ||| || ||  | || |||  |||
Db   263  CAATCAAAAGTTCAAGGGCCGGTCACAATCACTGCAGACACATCCACTAGCACAGCCTA    322

Qy   308  TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTCAAGAGCGGC    367
          |||| ||    ||  || |||||||||||| || || || |||| ||||||||
Db   323  CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGGCCGGTCTATTACTGTGCAAGAAATAG    382

Qy   368  CTGTATATGGACTACTGGGGTCAAGGTACCCTGTCACCGTCTCCTCAGGTGAGTCCTT     427
          ||    ||||| ||| ||||| |||||
Db   383  GGACTATAGTAACAACTGG------------------------------------------    401

Qy   428  AAAACCTCTAGAGCTTTCTGGGGGCAGCCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTG    487
          | ||  || |    ||| ||
Db   402  ------TACTTCGATGTCTGGGGCGAAGGGACCCTGGT-----------------------    433

Qy   488  GGCTAAGGTGAGGCAGGTGCGCCAGCCAGGTGCACACCCAATGCCGTGAGCCCAGACA     547
          |||||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Db   434  ------------------------------------------------------------    433

Qy   548  CTTGACCCTGCCTGGACCCTGTCGGTGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC    607
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Db   434  ------------------------------------------------------------    433

Qy   608  CCAGCTCGTGCCACCACGCGGTCACATGGCACACCTCTTCCAGCCTTCCACCAAGGG     667
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Db   434  --------------CACCGTCTCCTCAGCCTTCCACCAAGGG                 460

Qy   668  CCCATCGGTCTTCCCCCTGGCCCCTGCCAGGAGCACCTCCGAGAGCACAGCGCGCCCCT    727
          |||||||||||||||||| |||||||||  || |||||||| ||||||||||| ||||
Db   461  CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCGGGGGGCACAGCGGCCCT    520

Qy   728  GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC    787
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521  GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC    580

Qy   788  TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT    847
          |||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   581  CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT    640

Qy   848  CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT    907
          ||||||||||||||||||||||||||||||| |||||||||||| || |||||||||||||
Db   641  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT    700

Qy   908  AGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCTCAGG    967
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   701  GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGG    760

Qy   968  AGGGAGGGTGTCTGCAGGAGTCCTGGAAGCCAGGCTCAGCCCCTGCCTGGACGCACCCCGGCTGTG    1027
          |||||||||||||| ||||||||||||||||||| ||||| ||| |||||||||| ||
Db   761  AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCCCTGCCTGGACGCATCCCGGCTATG    820

Qy  1028  CAGCCCCCAGGCCAGCAAGGCAGGCCCATCTGCTCCTCACCGTGCCCTCCTCTGTCTGTG    1087
          |||| ||||||||||| |||||||||||  ||||| | |||||||||||||||||||||||
Db   821  CAGTCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGC    880

Qy  1088  CCGCCCCACTCATGCTCAGGGACAGGTGTTCTCCGGCTTTTTCCACCAGGCTCCAGGCAGG    1147
          |||||||||| |||| |||||| ||| |||| |||| ||||||  |||||||||||||||||
Db   881  CCGCCCCACTCATCTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC--CCAGGCTCTGGGCAGG    939

Qy  1148  CACAGGCTGGGTGCCCTACCCCAGGGCCCTTCACACAGGGGCAGGTGCTTGGCTCAGA    1207
          ||||||||||||||||  | ||| |||||  |||||| |||||||||||||||||||||
Db   940  CACAGGCTAGGTGCCCCTAACCCAGGCCCTGCACCAAAGGGGGCAGGTGCTGGGCTCAGA    999
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Sat Jul 19 10:01:52 2003

us-09-627-896b-23.rnpb

Search completed: July 18, 2003, 15:38:36
Job time : 554.679 secs

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Qy   1208  CCTGCCAAAGCCATATCCGGAGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCA   1267
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Db   1000  CCTGCCCAAGAGCCATATCCGGAGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCA  1059

Qy   1268  AACTGTCCACTCCCTCAGCTCGGACACCTTCTCCTCCCCAGATCCGAGTAACTCCCAAT  1327
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Db   1060  AACTCTCCACTCCCTCAGCTCGGACACCTTCTCCTCCCCAGATTCCAGTAACTCCCAAT  1119

Qy   1328  CTTCTCTCGCAGAGCCGCAAATGTTGTGTCGA--------GTGCCCACCGTGCCCAGGT  1378
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Db   1120  CTTCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGT  1179

Qy   1379  AAGCCAGCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC  1438
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Db   1180  AAGCCAGCCAGGCCCCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC  1239

Qy   1439  ATCCAGGGACAGGCCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC  1498
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Db   1240  ATCCAGGGGACAGGCCCCCAGCTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC  1299

Qy   1499  ---ACCTGCGGCGACACGTCAGTCTTCCTCTTCCTCCCCAAAACCCAAGGACACCCTCAT  1555
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Db   1300  TGAACTTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCTCCCCAAAACCCAAGGACACCCTCAT  1359

Qy   1556  GATCTCCCGGACACCCTGAGGTCACGTGCGTGGTGGACGTGAGCCACGAAGACCCCGA  1615
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Qy   1616  GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG  1675
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Db   1420  GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG  1479

Qy   1676  GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGA  1735
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Db   1480  GGAGGAGCAGTTCAACAGCACGTACCAGCACGTCCTCACCGTCCTGCACCAGGA  1539

Qy   1736  CTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGGCCTCCAACATCGTCCCAT  1795
           ||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||
Db   1540  CTGGCTGAATGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT  1599

Qy   1796  CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGTATGAGGGCCACATGACA  1855
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Qy   1916  CAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA  1975
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Db   1720  CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA  1779

Qy   1976  AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG  2035
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Qy   2036  AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACT  2095
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Qy   2096  CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG  2155
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Db   1900  CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG  1959

Qy   2156  GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA  2215
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Db   1960  GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA  2019

Qy   2216  GCCTCTCCCCGTCCCCGGGTAAATGAGTG  2244
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Db   2020  GCCTCTCCCCGTCCCCGGGTAAATGAGTG  2048
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us-09-627-896b-23.rni

Sat Jul 19 10:01:51 2003

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              GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    July 18, 2003, 09:26:19 ; Search time 119.256 seconds
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Title:          US-09-627-896B-23
Perfect score:  2249
Sequence:       1 tctagaccaccatgggtgg.........ccgggtaaatgagtgaattc 2249

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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1	1804	80.2	2560	2	US-07-916-098A-44	Sequence 44, Appl
2	1742.6	77.5	2287	5	PCT-US96-10043-8	Sequence 8, Appli
3	1651.6	73.4	2287	1	US-08-480-036-1	Sequence 1, Appli
4	1651.6	73.4	2287	2	US-08-461-968A-1	Sequence 1, Appli
5	1651.6	73.4	4723	4	US-08-462-571-1	Sequence 370, App
6	1611.8	71.7	4723	4	US-09-042-353-370	Sequence 218, App
7	1611.8	71.6	2029	2	US-08-758-417A-218	Sequence 43, Appli
8	1610.8	71.6	2482	3	US-07-916-098A-43	Sequence 3, Appli
9	1584.6	70.5	2482	3	US-08-477-460B-3	Sequence 3, Appli
10	1584.6	70.5	2482	3	US-08-379-516-3	Sequence 3, Appli
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15	1584.6	70.5	2770	4	PCT-US93-07422-3	Sequence 5, Appli
16	1548	68.8	2009	1	US-09-227-595-29	Sequence 4, Appli
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ALIGNMENTS

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RESULT 1
US-07-916-098A-44
; Sequence 44, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
-  APPLICANT:  BURKLY, LINDA C.
-  APPLICANT:  CHISHOLM, PATRICIA L.
-  APPLICANT:  THOMAS, DAVID W.
-  APPLICANT:  ROSA, MARGARET D.
-  APPLICANT:  ROSA, JOSEPH J.
   TITLE OF INVENTION:  ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
   TITLE OF INVENTION:  PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
   NUMBER OF SEQUENCES:  61
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
     STREET: 10 SOUTH WACKER DRIVE
     CITY: CHICAGO
     STATE: ILLINOIS
     COUNTRY: U.S.A.
     ZIP:  60606
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER TYPE:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  WORD PERFECT 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/07/916,098A
     FILING DATE:  July 24, 1992
     CLASSIFICATION:  424
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/US91/08843
     FILING DATE:  No. 587l732ember 27, 1991
     CLASSIFICATION:  424
     APPLICATION NUMBER:  07/618,542
     FILING DATE:  No. 587l732ember 27, 1990
     CLASSIFICATION:  424
   ATTORNEY/AGENT INFORMATION:
     NAME:  JOHN J. MC DONNELL
     REGISTRATION NUMBER:  26,949
     REFERENCE/DOCKET NUMBER:  92,310-G
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (312) 715-1000
     TELEFAX:   (312) 715-1234
     TELEX:   910/221-5317
   INFORMATION FOR SEQ ID NO:  44:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  2560 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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   NAME/KEY: sig_peptide
   LOCATION: 12..68
FEATURE:
   NAME/KEY: mat_peptide
   LOCATION: join(69..435, 712..1005, 1396..1431, 1550..1879,
             1977..2296)
FEATURE:
   NAME/KEY: intron
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FEATURE:
   NAME/KEY: intron
   LOCATION: 1006..1395
FEATURE:
   NAME/KEY: intron
   LOCATION: 1432..1549
FEATURE:
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   LOCATION: 1880..1976
FEATURE:
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   LOCATION: 1
   OTHER INFORMATION: /note= "pMDR1002 insert: pre-5A8
   OTHER INFORMATION: humanized heavy chain"
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   LOCATION: 12..435
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   LOCATION: 712..1005
FEATURE:
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   LOCATION: 1396..1431
FEATURE:
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   LOCATION: 1550..1879
FEATURE:
   NAME/KEY: exon
   LOCATION: 1977..2296
FEATURE:
   NAME/KEY: CDS
   LOCATION: join(12..435, 712..1005, 1396..1431, 1550..1879,
             1977..2296)
US-07-916-098A-44

Query Match    80.2%;   Score 1804;    DB 2;   Length 2560;
Best Local Similarity   89.2%;   Pred. No. 0;
Matches 2049;   Conservative   0;   Mismatches 185;   Indels   64;   Gaps   7;
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STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2287 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-10043-8

Query Match   77.5%;   Score 1742.6;   DB 5;   Length 2287;
Best Local Similarity   89.1%;   Pred. No. 0;
Matches 2038;   Conservative   0;   Mismatches 184;   Indels 65;   Gaps 12;

Qy   6 ACCACCATGGTTGGAACTGTA---TCATCTTCTTCTGGTTACCACAGCTACCAGGTGTG   62
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Db   7 ACCACCATGGACCTGGAGGTTCCTCTCTTCTTGTGTGGTGCAGCAGCTACAGGTGTC   66

Qy   63 CACTCCCAGGTCCAGTCGTGCAGTCGTGGGGCGTGAGGTGAAGAAGCCTGGGAGCTCAGTG   122
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Db   67 CAGTCCCAGGTGCAGTCGTGCAGTCGTGGGGCGTGAGGTGAAGAAGCCTGGGAGTCCTCCGTG   126

Qy   123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA   182
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Db   127 AAGGTCCTGCAAGGCTTCTGGAGGCACCATGCTCAGCAGCTATGCTATCAGCAGTGGGTGCGA   186

Qy   183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTACTGATAATAACA   242
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Qy   243 AACTACAACCAGAAGTTTAAGGGCCACAATGACTGTAGACAAGTCGACGAGCACA   302
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Db   247 AACTACGACACAGAAGTTCCAGGCGAGTCACGATTACCGCGGACAATCCACGAGCACA   306

Qy   303 GCCTATATGGAACTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCCAAGA   362
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Qy   363 GCGG--CCTGGTATATGGACTACTGGGGT   389
           || ||| ||||||||||||||||||||||
Db   367 GATAATGAGCGTATTGTAGTGTGTGGTTAGCTGCTGCTACTCGGGCGTGGTTCGACCCCTGGGGC   426

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Db   1445 GGCCTCGCGCCTCCAGCTCAAGGGCGGACAGGTGCCTGCCTGCCTGAGTAGCCTGCATCCAGGGACA   1504
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Qy   2047 AATGGGCAGCCGGAGAACAACTACAAGACCACCCCTCCCATGCTGGACTCCGACGGCTCC   2106

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RESULT 2
PCT-US96-10043-8
; Sequence 8, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

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Db    482  GCAGGCCAGCCTGACCTGGCTTGGGGCGGAGGGGGCTAAGGTGGAGGCAGGTGGCG  541

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Qy    570  TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCAGCTCGTCTCCCACACCGCGG  629
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Db    596  CGGACAGTTAAGAACCCCAGGGGGCCTCTGCG--CCTGGGCCCAGCTCGTCTCCCACACCGCGG  654

Qy    630  TCACATGGCACCACCTCTTCTTGCAGACTCCTCACCCAGGGCCCATGGTCTTCCCCTGCG  689
           ||||||||||||||||||||||||||  ||| |||||||||||||||||||||||||||
Db    655  TCACATGGCACCACCTCTTCTTGCAGCCTCCACCCAGGGCCCATGGTCTTCCCCTGCA  714

Qy    690  CCCTGCTTCCAGGAGCACCTCCAGAGCACAGCCCCTGGGCTGCCTGGTCAAGGACTAC  749
           ||||  | |||||||||||  |||||||||||||||||||||||||||||||||||||
Db    715  CCCTCCTCCCAGAGCACACCCTGGGGGCACAGCCCCTGGGCTGCCTGGTCAAGGACTAC  774

Qy    750  TTCCCGAACCGGTGACGGTGTCGTGAACTCAGGCGCTCTGACCAGCGGCGGTGCACACC  809
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    775  TTCCCGAACCGGTGACGGTGTCGTGAACTCAGGCGCTCTGACCAGCGGCGGTGCACACC  834

Qy    810  TTCCCAGCTGTCTGCTACAGTCTTCTACTCCCTCAGCACGTGTGACCGTGCCC  869
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    835  TTCCCGGCTGTCTGCTACAGTCTTCTACTCCCTCAGCACGTGTGACCGTGCCC  894

Qy    870  TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGGCCAGCAACACC  929
           |||||| ||| |||||||||||||||||||||||||||| ||||||||  ||||||||||
Db    895  TCCAGCAGCTTGGGCACCCAGACCTACACCTGCAACGTGAATCACAAGCCCAGCAACACC  954

Qy    930  AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGTGTCTGCTGGAAGC  989
           ||||||||||||| ||||||||||||||||||  ||||||||||||||||||||||||
Db    955  AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCCACAGGGAGGGAGGTGTCTGCTGGAAG-  1013

Qy    990  CAGGCTCAGCGCTTCCTGCTGGACGCACCCCGGTGTCGAGCCCCAGGGCAGCAA  1049
           |||||||||||||||||||||||||||  ||||| | ||||||||||||||||||
Db   1014  CAGGCTCAGCGCTTCCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCAGGGCAGCAA  1073

Qy   1050  GGCAGGCCCCATCTGTCTCCTCCCGAGGGCTCTGCCCGCCCACTCATGCTCAGGGA  1109
           ||||||||||  |||| ||||||||| |||||||||     |||||  || |||||
Db   1074  GGCAGGCCCCCGTCTCACCCGGA-GCTCTGCCCTTCACCCGGA-GCTCTGCAGGGA  1132

Qy   1110  GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTCGGTGCCCCTACCC  1169
           ||||| |||||| || ||| | ||||||||  |||||||  |  |||| ||||||||||||
Db   1133  GAGGGCTTCTGCGGGCTTTTC--CCAGGCTCGGGCAGGCTCGGGCAGCCACAGGCTCCCTAACC  1190

Qy   1170  CAGGCCCTTCACACAGGGCGGCAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG  1229
           |||||||| |||||||  ||  ||||||||||||||||||||    |  ||||| ||||||||||||
Db   1191  CAGGCCCTGCACACACAAAGGGGCAGGTGCTTGGCTCGGGCTCCAGAGCCCATATCCGGG  1250

Qy   1230  AGGACCCTGCCCCTAAGGCCCGACCCAAACTGTCCACTCCTTCCACTCGTCCTTCAGCTCG  1289
           |||| |||||||||||||||| ||||||||| ||||||| | ||| |||  | |||||||
Db   1251  AGGAGACCCTGCCCCTAAGGCCCCACCCCAAACTCTCCACTCCCTCCAGCTCG  1310

Qy   1290  GACACCTTCTCTCTCCTCCCAGATCGAGTAACTCCCAATCTCTTCTCTCTGAGAGCGCAAAT  1349
           |||||||||||||| |||||||||  |||||||||||||||||||||| | ||||||||||||
Db   1311  GACACCTTCTCTCTCTCCCAGATTCCAGTAACTCCCAATCTCTTCTCTGCAGAGCGCCAAAT  1370

Qy   1350  GTTGTGTCGA-------GTGCCCACCGTGCCCAGTGAGCCAGCCCAGGCCTCGCCCT  1400
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Db   1371  CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGTAGCCAGCCTGCCCAGGCCTCGCCCT  1430

Qy   1401  CCAGCTCAAGGCGCGGACAGGTGCCCAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG  1460
           ||||||||||||  || ||||||||||| |||||||||||||||||||||||||||| |||||||||| |
Db   1431  CCAGCTCAAGGCCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACACAGGCCCCAGCCG  1490

Qy   1461  GGTGCTGACACGTCCCCCTCCACCTCCATCTCTTCCTCCAGCACC--ACCTGCGGCGACCCGTCA  1517
           ||||||||||||| ||| ||||| |||||| | ||||||||||||   ||||   ||| |||| ||
Db   1491  GGTGCTGACACGTCACCCTCCATCTCCATCCTCCAGCACCTCCTGGGGGGGACCCTGAGTC  1550

Qy   1518  GTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCCTCATGATCTCCCGGACCCCTGAGTC  1577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1551  GTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCCTCATGATCTCCCGGACCCCTGAGGTC  1610
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Qy   1578  ACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTG  1637
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Db   1611  ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG  1670

Qy   1638  GACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCACGGGAGGAGCAGTTCAACAGCACG  1697
           ||||||||||||||||||||||||||||||||| || ||||||||||||||| ||||||||
Db   1671  GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG  1730

Qy   1698  TTCCGTGTGGTCAGCGTGCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTAC  1757
           | || ||||||||||||| |||||||  ||||||||||||||||||| |||||||||||||
Db   1731  TACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC  1790

Qy   1758  AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACC  1817
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Db   1791  AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC  1850

Qy   1818  AAAGGTGGGACCCGCGGGGTATGAGGCCACATGACAGAGAGGCCGGCTCGGCCCCACCCTC  1877
           |||||||||||||| ||||| | ||| ||||||||||||||||||  |  || |||||||||
Db   1851  AAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGACAGAGAGGCCACACCCTC  1910

Qy   1878  TGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCTACAGGGCAGCCCCGAGAACCACA  1937
           ||||||| ||||||||||||| |||||||||||| |||||||||||||||||||||||||
Db   1911  TGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAACCACA  1969

Qy   1938  GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG  1997
           |||||||||||||||||||||||||||| |||| |||||||||||||||||||||||||||
Db   1970  GGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG  2029

Qy   1998  CCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  2057
           ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   2030  CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  2089

Qy   2058  GGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTA  2117
           ||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||
Db   2090  GGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTA  2149

Qy   2118  CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT  2177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2150  CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT  2209

Qy   2178  GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAA  2237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2210  GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAA  2269

Qy   2238  ATGAGTG  2244
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Db   2270  ATGAGTG  2276
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RESULT 3
US-08-480-036-1
; Sequence 1, Application US/08480036
; Patent No. 5723583
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian et al.
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.00)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:

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;    APPLICATION NUMBER: US/08/480,036
;    FILING DATE:
;    CLASSIFICATION:      424
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US/07/618,314C
;    FILING DATE: No. 5723583ember 23, 1990
;    ATTORNEY/AGENT INFORMATION:
;    NAME: Clark, Paul T.
;    REGISTRATION NUMBER: 30,162
;    REFERENCE/DOCKET NUMBER: 00786/067001
;    TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (617) 542-5070
;    TELEFAX:   (617) 542-8906
;    TELEX:     200154
; INFORMATION FOR SEQ ID NO: 1:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH:    2287
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
US-08-480-036-1

Query Match             73.4%;  Score 1651.6;  DB 1;  Length 2287;
Best Local Similarity   87.2%;  Pred. No. 0;
Matches 1998;  Conservative    0;  Mismatches 219;  Indels 75;  Gaps 14;
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Qy     6  ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTTGGTTACCAGCTACAGGTGTG   62
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Db     7  ACCACCATGGACTGGAACTTCCTTCTTCTTCTTGTTGGTGGCAGCAGCTACAGGTGTC   66

Qy    63  CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG  122
          |||  ||||||   |||||| |||||||||||||      ||||||||||||||
Db    67  CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCCGTG  126

Qy   123  AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATATGCTACAGTGGGTGAGA  182
          |||||||||||| || ||||||||| ||     ||||  ||||||||||||
Db   127  AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA  186

Qy   183  CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGATATTAATTACTATGATAATACA      242
          |||||   |||||||||||||||||| |||     ||     |||||||||||
Db   187  CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCTTTTCCAGCTATCAGCA  246

Qy   243  AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA  302
          |||||       ||||||     | |||||| |||| |||||||||||||||
Db   247  AACTACGCACAGAAGTTCCAGGGCAGAGTCACCATTACCGCGGACAAATCCACGAGCACA  306

Qy   303  GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA  362
          |||||  |||||||||  || ||||||| ||||||||||||
Db   307  GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA  366

Qy   363  GCGG-----------------------CCTGGTATATGGACTACTGGGGT          389
          ||||                       |||||  ||||||||||||||
Db   367  GGGGGGTTTTGGTTCTCTGGGGCTGGTGGGTTCCCCGTGGTTCGGGGGAC          426

Qy   390  CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTT  449
          |||||     || |||||||||||||||||   |||     ||||||||
Db   427  CAGGGAACCCTGGTCACCGTCTCCTCAGAGCCCCAGACACTCCCCCATCCTCG  481

Qy   450  GCGAGCCCGGGCCTGGACTTTGGCTTTGGGCAGGAGGTGGGGCTAAGGTGAGGCAGGTGGCG  509
          |||| ||   |||||||||||||     ||||||||||
Db   482  GCAGGGCCAGGCCCAGGGGCCTCCTTTTTGGGGCTAAGGTGAGGCAGGTGGCG  541

Qy   510  CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGCCGCTGAGGACCCTCG  569
          |||| ||| |||| || ||   ||||| || |||||
Db   542  CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCGCT-----GAACCCTCG  595

Qy   570  TGGATAGACAAGAACCGGAGGGGGCCTCTGCGCCCCAGCTCTGTCCCACACCGCGG  629
          ||||   |||||||| ||||| |||||||||||||||
Db   596  CGGACAGTGAAGAACCCAGGAGGCCTCTTGCG-CCTGGCCCAGCTCTGTCCCACACCGCGG  654

Qy   630  TCAATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG  689
          ||||||||||||||||||||||||||||||||||||||||||||
Db   655  TCAATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA  714
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Qy   690  CCCTGCTTCCAGGAGCACTTCCGAGAGCACAGCGCCCTCGGGCTGCCTCCTGGTCAAGGACTAC  749
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Db   715  CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTCGGGCTGCCTGGTCGCCTGGTCAAGGACTAC  774

Qy   750  TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC  809
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Db   775  TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC  834

Qy   810  TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  869
          ||||||  ||| ||||||  |||||||||||||||||||||||||||||||||||||
Db   835  TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  894

Qy   870  TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC  929
          ||||||||||||  |||||||||||||||||||||||  || ||||||||||||||||
Db   895  TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC  954

Qy   930  AAGGTGGACAAGAGCAGTTGGTGAGAGGCCAGCTCAGGGCGTGTCTGCTGGAAGC  989
          ||||||||||||||||||  |||||||||||||||||||| |||||||||||||
Db   955  AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAG-  1013

Qy   990  CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCGTGCAGGGCAGCAA  1049
          ||||||||||||||||||| ||||| |||  ||| |||||||| ||||||
Db  1014  CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCCAGGGCAGCAA  1073

Qy  1050  GGCAGGCCCCATCGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCAGTCTCAGGGA  1109
          ||||||||| |||||| |||  |||||||||  ||||||||||||||||  |||||||
Db  1074  GGCAGGCCCGTCTGCCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA  1132

Qy  1110  GAGGGTCTTCTGGCTTTTTCCACCAGGGTCTGGGAGTGACCTGAGAAGCCTGGAGCTCAGTG  1169
          ||||| |||||||  |||  || |||||| |||||| ||| |||||||||||||||||
Db  1133  GAGGGTCTTCTGGCTTTTTC--CCAGGGTCTGGGCAGGCACAGCTGGGCTCGGGTGCCCCTAACC  1190

Qy  1170  CAGGCCCTTCACACAGGGCAGGTGCTGCTGGGCTCAGACCTGCCAAAAGCCATATCCGGG  1229
          ||||||||| |||||| ||||||||||||||||||||||||  |||||||
Db  1191  CAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG  1250

Qy  1230  AGGACCCTGCCCCTGACCTAAGCCACCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG  1289
          |||||||||||||||||||||||||||||  ||||||||||  ||||||||||||||
Db  1251  AGGACCCTGCCCCTGACCTAAGCCCAAACCCCAAAGCCAAACTCTCCACTCCCTCAGCTCG  1310

Qy  1290  GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCAATCTCTTCTCTGCGAGAGCCAAAT  1349
          |||||||||||||||||||||||  ||||| ||||||||||||| |||||||||||||
Db  1311  GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCAATCTCTTCTCTGCGAGAGCCAAAT  1370

Qy  1350  GTTGTCGA-------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT  1400
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Db  1371  CTTGTGACAAAACTCACACACGCCCTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT  1430

Qy  1401  CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGCAGGCAGAGGCACG  1460
          |||||||||||| |||||||||||||||||||||||||||  |||||||||  |||||||
Db  1431  CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGCAGGCCCCAGCGCG  1490

Qy  1461  GGTGCTGACACGTCCACCTCCATCTCTTCCTCCTCTAGAGCTTTCTGG  1517
          |||||||||||||||||||||||||| ||   |||||| ||
Db  1491  GGTGCTGACACGTCCACCTCCATCTCTTCCTCCTCAGCACCTGAACTCCTGGGGGGACCCCTGAGGTC  1550

Qy  1518  GTCTTCCTCTTCCCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC  1577
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Db  1551  GTCTTCCTCT-----AGGGGGGTTTGGTTCTCGTGGGAGTACTAGAGGGTCTGGGGAC  1605

Qy  1578  ACGTGCGT-----GGTGGTGGACGTGAGCCAGGAGCAGCCCGAGGTCCAGTTCAACTGT  1632
          ||| |      |||||||||||||||||||||||||||| |||||  ||||||||||||
Db  1606  TCCAGTGTACGCACCTTGGTGACACGTGAGCCACGAAGCAGCCCGAGTTCAAGTTCAACTGT  1665

Qy  1633  ACGTGGACGGCGGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACA  1692
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Db  1666  ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA  1725

Qy  1693  GCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG  1752
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;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 2287
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
; US-08-461-968A-1

Query Match             73.4%;  Score 1651.6;  DB 1;  Length 2287;
Best Local Similarity   87.2%;  Pred. No. 0;
Matches 1998;  Conservative 0;  Mismatches 219;  Indels 75;  Gaps 14;

Qy      6 ACACCATGGGTTGGAACTGTA---TCATCTTCTTCTGGTTACCACAGTCACAGGTGTG   62
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Db      7 ACCACCATGGACCTGGACGTTCCTTCCTCTTGTGGTGGCAGCAGTCACAGGTGTC      66

Qy     63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG  122
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Db     67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGTCCTCGGTG  126

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Qy    183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGAGTTATTAATATTTACTATGATAATACA  242
            ||||| |||||||| |||||||||||||||||||||||||  | |  || || | ||
Db    187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGGATCATCCCTATCTTTGGTACAGCA  246

Qy    243 AACTACAACCAGAAGTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA  302
            |||| |||| |||||||  |  |  || || |  |||||||||| | |||| ||| |||
Db    247 AACTACCGCCACAGAAGTTCCAGGGCCAGGTCACCATTACCGCGGACACGAGCACACACA  306

Qy    303 GCCTATATGAACTTAGTTCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA  362
            |||||| ||| ||   || ||||||||||||||||||||| ||| ||| || ||||||
Db    307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA  366

Qy    363 GCGG-----------------------------CCTGGTATATGGACTACTGGGGT  389
            | ||                             ||  |  | |||| || |||||
Db    367 GATAATGGAGCGTATTGTAGTAGTACCTCGGGTCACTCGGCTGGTTCGACCCCCTGGGGC  426

Qy    390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCTCAGGAGCTTTCTGG  449
            |||||||||||||||  ||||||||| |||||| || || || || ||||
Db    427 CAGGGAACCCTGGTCACCGTCTCACCGTCTCAGGGAGTGCATCCGCCAAGAACTCAGCTTCCTGG  481

Qy    450 GCGAGCCGGGCCTGACTTGGCTTGGCTTTGGGCAGGAGTGGGGCAGGTGGCGG  509
            |||||||||||||||||||||||||||  ||||||||||||||| |||||
Db    482 GCAGGCCCAGGCCTGACCTGGCTTGGCTTTGGGGCAGGCAGGCAGGTGGCG  541

Qy    510 CAGCCAGGTGCACACCAATGCCCGTGAGCCCGACCTGCCTGGACCCTCG  569
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Db    542 CCAG-CAGTGCACACCAATGCCCATGAGCCCATGAGCCCAGCCCGACGCT-----GAACCTCG  595

Qy    570 TGGATAGACAAGAACCGAGGGGCCCTCGCCCCAGCTCGTCCCCACACCGCGG  629
            || |  ||||  |||| || ||||||||||||| || || || || ||||||
Db    596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG--CCTGGGCCCAGCTCGTCTGTCCCACACCGCGG  654

Qy    630 TCACATGGCACCACCTCTTGCAGCCTCCACAAGGGCCCATCGGTCTCCCCCTGGGC  689
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Db    655 TCACATGGCACCACCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTCCCCCTGGCA  714

Qy    690 CCCTGCTTCCAGGAGCACACCCGAGAGCACAGCAGCGCCCTGGGCTGCCTGGTCAAGGACTAC  749
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Db    715 CCCTCCTTCCCCAAGGACACCCTCGGGGGCACACCCGAGAGCCCAGCCCGGCGCTGCCTGGTCAAGGACTAC  774

Qy    750 TTCCCGGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC  809
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Db    775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC  834

Qy    810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  869
            |||||  | || | |  || |||| ||||||  |||||||| || ||||||||||||||||
Db    835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC  894

Qy    870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC  929
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Qy   1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCTCCCAGCCCCATCGAGAAAACCATCTCCA  1812
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 AGTACAAGTGCAAGGTCTCCAACAAAGGCTCCCAGCCCCATCGAGAAAACCATCTCCA  1845

Qy   1813 AAACCAAAGGTGGGACCCGCGGGGGTATGAGGGGCACATGGACAGAGGCCGCTCGGCCCA  1872
            |||||||||||||||||||||||||     ||||||   ||||||||||||||||||||||
Db   1846 AAGCCAAAGGTGGGACCCGCGGGGTGCGAGGGGCACCACATGGACAGAGGCCGCTCGGCCCA  1905

Qy   1873 CCCTCTGCCCTGGGAGTGACCGCGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA  1932
            ||||||||||||||||||||||||||      | |||||||||||||||||||||||||
Db   1906 CCCTCGCCCTGAGAGTGACCGCCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAA  1964

Qy   1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG  1992
            |||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db   1965 CCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTG  2024

Qy   1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG  2052
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG  2084

Qy   2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC  2112
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC  2144

Qy   2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC  2172
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC  2204

Qy   2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCGTCCCCG  2232
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG  2264

Qy   2233 GGTAAATGAGTG  2244
            ||||||||||||
Db   2265 GGTAAATGAGTG  2276
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RESULT 4
US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
; GENERAL INFORMATION:
;   APPLICANT: Seed et al., Brian
;   TITLE OF INVENTION: INHIBITION OF CELL ADHESION
;   TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 0210-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/461,968A
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/618,314
;   FILING DATE: 23-NOV-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lech, Karen F.
;   REGISTRATION NUMBER: 35,238
;   REFERENCE/DOCKET NUMBER: 00786/067003
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   TELEX: 200154

Db   1965 CCACAGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAGACCAGTCAGCCTG 2024
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG 2052
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 ACCTGCCTGGTCAAAGGCTTCATCCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084

Qy   2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 CAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC 2144

Qy   2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2204

Qy   2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTCCCCG 2232
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTCTCCG 2264

Qy   2233 GGTAAATGAGTG 2244
           ||||||||||||
Db   2265 GGTAAATGAGTG 2276

Qy Query Match   73.4%; Best Local Similarity   87.2%; Score 1651.6; DB 2; Length 2287;
    Matches 1998; Conservative   0; Mismatches 219; Indels 75; Gaps 14;

Qy   6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCAGCTACAGGTGTG 62
           |||||||||||||||||||||| || ||||||||||||||||||||||||||||||

Db   895 TCCAGCAGTTGGGCCACCCAGCCAGATCTGCAAGCTGAATCACAACGCCCAGCAACACC 954
           |||||||||| ||||| |||||||||||||||||||||||||||||||||||||||||
Qy   930 AAGGTGGACAAGAGCAGTTGGTGAGAGGCCAGCTCAGGGAGGAGGGGTGTCTGCTGGAAGC 989
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   955 AAGGTGGACAAGAGAAGTTGGTGAGAGGCCAGCAGCAGGGAGGAGGGGTGTCTGCTGGAAG- 1013

Qy   990 CAGGCTCAGCCCTTCCTCGCTGGACGCGCAGCCCGGCGTGTGCCAGGGCAGCAA 1049
           |||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db   1014 CAGGCTCAGCGCTGCTGCCTGGACGCATCCCGGCATCCGGCTATGCAGCCCAGTCCAGGGCAGCAA 1073

Qy   1050 GGCAGGCCCCATCTGTCTCCTCACCGGAGGCCTTCGCCGCCCCACTCATGCTCAGGGA 1109
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1074 GGCAGGCCCCGTCTGCCGTCCTCTTCACCCGGA-GCCTCTGCGCCCCACTCATGCTCAGGGA 1132

Qy   1110 GAGGGTGTCTTGGCTTTTTCCACCAGGCTCAGGCAGGCACAGGTGGGTGCCCCTACCC 1169
           ||||||||||||||| |||| |||||||||||||||||||| |||||||||||||
Db   1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGCAGGCACAGGCTAGGTGCCCCTAACC 1190

Qy   1170 CAGGCCCTTCACACACAGGGGCAGGTGCTGCTGCTCAGACCTTGCCAAAAGCCATATCCCGG 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1191 CAGGCCCTGCACACACAAAGGGGCAGGTGCTGCTGCTCAGACCTTGCCAAAAGCCATATCCCGG 1250

Qy   1230 AGGACCCTGCCCTGACCTAAGCGACCCCAAACTGTCCACTCCCTCAGCTCG 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1251 AGGACCCTGCCCTGACCTAAGCCACCCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy   1290 GACACCTTCTCTCTCCCCAGATCCGAGTAACTCCAATCTTCTCTGCAGAGCGCAAAT 1349
           ||||||||||||||||||| |||||||||||||||||||||| ||||
Db   1311 GACACCTTCTCTCTCCCCAGATTCCAGTAACTCCAATCTTCTCTGCAGAGCCCAAAT 1370

Qy   1350 GTTGTGTCGA--------GTGCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
           ||||| || | ||||||||||||||||||||||||||||||||||||||
Db   1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy   1401 CCAGCTCAAGGCGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1431 CCAGCTCAAGGCGGGACAGCAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy   1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGGCAGCACCGTCA 1517
           ||||||||||||||||||||||||||||||||||||| ||||| |||||||||||||
Db   1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGGTCA 1550

Qy   1518 GTCTTCCTCTTCCCCCAAAACCCAAGGACACACCCTCATGATCTCCCGGACCCCTGAGTC 1577
           ||||||| ||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1551 GTCTTCCTCT-----AGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGGAC 1605

Qy   1578 ACGTGCGT--------GGTGTGGACGTGAGCCACGAGGTCCAGTTCAACTGGT 1632
           ||||| || |||| |||||||||||||||||||||||||||||||
Db   1606 TCCAGTGTACGGACCTGGTGGACGTGAGCCACGAGGTCAAGTTCAACTGGT 1665

Qy   1633 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACA 1692
           ||||||||| ||||||||||||||||||||||| |||||||||||||||||||||||||
Db   1666 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 1725

Qy   1693 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGG 1752
           ||||| |||| |||||| |||||||| ||||||||||||||||||||||||||||||
Db   1726 GCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 1785

Qy   1753 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCA 1812
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1845

Qy   1813 AAACCAAAGGTGGGACCCGCGGGGTATGGAGGGCCACATGACAGAGGCCGCTCGCCCCA 1872
           || ||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1846 AAGCCAAAGGTGGGACCCGTGGGGTGCCACAGTGCCCACATGACAGAGGCCGCTCGGCCCA 1905

Qy   1873 CCCTCTGCCCTGGAGTGACCGGTCAGCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGCAGCCCCAGAA 1932
           |||||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 CCCTCTGCCCTGAGAGTGACCGGTGTACCAACCTCTGT-CCTACAGGGCAGCCCCCGAGAA 1964

Qy   1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGATGAGATGACCAAGAACCAGTCAGCCTG 1992
           |||||||||||||||||||||||||||| ||| ||||||||||| |||||||||||||

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Qy     2173  TCCGTGATGCATGAGGCTTCTGCACAACCACTACACGCGAGAAGAGCCCTCCCTGTCCCCG  2232
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     2205  TCCGTGATGCATGAGGCTTCTGCACAACCACCACTACACGCGAGAAGAGCCCTCCCTGTCTCCG  2264

Qy     2233  GGTAAATGAGTG  2244
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Db     2265  GGTAAATGAGTG  2276
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RESULT 6
US-09-042-353-370

; Sequence 370, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils
;   APPLICANT: Kay, Robert M.
;   TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
;   TITLE OF INVENTION: Producing Heterologous Antibodies
;   NUMBER OF SEQUENCES: 421
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/042,353
;   FILING DATE: 13-MAR-1998
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/810,279
;   FILING DATE: 17-DEC-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/853,408
;   FILING DATE: 18-MAR-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/904,068
;   FILING DATE: 23-JUN-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/990,860
;   FILING DATE: 16-DEC-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/053,131
;   FILING DATE: 26-APR-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/096,762
;   FILING DATE: 22-JUL-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/155,301
;   FILING DATE: 18-NOV-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/161,739
;   FILING DATE: 03-DEC-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/165,699
;   FILING DATE: 10-DEC-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/209,741
;   FILING DATE: 09-MAR-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/352,322
;   FILING DATE: 07-DEC-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/544,404
;   FILING DATE: 10-OCT-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/728,463
;   FILING DATE: 10-OCT-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US96/16433
;   FILING DATE: 10-OCT-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/758,417
;   FILING DATE: 02-DEC-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US97/21803
;   FILING DATE: 01-DEC-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 014643-00940US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 370:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4723 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
; US-09-042-353-370

Query Match   71.7%; Score 1611.8; DB 4; Length 4723;
Best Local Similarity   94.3%; Pred. No. 0;
Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4;
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Qy      430  AACCTCTAGAGCTTTCTGGGGGGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGG  489
             ||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||
Db        8  AGCAGCTGAAGCTTTCTGGGGCAGGCCCAGGCCCTGACCTTGGCTTTGGGGCAGGGAGGGGG  67

Qy      490  CTAAGGTGAGGCAGGTGGCGCCAGCAGTGCACACCCAATGCCGTGAGCCCAGACACT  549
             ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       68  CTAAGGTGAGGCAGGTGGCGCCAGCAGTGCACACCCAATGCCCATGAGCCCAGACACT  127

Qy      550  GGACCCTGCCTGACCCTCGTGATGACAAGAACCGAGGGGCCTCTGGGCCCTGGGCCC  609
             |||||||      |||||   ||||||||||||||||||||  |||||||||||||||
Db      128  GGACGCT------GAACCTCGGCGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC  182

Qy      610  AGTCTCGTCCCACACCCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC  669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183  AGTCTCGTCCCACACCCGGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGC  242

Qy      670  CATCGGTCTTCCCCCTGGCGCCCTGCTTCCCGGACCGGTGCGGTGTCGTGGAACTCAGGCGCTC  729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      243  CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTGCTGGGGCACAGCGGCCCCTGG  302

Qy      730  GCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC  789
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      303  GCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC  362

Qy      790  TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGCACTTACACCTACTCCCTCA  849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      363  TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGCACTTACACCTACTCCCTCA  422

Qy      850  GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACGAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG  909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      423  GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA  482

Qy      910  ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG  969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      483  ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG  542

Qy      970  GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTTCCTGCCTGACGCGCACCCCGGCTGTGCA  1029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      543  GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCGTTCCTGCCTGACGCGCATCCCGGCTATGCA  602

Qy     1030  GCCCAGCCCAGGCAGCAAGGCAGGCCCCATCTGTCTCCACCCGAGGGCCTCTGCCC  1089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      603  GCCCCAGTCCAGGCAGCAAGGCAGCAGGCCCCGTCTGCCTTCACCCGAGGGCCTCTGCGCC  662
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Qy  2158 AACGTCTTCATGCTCCGTGATGCATGAGGCTCTCGCACAACCACTACACGCGCAGAAGAGC 2217
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1742 AACGTCTTCATGCTCCGTGATGCATGAGGCTCTCGCACAACCACTACACGCGCAGAAGAGC 1801

Qy  2218 CTCTCCCTGCTCCCGGGTAAATGAGTG 2244
         ||||||||| ||||||||||||||||
Db  1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
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RESULT 7
US-08-758-417A-218
; Sequence 218, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
;   Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;   Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 9411-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/758,417A
;   FILING DATE: 02-Dec-1996
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/728,463
;   FILING DATE: 10-OCT-1996
;   APPLICATION NUMBER: US 08/544,404
;   FILING DATE: 10-OCT-1995
;   APPLICATION NUMBER: US 08/352,322
;   FILING DATE: 07-DEC-1994
;   APPLICATION NUMBER: US 08/209,741
;   FILING DATE: 09-MAR-1994
;   APPLICATION NUMBER: US 08/165,699
;   FILING DATE: 10-DEC-1993
;   APPLICATION NUMBER: US 08/161,739
;   FILING DATE: 03-DEC-1993
;   APPLICATION NUMBER: US 08/155,301
;   FILING DATE: 18-NOV-1993
;   APPLICATION NUMBER: US 08/096,762
;   FILING DATE: 22-JUL-1993
;   APPLICATION NUMBER: US 08/053,131
;   FILING DATE: 26-APR-1993
;   APPLICATION NUMBER: US 07/990,860
;   FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Serafini, Andrew T.
;   REGISTRATION NUMBER: 41,303
;   REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4723 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-08-758-417A-218
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Qy  1090 GCCCCACTCATGCTCAGGAGGAGGGTCTTCTGGCTTTTCCACCAGGCTCCAGGCAGGCA 1149
         |||||||||||||||||||||||||||||||||||||| || |||||||| ||||||||
Db  663  GCCCCACTCATGCTCAGGAGGAGGGTCTTCTGGCTTTTTCC--CCAGGCTCTGGGCAGGCA 721

Qy  1150 CAGGCTGGGTGCCCTACCCCAGGCCCTTCACACAGGGGCAGGTGCTTGGCTTCAGACC 1209
         ||| | || | |||||||| |||||||| ||||| |||||||||||||| |||||||||
Db  722  CAGCTAGTGCGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTTCAGACC 781

Qy  1210 TGCCAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAGGCCACCCCCAAAGGCCAAA 1269
         |||||||||||| | ||||||||||||| ||||||| |||| ||||| ||||||||||
Db  782  TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCCAAACCCCCAAAGGCCAAA 841

Qy  1270 CTGTCCACTCCCTCAGCTCGGACACACCTTCTCTCTCCCAGATCCGAGTAACTCCCAATCT 1329
         || ||||||||||||||||| ||||||| ||||||||| |||| |||||||| ||||||
Db  842  CTCTCCACTCCCTCAGCTCGGACACACCTTCTCTCTCCCAGAITTCCAGTAACTCCCAATCT 901

Qy  1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA-------GTGCCACCGTGCCCAGGTAA 1380
         |||||| ||||| || |||| ||| || ||       ||||||||||||| |||||
Db  902  TCTCTCTGCAGAGCACCCAAATCTTGTGACAAAACTCACACATGCCCCACCGTGCCCAGGTAA 961

Qy  1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
         ||||||||||| |||||||| |||||| |||| ||||| |||| ||||||||||||||||
Db  962  GCCAGCCCAGGCCTGCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy  1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
         ||||||||||| |||||||||||||||| |||||| ||| ||||||||||||||||||
Db  1022 CCAGGGACAGGCCCCAGCCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCCTG 1081

Qy  1499 -ACCTGCGGCAGCACGTCAGTCTTCCTCTCTCCCCAAAACCAAGGACACCCTTCATGA 1557
          ||||| ||||| ||||| ||||||||||| ||||||| ||||||||||||||||||
Db  1082 AACTCCTGGGGCAGCACGTCAGTCTTCCTCTCTCCCCAAAACCAAGGACACCCTTCATGA 1141

Qy  1558 TCTCTCCGCACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAGACCCCGAGG 1617
         |||||| |||||||||||||| ||||| |||||||||||||||||||||| ||||||||
Db  1142 TCTCTCCGGACCCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGACCCCTGAGG 1201

Qy  1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
         |||||||||||||||| |||||| ||||||||||||||||| |||||| ||||||||||
Db  1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy  1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGTCCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
         ||||||||||||||||||| |||| |||||||| ||||||||||||| ||||||||||||
Db  1262 AGGAGCAGTTCAACAGCACGTACCGTGTGTCCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy  1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
         ||||||||||||||||||||||||||||| |||||||||||| |||||||||||||||
Db  1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy  1798 AGAAAACCATCTCAAAACCAAAGGTGGGACCCGCGGGTATGAGGGCCACATGGACAGA 1857
         |||||||||||| ||||||||||| |||||||| ||||| ||||||||||||||||||
Db  1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy  1858 GGCCGGCTCGGCCCACCCTGTGCCCAGGGTGCTGTGCCAACCTCTGTCCCTACA 1917
         ||||||||||||||||| |||||||||| |||||| |||||||| ||||||||||
Db  1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy  1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCGGGGAGGAGATGACCAAG 1977
         |||||||||||||||||||||||||||| |||||||| |||||||||||
Db  1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy  1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
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Db  1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy  2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCATGCTGGACTCC 2097
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Db  1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCC 1681

Qy  2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
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Db  1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741
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Query Match       71.7%;   Score 1611.8;   DB 4;   Length 4723;
Best Local Similarity 94.3%;   Pred. No. 0;
Matches 1722;   Conservative 0;   Mismatches 87;   Indels 18;   Gaps 4;

Qy   430 AACCTTCAGAGCTTTCTGGGGCGAGCCGGGCCGGGCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
         |||||||||||||||| ||||||| ||||| ||||| ||||| |||||||||||||||||| |||
Db     8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy   490 CTAAGGTGAGGCAGGTGGCGCAGCCAGTGCACCCAATGCCGTGAGCCCAGACACT 549
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    68 CTAAGGTGAGGCAGGTGGCGCAGCCAGTGCACCCAATGCCCATGAGCCCAGACACT 127

Qy   550 GGACCCTGCCTGACCCTCGTGATAGACAAGAACCGAGGGGGCCTGTGCGCCCTGGGCCC 609
         |||||||||||        |||||| |||| |||||||||||||||||||||||||||||
Db   128 GGAACCTGCGGACAGTTAAGAACCCAGGGGGCCTGTGCGCCCTGGGCCC 182

Qy   610 AGCTCTGTCCCACCACGCGGTCACATGGCACCACCTTCTTGCAGCCTTCCACCAAGGGCC 669
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Db   183 AGCTCTGTCCCACCACCGCGGTCACATGGCACCACCTTCTTGCAGCCTCCACCAAGGGCC 242

Qy   670 CATCGGTCTTCCCCCTGGGGCGCCCCTGCTCCGAGAGCACCTCCGAGGACACAGCGGCCCCTGG 729
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 CATCGGTCTTCCCCCTGGGGCGCACCCTGCTCCGAGAGCACCTCCGAGGACACAGCGGCCCCTGG 302

Qy   730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy   790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCCTCAGGACTCTACTCCCTCA 849
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCCTCAGGACTCTACTCCCTCA 422

Qy   850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACACCTGCAACGTGA 482

Qy   910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
         ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCAGCACGGGAG 542

Qy   970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCTGCTGCTGACGCGCCACCCCGGCTGTGCA 1029
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Db   543 GGAGGGGGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCTGCTGCTGCTGACGCCGCTATCCCGGCTATGCA 602

Qy  1030 GCCCCAGCCCAGGCCAGCAAGGCAGGAGGCCCCATCGTCTCCTCCACCACCGTGTCTGCTCCC 1089
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Db   603 GCCCCAGTCCAGGCCAGCAAGGCAGGAGGCCCCGTCGTCTCCTCTTCACCCCGAGGGGCCTCGCCC 662

Qy  1090 GCCCCACTCATCGTCAGGGAGAGGGTCTTCTGGCTTTTCCACCCAGGCTCCAGGCAGGCA 1149
         |||||||||||| ||||||||||||||||||||||||||||  |||||||||||||||||
Db   663 GCCCCACTCATGTCAGGGAGAGGGTCTTCTGGCTTTTCC--CCAGGCTCTGGGCAGGCA 721

Qy  1150 CAGGCTGGGTGGCCCCTACCCCCAGGGGGCAGGGGCAGGTGCTTGGCTCAGACC 1209
         ||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   722 CAGGCTAGGTGGCCCCTAACCCCAGGGGGCAGGGGCAGGTGCTTGGCTCAGACC 781

Qy  1210 TGCCAAAAGCCATATCCCGGAGAACCCTGCCCTGCCACCCCAAAGGCCAAA 1269
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Db   782 TGCCAAGAGCCATATCCCGGAGAACCCTGCCCTGCCACCCCAAAGGCCAAA 841

Qy  1270 CTGTGCCACTCCCTCGGACACCTTCTCCTCTCTCCGATCCCGAGTCAACTCCCAATCT 1329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   842 CTCTCCACTCCCTCGGACACCTTCTCTCCCTCTCCGATTCCCGAGTAACTCCCAATCT 901

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy  1441 CCAGGGACAGGCCCCAGCTGGGCTGCTGACACGTGCCACCTCCATCTCTTCCTTCAGCACC-- 1498
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Db  1499 -ACCTGCGGCAGCACCGTCAGTTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGA 1557

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Qy  1499 -ACCTGCGGCAGCACCGTCAGTTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGA 1557

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Qy  1558 TCTCCCGGACACCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617

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Qy  1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737

Db  1262 AGGAGCAGTTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321
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Qy  1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797

Db  1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381
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Qy  1798 AGAAAACCATCTCAAAACCAAAGGTGGGACCCGGGTATGAGGGCCACATGGACAGA 1857

Db  1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441
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Qy  1858 GGCCGGCTCGGCCCACCCTCTGGGAGTGACCGCTGTGCCAACCTCTGTCCTACAGG 1917

Db  1442 GGCCGGCTCGGCCCACCCTCTGAGAGTGACCGCTGTACCAACCTCTGTCCTACAGG 1501
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Qy  1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977

Db  1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561
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Qy  1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037

Db  1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621
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Qy  2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCC 2097

Db  1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681
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Qy  2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157

Db  1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741
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Qy  2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217

Db  1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801
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Qy  2218 CTCTCCCTGTCTCCGGGTAAATGAGTG 2244

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RESULT 8
US-07-916-098A-43
; Sequence 43, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO

STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 2029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "pBAG101 insert"
US-07-916-098A-43

Query Match   71.6%;   Score 1610.8;   DB 2;   Length 2029;
Best Local Similarity 94.6%;   Pred. No. 0;
Matches 1712;   Mismatches 92;   Conservative 0;   Indels 6;   Gaps 4;

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Qy  438 GAGGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGCGCAGGAGTGGGCTAAGGTG 497
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Db    2 GAGCTTTCTGGGGCGCAGGCCAGGCCTGACCTTGGC-TGGGGGCAGGGAGGGGGGCTAAGGTG 60

Qy  498 AGGCAGGGTGGCGCCCAGCCAGGTGCACACCCAGTGCTGCCCCTGAGCCCCGACCCCTG 557
        ||||||||||||||||||||||||||||||||||  |||||||| || |||||||||||
Db   61 ACGCAGGGTGGCGCCCAGCCAGGTGCACACCCAGTGCCCAATGCCCAGAGCTCCGCGCCCTG 120

Qy  558 CCTGGACCCCTCGTGGATAGACAAGAACCAGAGGGCCTCGCGCCCAGCTCTGT 617
        ||  |||||| ||| ||| |||||||| |||||||||||||||||||||||||
Db  121 CATGGACCCATCGGGGATAGAACAAGAACCAGAGGGCCTCGCGCCCCTGGGCCCTGT 180

Qy  618 CCCACACCCGCGGTCACATGGCACCACCTCTTGCAGCCCCACCCAAGGGGCCCCATCGGTC 677
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Db  181 CCCACACCCGCGGTCACATGGCACCACCTCTTGCAGCCCCACCCAAGGGGCCCCATCCGTC 240

Qy  678 TTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGACCGGTGACGTGTCGTGACCAGC 737
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Db  241 TTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCAGTGTGTCGTGTCGGAACTCAGCC 300

Qy  738 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGC 797
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Db  301 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC 360

Qy  798 GGCGTGCACACCTTCCCAGCTGTCCTACAGTCTCTACTCCCCTCAGCAGCGTG 857
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Db  361 GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCCTACTCCCTCAGCAGCGCGTG 420
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Qy  858 GTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAG 917
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Qy  918 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGAGGGGTG 977
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Qy 1038 CCAGGCAGCCAAGGCAGGCAGCCCCATCTGTCTCCTCACCCGGCCTCGCCCGCCCCACT 1097
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Db  601 CCAGGCAGCCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACCACCCACT 660

Qy 1098 CATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGCGTCCAGGCTCCAGCAGGCTGG 1157
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Db  661 CATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGCGTCCGGCA-CCACAGGCTGG 719

Qy 1158 GTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAA 1217
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Db  720 ATGCCCCTACCCCAGCCCTGCGCATACA-GGGCAGGTGCTCGCGCTCAGACCTGCCAAGA 778

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Db  779 GCCATATCCGGGAGGACCCTGCCCTGCCCTGACCTAAGCCCACCCCAAAGCCAAACTCTCCAC 838

Qy 1278 TCCCTCAGCTCGGACACCTTCTCTGCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTG 1337
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Db  839 TCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTG 898

Qy 1338 CAGAGCCAAATGTTGTGTGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGC 1397
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Db  899 CAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCAGCCTCGC 958

Qy 1398 CCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGACCAGGCCCCAG 1457
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Db  959 CCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGACCAGGCCCCAG 1018

Qy 1458 CTGGGTGCTGACAGTCCACCTGACATCCTCCCACC---ACCTGGCGCAGCGACCACCG 1514
        | |||||||||| | ||| || |||| |||| ||||   |||| |||||||||||||
Db 1019 CCGGGTGCTGACGCATCCAACCTCCAGCACCTGAGTTCCTGGGGGACCA 1078

Qy 1515 TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCCGACCCCTGAG 1574
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Db 1139 GTCACGTGCGTGGTGGTGGACGTGGGACGTGAGCCAGGAGGTCCAGTTCAACTGGTAC 1198

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Db 1259 ACGTACCGTGTGTGCAGCGTCCTCCACCGTCCTGCACCAGGACTGGCTGGCGCAAGGAG 1318

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Db 1319 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAA 1378

Qy 1815 ACCAAAGGTGGGACCCCGGGGTATGAGGGCCACATGGACAGAGGGCCGGCTCGGCCCACC 1874
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Db 1379 GCCAAAGGTGGGACCCCACGGGGTGCGAGGGCCACCACGAGGGCCAGCTGCGGCCCACC 1438

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        |||||||||||||||||||||||||||||||| ||   |||||||||||||||||||||||| ||
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Query Match        70.5%;  Score 1584.6;  DB 3;  Length 2482;
Best Local Similarity 99.7%;  Pred. No. 0;
Matches 1587;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

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Db     688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACTCCGAG  747

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Db     748 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG  807

Qy     774 TGGAACTCAGGCGGCTCTGACAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA  833
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Db     808 CTACAGCAGCGGCTCTGACAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA  867

Qy     834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  927

Qy     894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  953
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Db     928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  987

Qy     954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCAGGCAGCCCAGGCCAGGCCCTCGCCCTGGAC  1013
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Db     988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGAC  1047

Qy    1014 GCACCCCGGCTGTGCAGCCCCACTCAGGGCCAGGCCAGGCCCATCGTCTCCTCAC  1073
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Db    1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCCAGGCCCATCGTCTCCTCAC  1107

Qy    1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC  1133
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Db    1108 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC  1167

Qy    1134 AGCTCCAGGCAGGCCACAGGCTGGGTGCCCAGGCCCTACCCCAGGCCCTCCACACAGGGGCAG  1193
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Db    1168 AGCTCCAGGCAGGCCACAGGCTGGGTGCCCAGGCCCTACCCCAGGCCCTCCACACAGGGGCAG  1227

Qy    1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGAGGACCCTGCCCTGCCCTAAGCC  1253
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Db    1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGAGGACCCTGCCCTGCCCTAAGCC  1287

Qy    1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCTCCCAGATCC  1313
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Db    1288 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCTCCCAGATCC  1347

Qy    1314 GAGTAACTCCCAATCTTCTCTCTGCGAGAGCCCAAATGTTGTGTCGAGTGCCCACCGTGCC  1373
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Db    1348 GAGTAACTCCCAATCTTCTCTCTGCGAGAGCCCAAATGTTGTGTCGAGTGCCCACCGTGCC  1407

Qy    1374 CAGGTAAGCCAGCCCAGGCCTCGCCCTCAAGGCCCTCAAGGCGGGACAGTGCCCTAGAGTAG  1433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1408 CAGGTAAGCCAGCCCAGGCCTCGCCCTCAAGGCCCTCAAGGCGGGACAGTGCCCTAGAGTAG  1467

Qy    1434 GCACCACCTGCGGCAGCAGGACCACGTTCAGTCTTCCTTCCTCTTCCCCCAAAAACCCAAGGACACCCTC  1493
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1468 CCTGCATCCAGGACACGGCAGGACCACGTTCAGTCTTCCTTCCTCTTCCCCCAAAAACCCAAGGACACCCTC  1527

Qy    1494 GCACCACCTGCGGCAGCACGTTCAGTCTTCCTTCCTCTTCCCCCAAAAACCCAAGGACACCCTC  1553
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    1528 GCACCACCTGTGGCAGGACCGTCAGTCTTCCTTCCTCTTCCCCCAAAAACCCAAGGACACCCTC  1587

Qy    1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  1613
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  1647

Qy    1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA  1673
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA  1707

Qy    1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG  1733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1935 ACAGGTGTACACCTGCCCCCATCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC  1994
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1499 ACAGGTGTACACCTGCCCCCATCCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC  1558

Qy    1995 CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA  2054
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Db    1559 CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA  1618

Qy    2055 GCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCT  2114
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Db    1619 GCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT  1678

Qy    2115 CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC  2174
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Db    1679 CTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTTCATGCTC  1738

Qy    2175 CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGG  2234
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Db    1739 CGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGG  1798

Qy    2235 TAAATGAGTG  2244
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Db    1799 TAAATGAGTG  1808
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RESULT 9
US-08-477-460B-3
; Sequence 3, Application US/08477460B
; Patent No. 6034223
GENERAL INFORMATION:
    APPLICANT: Progenics Pharmaceuticals, Inc.
    TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
    TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Cooper & Dunham
        STREET: 30 Rockefeller Plaza
        CITY: New York
        STATE: New York
        COUNTRY: USA
        ZIP: 10112
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.24
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/477,460B
        FILING DATE: 07-JUN-1995
        CLASSIFICATION: 530
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/927,931
        FILING DATE: 07-AUG-1992
    ATTORNEY/AGENT INFORMATION:
        NAME: White, John P.
        REGISTRATION NUMBER: 28,678
        REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 977-9550
        TELEFAX: (212) 977-9809
        TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2482 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: unknown
    MOLECULE TYPE: cDNA
    ORIGINAL SOURCE:
        ORGANISM: homo sapien
        CELL TYPE: lymphocyte
US-08-477-460B-3
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Db   1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTGGTCAGGGTCCTCACCGTTGTGCACCAG 1767
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Db    748 AGCACAGCGCGCCCTGGGCTGCCTGGTCAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy   1734 GACTTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
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Qy    774 TGGAACTCAGGCGGCTTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833

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Qy   1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGACCCGCGGGGTATGAGGGCCACATGA 1853
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Qy    834 GGACTCTACTCCCTCAGCAGCGTGTGCACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893

Db   1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1887
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Db    868 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy   1854 CAGAGGCCCGCGTCGGCCCACCCTCGCCCTGGGAGTGACCGCTTGTGCCAACCTCTGTCCC 1913
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Qy    894 TACACCTGCAACGTAGATCAACAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953

Db   1888 CAGAGGCCGCGTCGGCCCACCCTCGCCCTGGGAGTGACCGCCTGTGCCAACCTCTGTCCC 1947
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928 TACACCTGCAACGTAGATCAACAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy   1914 TACAGGGCAGCCCCGAGAACCACAGTGTACACCCCTGCCCCATCCCGGGAGGAGATGAC 1973
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    954 AGGCCAGCTCAGGAGGGTGTCTGCTGAAGCCAGGTCAGCCCTGCACCCTCCTGCCTGGAC 1013

Db   1948 TACAGGGCAGCCCCGAGAACCACAGTGTACACCCCTGCCCCATCCCGGGAGGAGATGAC 2007
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Db    988 AGGCCAGCTCAGGAGGGTGTCTGCTGAAGCCAGGTCAGCCCTGCACCCTCCTGCCTGGAC 1047

Qy   1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Qy   2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCATGCTGGA 2093
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Qy   1074 CCGGAGGCCTTGTGCGCCCCACTCAGGCTGCCCACCCAGGGCCTTCACACACAGGGGCAG 1133

Db   2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCATGCTGGA 2127
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Db   1108 CCGGAGGCCTTGTGCGCCCCACTCAGGCTGCCCACCCAGGGCCTTCACACACAGGGGCAG 1167

Qy   2094 CTCCGACGGCTCCTTCTTCCTACAGCAAGCAAGCTGACCTGAGAGCCAGGTGGCAGCA 2153
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Qy   1134 AGGCTCCAGGAGCACAGGCTGGGTGCCCCACCCAGGCCCTTCACACCAGGGGCAG 1193

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1168 AGGCTCCAGGACCAGGCTGGGTGCCCCACCCAGGCCCTTCACACCAGGGGCAG 1227

Qy   2154 GGGGAACGTCTTCTCCTGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Qy   1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCTGACCTAAGCC 1253

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Db   1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCTGACCTAAGCC 1287

Qy   2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
          ||||||||||||||||||||||||||||||||
Qy   1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCGGAGCGCCAAATGTGTGTCGAGTGCCCACCGTGCC 1313

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                                                           Qy   1314 GAGTAACTCCCAATCTTCTCTCTGCGAGCGCCAAATGTGTGTCGAGTGCGCGCCAGTGTGCCAGTAG 1373
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                                                           Db   1348 GAGTAACTCCCAATCTTCTCTCTGCGAGCGCCAAATGTGTGTCGAGTGCGCGCCAGTGTGCCAGTAG 1407

                                                           Qy   1374 CAGTAAGCCAGCCAGCCCAGGCCTTCGCCCTCGCCCTCAGCTCAAGGCGGACAGGTGCCTAGAGTAG 1433
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                                                           Db   1408 CAGTAAGCCAGCCAGCCCAGGCCTTCGCCCTCGCCCTCAGCTCAAGGCGGACAGGTGCCTAGAGTAG 1467

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                                                           Db   1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACTTCACCTCTTCCTCA 1527

                                                           Qy   1494 GCACCACTGGGCAGCAGCACCGACCCTGAGGTGCACGTGGCACGTGAGCCACGAGGACCCTC 1553
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                                                           Db   1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

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RESULT 10
US-08-379-516-3
; Sequence 3, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; TITLE OF INVENTION: Immunoconjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER APPLICATION FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER APPLICATION FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH:.2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-379-516-3

Query Match   70.5%;   Score 1584.6;   DB 3;   Length 2482;
Best Local Similarity   99.7%;   Pred. No. 0;
Matches 1587;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

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Db    688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

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us-09-627-896b-23.rni

Sat Jul 19 10:01:51 2003

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Db  1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1887
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Qy  1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGGTGCCAACCTCTGTCCC 1913
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Db  1888 CAGAGGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGGTGCCAACCTCTGTCCC 1947

Qy  1914 TACAGGGCAGCCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGGGACATCGCCGT 1973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1948 TACAGGGCAGCCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGGGACACCGCCGT 2007

Qy  1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Qy  2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACCCCTCCCATGCTGGA 2093
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Db  2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACCCCTCCCATGCTGGA 2127

Qy  2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153
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Db  2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy  2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Db  2188 GGGGAAGGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy  2214 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2244
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Db  2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278
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RESULT 11
US-09-329-916-3, Application US/09329916
; Sequence 3, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
;   CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION DATA: 08/477,460
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 07-JUN-1995
; FILING DATE: US 07/927,931
; APPLICATION NUMBER: 07-AUG-1992
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P. 28,678
; REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH 2482 base pairs
; TYPE nucleic acid

STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte

US-09-329-916-3   Score 1584.6;   DB 4;   Length 2482;   0;
                                   Pred. NO. 0;   4;   Indels   0;   Gaps   0;
Query Match   70.5%;   Mismatches   0;
Best Local Similarity   99.7%;   Conservative   0;
Matches 1587;

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Qy   654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
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Db   688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy   714 AGCACAGCGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
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Qy   774 TGGAACTCAGGCGCTGTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
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Db   808 TGGAACTCAGGCGCTGTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy   834 GGATCTTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
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Db   868 GGACTCTTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy   894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953
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Db   928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy   954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGGTGCCTGGTCCCATCGTCTCCTCAC 1013
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGGTGCCTGGTCCCATCGTCTCCTCAC 1047

Qy  1014 GCACCCCGGCGTGCAGCCCCAGCCCCACTGCTCAGGAGCAGGGTCTTCTGGCTTTTCCACC 1073
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Qy  1074 CCGGAGGCCCTGCGGCCCACCTCCTCCTGCAGAGCGCAAATGTTGTGTCAGAGGGCAG 1133
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Db  1108 CCGGAGGCCCTGCGGCCCACCTCCTCCTGCAGAGCGCAAATGTTGTGTCAGAGGGCAG 1167

Qy  1134 AGGCTCCAGGAGGCACAGGGCTGGGTGCCCTACCCCAGCCCCTGACCTAAGCC 1193
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Qy  1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCCCATATCCCCAGATCC 1253
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Db  1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCCCATATCCCCAGATCC 1287

Qy  1254 GACCCCAAAGGCCAAACTGCCACCTCCCTGCAGAGCGCAAATGTTGTGTCAGAGTGCCGCC 1313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1288 GACCCCAAAGGCCAAACTGCCACCTCCCTGCAGAGCGCAAATGTTGTGTCAGAGTGCCGCC 1347

Qy  1314 GAGTAACTCCAATCTTCTCTGCAGAGGCGGGACAGGTGCCCTAGAGTAG 1407
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Db  1348 GAGTAACTCCAATCTTCTCTGCAGAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy  1374 CAGGTAAGCAGCCAGCCAGCCAGCACGTCCACCTCAGTCTTCCTCA 1493
             ||||||||||||||||||||||||||||||||||||||||||||||
Db  1408 CAGGTAAGCAGGCACAGGGCCAGCACGTCCACCTCAGTCTTCCTCA 1527

Qy  1434 CCTGCATCCAGGGACAGGGCCCACCCTTCAGTCTTCCTTCCCCCCAAAACCCAGGACACCCTC 1553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1468 CCTGCATCCAGGGACAGGGCCCACCCTTCAGTCTTCCTTCCCCCCAAAACCCAAGGACACCCTC 1587

Qy  1494 GCACACCTCGGCGACGCTCAGTCTTCTTCTTCCTCCCCCCAAAACCCAAGGACACCCTC 1613
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Db  1528 GCACCACCTGTGCAGACACCCTGAGTCACGTGGCGTGGTGACGTGAGCCACGGAAGACCCCC

Qy  1554 ATGATCTCCCGAGCCCCTGAGGTCACGTGGCGTGGTGACGTGAGCCACGGAAGACCCCC 1613
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PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/476,227
    FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
    NAME: White, John P.
    REGISTRATION NUMBER: 28,678
    REFERENCE/DOCKET NUMBER: 37690-II-A
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 278-0400
    TELEFAX: (212) 391-0525
    TELEX:

INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2482 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: unknown
    MOLECULE TYPE: cDNA
    ORIGINAL SOURCE:
        ORGANISM: homo sapien
        CELL TYPE: lymphocyte
US-08-485-372A-3

Query Match
Best Local Similarity   70.5%;   Score 1584.6;   DB 4;   Length 2482;
Matches 1587;   Conservative   0;   Pred. No. 0;   Indels   0;   Gaps   0,
                99.7%;   0;   Mismatches   4;

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Qy    654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCCGAG  713
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Db    688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG  747

Qy    714 AGCACAGCGCCGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG  773
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 AGCACCTCCGAGAGCACAGCGGCGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG  807

Qy    774 TGGAACTCAGGCGCTCTGACCAGCGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA   833
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 TGGAACTCAGGCGCTCTGACCAGCGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA   867

Qy    834 GGACTCTACTTCCCTGCCGTGGAGGACAACTGGCACCCAGACCAACTTCGGCACCACCAGACC  893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868 GGACTCTACTTCCCTGCCGTGGAGGACAACTGGCACCCCAGCAACACTTCGGCACCACCAGACC  927

Qy    894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  953
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Db    928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  987

Qy    954 AGGCCAGCTCAGGGAGGAGGGAGGGCCGTTCTGCTGGAAGCCAGGCTCAGCCCCTGGGAC 1013
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Db    988 AGGCCAGCTCAGGGAGGAGGGAGGGCTGTTCTGCTGGAAGCCAGGCTCAGCCCCTGCTGAC 1047

Qy   1014 GCACCCCGGCTGTGCAGCCCCAGGGCCCAGGCAGCAGGCCCCATCGTCTCCTCAC 1073
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Db   1048 GCACCCCGGCTGTGCAGCCCCAGGGCCCAGGGCAGCAGGCAGGCCCCATCGTCTCCTCAC 1107

Qy   1074 CCGGAGGCCCTGCCCGCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTTCCACC 1133
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Db   1108 CCGGAGGCCCTGCCCGCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTTCCACC 1167

Qy   1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193
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Qy   1194 GTGCTTGGCTCAGACCTGCAAAAGCCATATCCGGAGACCCTGCCCCTGCCCTAAGCC 1253
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Db   1228 GTGCTTGGCTCAGACCTGCAAAAGCCATATCCGGAGACCCTGCCCTGCCCTAAGCC 1287

Qy   1254 GACCCCAAAGGCAAACTGTCCACTCCCTCAGCTCGGACACCTTGTGTTGTGCCCACGATCC 1313
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Qy   1314 GAGTAACTCCCAATCTTCTCTCGAGAGGCCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373
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Db   1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy   1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733
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Db   1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1767

Qy   1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827

Qy   1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1853
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Db   1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1887

Qy   1854 CAGAGGCCGGCTCGGCCCACCCCTCTGCCCTGGGAGTGACCGTGTGCCAACCTCTGTCCC 1913
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1888 CAGAGGCCGGCTCGGCCCACCCCTCTGCCCTGGGAGTGACCGTGTGCCAACCTCTGTCCC 1947

Qy   1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy   2008 CAAGAACCAAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Db   2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2067

Qy   2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2127

Qy   2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2187

Qy   2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Db   2214 GAGCCTCTCCCTGTCTCCGGGTAAAATGAGTG 2244

Qy   2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278
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RESULT 12
US-08-485-372A-3
Sequence 3, Application US/08485372A
Patent No. 6187748
GENERAL INFORMATION:
    APPLICANT: Beaudry, Gary A.
    APPLICANT: Maddon, Paul J.
    TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Cooper & Dunham LLP
        STREET: 1185 Avenue of the Americas
        CITY: New York
        STATE: New York
        COUNTRY: USA
        ZIP: 10036
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.24
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/485,372A
        FILING DATE:
        CLASSIFICATION: 435

ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2482 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-409-006A-3

Query Match   70.5%;   Score 1584.6;   DB 4; Length 2482;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1587; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

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Db    688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG  747

Qy    714 AGCACAGGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG  773
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Db    748 AGCACAGGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG  807

Qy    774 TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA  833
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Db    808 TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA  867

Qy    834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  893
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Db    868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  927

Qy    894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  953
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Db    928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  987

Qy    954 AGGCCAGCTCAGGGAGGAGGGTGTCTGTGGAAGCCAAGGGCAGGCCTCAGCCCTCCTGCTGAC 1013
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Db    988 AGGCCAGCTCAGGGAGGAGGGTGTCTGTGGAAGCCAAGGGCAGGCCTCAGCCCTCCTGCTGAC 1047

Qy   1014 GCACCCCGGCTGTGCAGCCCGAGCGCCCCATCGTCTCCTCAC 1073
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Db   1048 GCACCCCGGCTGTGCAGCCCGAGCGCCCCATCGTCTCCTCAC 1107

Qy   1074 CCGGAGGCCTTGCCCGCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133
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Db   1108 CCGGAGGCCTTGCCCGCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1167
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Db   1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

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Qy   1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGACGTGAGCCACGAAGACCCC 1613
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Db   1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGACGTGAGCCACGAAGACCCC 1647

Qy   1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
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Db   1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy   1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGTCACCAG 1733
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Db   1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGTCACCAG 1767

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Qy   1794 ATCGAGAAAACCATCTCCAAAACCAAAGTGGGACCCGGGGGTATGAGGGCCACATGGA 1853
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1828 ATCGAGAAAACCATCTCCAAAACCAAAGTGGGACCCGGGGGTATGAGGGCCACATGGA 1887

Qy   1854 CAGAGGCCGGCTCGGGCTCCACCCCTCTGCCCTGGGAGTGACCGTGCCAACCTCTGTCCC 1913
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1888 CAGAGGCCGGCTCGGGCTCCACCCCTCTGCCCTGGGAGTGACCGTGCCAACCTCTGTCCC 1947

Qy   1914 TACAGGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1948 TACAGGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy   1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Db   2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

Qy   2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGTCTGGA 2093
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Qy   2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153
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Db   2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy   2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Db   2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy   2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db   2248 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2278
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RESULT 13
US-09-409-006A-3
; Sequence 3, Application US/09409006A
; Patent No. 6342586
GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:

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Qy   2214 GAGGCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db   2248 GAGGCTCTCCCTGTCTCCGGGTAAATGAGTG 2278
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RESULT 14
US-08-484-681-3
; Sequence 3, Application US/08484681
; Patent No. 6451313
; GENERAL INFORMATION:
;   APPLICANT: Beaudry, Gary A.
;   APPLICANT: Maddon, Paul J.
;   TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper & Dunham LLP
;   STREET: 1185 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10036
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/484,681
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: White, John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 37690-II-B
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 278-0400
;   TELEFAX: (212) 391-0525
;   TELEX:
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2482 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;   ORGANISM: homo sapien
;   CELL TYPE: lymphocyte
US-08-484-681-3

Query Match   70.5%; Score 1584.6; DB 4; Length 2482;
Best Local Similarity   99.7%; Pred. No. 0;
Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy    654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCCCCTGCTCCAGGAGCACCTCCGAG 713
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Db    688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy    714 AGCACAGCGGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
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Db    748 AGCACAGCCGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy    774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
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Db    808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy    834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy    894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953
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Db    928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987
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Qy   1134 AGGGCTCCAGGCAGGCAGGACCAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1168 AGGGCTCCAGGCAGGCAGGACCAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1227

Qy   1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253
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Db   1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1287

Qy   1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACTTCTCTCCTCCCAGATCC 1313
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Db   1288 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1347

Qy   1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTCTGAGTGCCCACCGTGCC 1373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1348 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTCTGAGTGCCCACCGTGCC 1407

Qy   1374 CAGGTAAGCCAGCCCAGGCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 CAGGTAAGCCAGCCCAGGCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy   1434 CCTGCATCCAGGGACAGGCCCCCAGCTGGGTGCTGCACGTCCACCTCCATCTCTTCCTCA 1493
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Db   1468 CCTGCATCCAGGGACAGGCCCCCAGCTGGGTGCTGCACGTCCACCTCCATCTCTTCCTCA 1527

Qy   1494 GCACCACCTGCGCAGCACCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCTC 1553
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Qy   1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613
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Qy   1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
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Qy   1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733
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Qy   1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
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Qy   1794 ATCGAGAAAACCATCTCAAAAACCAAAGGTGGGACCCCGGGGTATGAGGGCCACATGGA 1853
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Qy   1854 CAGAGGCCCGGCTCGGCCCACCCTCTGCCCCGGGAGTGACCGCGTGTGCCAACCTCTGTCCC 1913
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Qy   1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
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Db   1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy   1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Qy   2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093
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Db   2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2127

Qy   2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGACAAGAGCAGGTGCAGCA 2153
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Db   2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGACAAGAGCAGGTGCAGCA 2187

Qy   2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Db   2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247
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Qy 2034 GGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGAGACCACACACCTCCATGCTGGA 2093
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Db 2068 GGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACACAGAGACCACACACCTCCATGCTGGA 2127

Qy 2094 CTTCGACGGCTCCTTCTTCCTCTACACGCAAGTCACCGTGGACAAGAGCAGTGGCAGCA 2153
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Db 2128 CTTCGACGGCTCCTTCTTCCTCTACACGCAAGTCACCGTGGACAAGAGCAGTGGCGAGCA 2187

Qy 2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Qy 2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 15
PCT-US93-07422-3
; Sequence 3, Application PC/TUS9307422
; GENERAL INFORMATION:
;   APPLICANT: Progenics Pharmaceuticals, Inc.
;   TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
;   TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper & Dunham
;   STREET: 30 Rockefeller Plaza
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10112
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US93/07422
;   FILING DATE: 19930806
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/927,931
;   FILING DATE: 07-AUG-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME: White, John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 977-9550
;   TELEFAX: (212) 977-9809
;   TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2482 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;   ORGANISM: homo sapien
;   CELL TYPE: lymphocyte
PCT-US93-07422-3

Query Match   70.5%;   Score 1584.6;   DB 5;   Length 2482;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1587; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCCGCCCTGCTCCCAGGAGCACCTCCGAG 713
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Db   688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCCGCCCTGCTCCCAGGAGCACCTCCGAG 747

Qy   714 AGCACAGCGGGCCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773

Qy   954 AGGCCAGCTCAGGGAGGGAGGGGTGTCTGCTGGAAGCTCAGGCTCAGCCGTCTGCCTGGAC 1013
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Db   988 AGGCCAGCTCAGGGAGGGAGGGGTGTCTGCTGGAAGCCAGGCCAGCCGTCTGCCTGGAC 1047

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Db 1048 GCACCCCGGCTGTGCAGCCCAGGCAGCAAGGCAGGAGGGCCCATCTGTCTCCTCAC 1107

Qy 1074 CCGGAGGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCACC 1133
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Qy 1134 AGGCTCCAGGCAGGCAGGCCACAGGCTGGGTGCCCTACCCCCAGGCCCTTCACACAGGGGCAG 1193
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Qy 1434 CCTGCATCCAGGGACAGCAGCCCCCAGCTGGTGGTGTGACACGTCCACCTCCATCTCTTCCTCA 1493
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Db 1468 CCTGCATCCAGGGACAGCAGCCCCCTGAGCTGGTGGTGTGACACGTCCACCTCCATCTCTTCCTCA 1527

Qy 1494 GCACCACCTGCGGCAGCAGCCGTCAGTCTTCCCTCCTCCCCCAAAACCCAAGGACACCCTC 1553
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Db 1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy 1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGTCACCGGTTGTGCACCAG 1733
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Db 1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGTCACCGGTTGTGCACCAG 1767

Qy 1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
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Qy 1854 CAGAGGCCGGCTCGGCCCACCCTCTGGCCTCGGCCCCATCCCGGGAGTGACCGTGTCCC 1913
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Db 1888 CAGAGGCCGGCTCGGCCCACCCTCTGGCCTCGGCCCCATCCCGGGAGTGACCGTGTCCC 1947

Qy 1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
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Db         |||||||||  |||||||||||||||||||||||||||||||||||||
    748    AGCACGACCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG  807

Qy  774    TGGAACTCAGGCGCTGACACGGCGGTGACCGGTGCTGCCTCCAGCTGTCTCCTACAGTCCTCA  833
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Db  808    TGGAACTCAGGCGCTCTGACCAGCGGCGTGACCACCTGTCCTCCAGCTGTCTCCTACAGTCCTCA  867

Qy  834    GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  893
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Db  868    GGACTTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  927

Qy  894    TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  953
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Db  928    TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG  987

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Db  988    AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC  1047

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Db  1048   GCACCCCGGCTGTGCAGCCCAGGCAGCAAGGCAGAGGCCAGGCCCCCATCTGTCTCCTCAC  1107

Qy  1074   CCGGAGGCCTCTGCCCGCCCCCACTCATGCTTCAGGGAGGAGAGGTCTTCTGGCTTTTTCCACC  1133
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Db  1108   CCGGAGGCCTCTGCCCGCCCCCACTCATGCTTCAGGGAGGAGAGGTCTTCTGGCTTTTTCCACC  1167

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Db  1348   GAGTAACTCCCAATCTCTCTCTGCAGAGCGCAAATGTTGTCGAGTGCCACCGTGCC  1407

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Db  1408   CAGGTAAGCCAGGACCAGGACAGGCCCCAGCTGGGTGCTGACAGTGCCACCTTCCATCTCTTCCTCA  1467

Qy  1434   CCTGCATCCAGGAGACAGGCCCCAGCTGGGTGCTGACAGTGCCACCTCCATCTCTTCCTCA  1493
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Db  1768   GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC  1827

Qy  1794   ATCGAGAAAACCATCTCCAAAACCAAAGGTGGACCCGCGGGGTATGAGGGCCACATGGA  1853
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Db  1888   CAGAGGCCGGCTGGCTCTCGACCCCTCTGGGAGTGACCGGCTGTGCCAACCTCTGTCCC  1947

Qy  1914   TACAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCATCCGGAGGAGATGAC  1973
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Db  1948   TACAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCATCCGGAGGAGATGAC  2007

Qy  1974   CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT  2033
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Db  2068   GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA  2127

Qy  2094   CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA  2153
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Db  2128   CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA  2187

Qy  2154   GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA  2213
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Qy  2214   GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2244
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Db  2248   GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG  2278
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Search completed: July 18, 2003, 19:59:05
Job time : 124.256 secs

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 18, 2003, 04:46:48 ; Search time 915.261 Seconds
                                      (without alignments)
                                      10397.705 Million cell updates/sec

Title: US-09-627-896B-25
Perfect score: 327
Sequence: 1 gacatccagatgacccagtc.........ccaaggtggaaatcaaacgt 327

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1455140287B residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

GenCore version 5.1.6

Database :   GenEmbl:*
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    2: gb_htg:*
    3: gb_in:*
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    9: gb_pr:*
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   28: em_un:*
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   41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	304.8	93.2	743	6	AX258853	AX258853 Sequence
3	300.4	91.9	338	9	HSU86803	U86803 Human Ig ka
4	300.4	91.9	395	9	HSIGKLV41	X72462 H.sapiens m
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7	297.2	90.9	324	9	AB063945	AB063945 Homo sapi
8	296	90.5	328	9	AY043160	AY043160 Homo sapi
9	295.6	90.4	324	9	AF035044	AF035044 Homo sapi
10	295.2	90.3	752	6	AX258847	AX258847 Sequence
11	295.2	90.3	324	9	AX258851	AX258851 Sequence
12	295.2	90.3	752	6	AX258895	AX258895 Sequence
13	290.2	88.7	450	9	HUMIGHGU	L03156 Homo sapien
14	289.2	88.4	390	9	AF103772	AF103772 Homo sapi
15	289	88.4	316	9	AF193852	AF193852 Homo sapi
16	289	88.4	321	9	HSIGKVBAC	Z18827 Homo sapien
17	288	88.1	1073	9	HSIKLVA20	X63398 H.sapiens D
18	288	88.1	36886	9	AP001238	AP001238 Homo sapi
19	288	88.1	172465	9	AC110080	AC110080 Homo sapi
20	287	87.8	287	9	HSIGDPK4	X93622 H.sapiens g
21	285.4	87.3	330	9	AF103536	AF103536 Homo sapi
22	284.6	87.0	312	9	AF103486	AF103486 Homo sapi
23	284.6	87.0	332	9	AF103489	AF103489 Homo sapi
24	284	86.9	321	9	HSIGKLV55	X72476 H.sapiens m
25	284	86.9	324	9	AF099196	AF099196 Homo sapi
26	283.4	86.7	325	9	AY043164	AY043164 Homo sapi
27	282.8	86.5	372	9	HSIGKLV25	X72446 H.sapiens m
28	281.2	86.0	393	9	AF103771	AF103771 Homo sapi
29	281.2	86.0	432	9	HUMIGKVCA	L01279 Homo sapien
30	280.6	85.8	325	9	HSIGKLV19	X72440 H.sapiens m
31	279.2	85.4	321	6	AR162137	AR162137 Sequence
32	279	85.3	333	9	HUMPRBH	L09083 Homo sapien
33	278.6	85.2	322	9	AY043092	AY043092 Homo sapi
34	278.6	85.2	322	9	AY043138	AY043138 Homo sapi
35	278	85.0	342	9	HSU97250	U97250 Homo sapien
36	278	85.0	387	9	HUMIGKVJAA	L26890 Homo sapien
37	277.4	84.8	320	9	HUMFRAQ	L08900 Homo sapien
38	277.4	84.8	329	9	HUMFRBJ	L09085 Homo sapien
39	276.4	84.5	327	9	AF107244	AF107244 Homo sapi
40	276.4	84.5	650	9	HSA010446	AJ010446 Homo sapi
41	275.8	84.3	324	9	AF146408	AF146408 Homo sapi
42	275.6	84.3	322	9	AY043133	AY043133 Homo sapi
43	275.4	84.2	322	9	AY043139	AY043139 Homo sapi
44	275.4	84.2	1247	9	HSIGK6	Z00004 Human germl
45	275.4	84.2	1248	9	HUMIGKAH	M23848 Human Ig re

ALIGNMENTS

RESULT 1
HSVKI12RM
LOCUS   HSVKI12RM   327 bp   DNA   linear   PRI 17-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody light chain variable
            region,subgroup V(K)1 (III-2R IgM line).
ACCESSION   X70459
VERSION   X70459.1   GI:38436
KEYWORDS   anti-DNA antibody; complementarity determining region; Ig kappa
            light chain; Ig light chain; Ig variable region; IgM;
            immunoglobulin; systemic lupus erythematosus.
SOURCE   Homo sapiens
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 327)

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BASE COUNT   163 a   195 c   218 g   167 t
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Best Local Similarity   98.5%;   Pred. No. 2.6e-87;
Matches 319;   Conservative   0;   Mismatches   2;   Indels   3;   Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db   415 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 474

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db   535 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 594

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db   655 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTATAAACAGTGCCCCT---TGGACGTTCGGC 711

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
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Db   712 CAAGGGACCAAGGTGGAAATCAAA 735

RESULT 3
HSU86803
LOCUS   HSU86803   338 bp   mRNA   linear   PRI 04-MAR-1997
DEFINITION Human Ig kappa chain V-region (VL-COL) mRNA, partial cds.
ACCESSION U86803
VERSION   U86803.1   GI:1864136
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS   Pritsch,O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
TITLE   V gene usage by seven hybrids derived from CD5+ B-cell chronic
           lymphocytic leukemia and displaying autoantibody activity
JOURNAL   Blood 82 (10), 3103-3112 (1993)
MEDLINE   94033522
PUBMED   7693035
REFERENCE 2 (bases 1 to 338)
AUTHORS   Pritsch,O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
TITLE   Direct Submission
JOURNAL   Submitted (24-JAN-1997) Unite d'Immunohematologie et
           d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
           75724, France
FEATURES   Location/Qualifiers

AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
           and Diamond,B.
TITLE   Molecular characteristics of antibodies bearing an
           anti-DNA-associated idiotype
JOURNAL   J. Exp. Med. 174 (6), 1633-1652 (1991)
MEDLINE   92078875
PUBMED   1660528
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ORIGIN

Query Match   100.0%;   Score 327;   DB 9;   Length 327;
Best Local Similarity   100.0%;   Pred. No. 1.8e-94;
Matches 327;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300

Qy   301 CAAGGGACCAAGGTGGAAATCAAACGT 327
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Db   301 CAAGGGACCAAGGTGGAAATCAAACGT 327

RESULT 2
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LOCUS   AX258853   743 bp   DNA   linear   PAT 26-OCT-2001
DEFINITION Sequence 2352 from Patent WO0172771.
ACCESSION AX258853
VERSION   AX258853.1   GI:16508406
KEYWORDS   .
SOURCE   synthetic construct.
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE 1
AUTHORS   Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
           Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
           Hansen,P.H., Ravera,M. and Hsiao,K.C.
TITLE   Insulin and igf-1 receptor agonists and antagonists
JOURNAL   Patent: WO 0172771-A 2352 04-OCT-2001; Novo Nordisk A/S (DK)
           DGI Biotechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)

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                Query Match        91.9%;   Score 300.4;  DB 9;  Length 395;
                Best Local Similarity   97.2%;   Pred. No. 7.1e-86;
                Matches   317;  Conservative  0;  Mismatches   6;  Indels  3;  Gaps  1;

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                LOCUS       AX258845         761 bp   DNA       linear   PAT 26-OCT-2001
                DEFINITION  Sequence 2344 from Patent WO0172771.
                ACCESSION   AX258845
                VERSION     AX258845.1   GI:16508398
                KEYWORDS    synthetic construct.
                SOURCE      synthetic construct
                ORGANISM    artificial sequences
                REFERENCE   1
                AUTHORS     Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
                            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
                            Hansen,P.H., Ravera,M. and Hsiao,K.C.
                TITLE       Insulin and igf-1 receptor agonists and antagonists
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                BASE COUNT   84 a    92 c    81 g    81 t
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                Query Match        91.9%;   Score 300.4;  DB 9;  Length 338;
                Best Local Similarity   97.2%;   Pred. No. 7.2e-86;
                Matches   317;  Conservative  0;  Mismatches   6;  Indels  3;  Gaps  1;

    Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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    Db     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

    Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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    Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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    Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
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    Db   298 GGAGGGACCAAGGTGGAGATCAAACG 323

                RESULT 4
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                LOCUS       HSIGKLV41        395 bp    mRNA      linear   PRI 31-JAN-1994
                DEFINITION  H.sapiens mRNA for rearranged Ig kappa light chain variable region
                            (I.40).
                ACCESSION   X72462
                VERSION     X72462.1   GI:441392
                KEYWORDS    C-region; immunoglobulin; J-segment; kappa light chain; V-region.
                SOURCE      Homo sapiens
                ORGANISM    Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                REFERENCE   1  (bases 1 to 395)
                AUTHORS     Zachau,H.G.
                TITLE       Direct Submission
                JOURNAL     Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische
                            Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2,
                            FRG
                REFERENCE   2  (bases 1 to 395)
                AUTHORS     Klein,R., Jaenichen,R. and Zachau,H.G.
                TITLE       Expressed human immunoglobulin kappa genes and their hypermutation
                JOURNAL     Eur. J. Immunol. 23 (12), 3248-3262 (1993)
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JOURNAL     Patent: WO 0172771-A 2344 04-OCT-2001;
            DGI Biotechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
FEATURES    Location/Qualifiers
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BASE COUNT  179 a    201 c    219 g    162 t
ORIGIN
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Query Match   91.3%;   Score 298.4; DB 6; Length 761;
Best Local Similarity 97.2%;   Pred. No. 3.1e-85;
Matches   315; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

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Qy      1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Qy    301 CAAGGGACCAAGGTGGAAATCAAA 324
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Db    730 GGAGGGACCAAGGTGGAGATCAAA 753
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RESULT 6
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LOCUS       HUMIGHGQ                447 bp    mRNA    linear   PRI 03-MAY-2000
DEFINITION  Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
            (IGHV@) mRNA, partial cds.
ACCESSION   L03152
VERSION     L03152.1  GI:185387
KEYWORDS    .
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
AUTHORS     Collet,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.
            and Lerner,R.A.
TITLE       A binary plasmid system for shuffling combinatorial antibody
            libraries
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE     93066172
PUBMED      1438192
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            /protein_id="AAA52924.1"
            /db_xref="GI:567146"
            /translation="ELTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKL
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            EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPERTKVQWKVV"
V_region    <1..>447
            /gene="IGHV@"
            /note="G00-128-528"
BASE COUNT  110 a    119 c    108 g    110 t
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Query Match   91.2%;   Score 298.2; DB 9; Length 447;
Best Local Similarity 98.1%;   Pred. No. 3.6e-85;
Matches   313; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

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Qy      8 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 61

Qy     68 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121

Qy    128 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCATCTCGGTTCA 187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCATCTCGGTTCA 181

Qy    188 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 241

Qy    248 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGGGA 307
          ||||||||||||||||||||||||||||||||||||||||||     ||||||||||||
Db    242 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GGACGTTCGGCCAAGGGA 298

Qy    308 CCAAGGTGGAAATCAAACG 326
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Db    299 CCAAGGTGGAAATCAAACG 317
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RESULT 7
AB063945
LOCUS       AB063945                324 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
            region, partial cds, clone:K118.
ACCESSION   AB063945
VERSION     AB063945.1  GI:21669096
KEYWORDS    .
SOURCE      Homo sapiens
ORGANISM    Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:K118.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
TITLE       Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
JOURNAL     Unpublished
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REFERENCE   2 (bases 1 to 324)
AUTHORS   Kurosawa,Y.
TITLE   Direct Submission
JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
COMMENT   (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
            Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES   Location/Qualifiers
     source   1..324
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="K118"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene   1..324
                     /gene="IGK"
     CDS   <1..>324
                     /gene="IGK"
                     /codon_start=1
                     /product="immunoglobulin kappa light chain VLJ region"
                     /protein_id="BAC01573.1"
                     /db_xref="GI:21669097"
                     /translation="DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
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                     KVDIER"

BASE COUNT   80 a   89 c   76 g   79 t
ORIGIN

Query Match   90.9%;   Score 297.2; DB 9;   Length 324;
Best Local Similarity   96.6%;   Pred. No. 7.8e-85;
Matches 315;   Conservative   0;   Mismatches   8;   Indels   3;   Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTTTTAGCCTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCGGTACGTTCGGC   300
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Db   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GGACTTTCGGC 297

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db   298 CCTGGGGACCAAAGTGGATATCGAACG 323

RESULT 8
AY043160
LOCUS   AY043160   328 bp   mRNA   linear   PRI 31-DEC-2001
DEFINITION Homo sapiens MCLl141 immunoglobulin light chain variable region
            mRNA, partial cds.
ACCESSION   AY043160
VERSION   AY043160.1 GI:18025709
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 328)

AUTHORS   Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,
            Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.
TITLE   Ig VL gene repertoire in B cell type chronic lymphocytic leukemia
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 328)
AUTHORS   Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,
            Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.
TITLE   Direct Submission
JOURNAL   Submitted (29-JUN-2001) North Shore-LIJ Research Institute, 350
            Community Drive, Manhasset, NY 11030, USA
FEATURES   Location/Qualifiers
     source   1..328
                     /organism="Homo sapiens"
                     /isolate="MCLl141"
                     /db_xref="taxon:9606"
                     /cell_type="B lymphocyte from patient with IgM+ chronic
                     lymphocytic leukemia (CLL)"
     CDS   <1..>328
                     /codon_start=1
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                     /protein_id="AAK94864.1"
                     /db_xref="GI:18025710"
                     /translation="DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
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                     GTKLEIK"

BASE COUNT   83 a   90 c   76 g   79 t
ORIGIN

Query Match   90.5%;   Score 296; DB 9;   Length 328;
Best Local Similarity   96.0%;   Pred. No. 1.9e-84;
Matches 315;   Conservative   0;   Mismatches   10;   Indels   3;   Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60
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Db   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
           ||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCATCAGGGGTCCCATCT 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCATCAGGGGTCCCATCT 180

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---CGGAGTACGTTC 297
           |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCGTATGTACACTTTT 300

Qy   298 GGCCAAGGGACCAAGGTGGAAATCAAAC 325
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Db   301 GGCCAGGGGACCAAGCTGGAGATCAAAC 328

RESULT 9
AF035044
LOCUS   AF035044   324 bp   mRNA   linear   PRI 24-SEP-1999
DEFINITION Homo sapiens clone FD2K myosin-reactive immunoglobulin light chain
            variable region mRNA, partial cds.
ACCESSION   AF035044
VERSION   AF035044.1 GI:5921640
KEYWORDS   .
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 324)
AUTHORS   Wu,X., Liu,B., Van der Merwe,P.L., Kalis,N.N., Berney,S.M. and
            Young,D.C.
TITLE   Myosin-reactive autoantibodies in rheumatic carditis and normal

us-09-627-896b-25.rge

Sat Jul 19 10:01:57 2003

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JOURNAL    fetus
MEDLINE    Clin. Immunol. Immunopathol. 87 (2), 184-192 (1998)
PUBMED     98277139
REFERENCE  9614934
AUTHORS    2  (bases 1 to 324)
TITLE      Young,D.C.
JOURNAL    Direct Submission
           Submitted (19-NOV-1997) Department of Pathology and Laboratory
           Medicine, University of Texas Health Science Center, 6431 Fannin,
           Houston, TX 77030, USA
FEATURES   Location/Qualifiers
   source  1..324
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /clone="FD2K"
   CDS     <1..>324
           /note="FD2K"
           /codon_start=1
           /product="autoantibody"
           /note="myosin-reactive immunoglobulin light chain
           variable region"
           /protein_id="AAD56280.1"
           /db_xref="GI:5921641"
           /translation="DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
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           KLEIKR"
BASE COUNT 82 a    89 c    75 g    78 t
ORIGIN

Query Match   90.4%;  Score 295.6;  DB 9;  Length 324;
Best Local Similarity  96.3%;  Pred. No. 2.6e-84;
Matches 314;  Conservative 0;  Mismatches 9;  Indels 3;  Gaps 1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GCACTTTTGGC 297

Qy   301 CAAGGGACCAAGGCTGGAGATCAAACG 326
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Db   298 CCAGGGACCAAGGCTGGAGATCAAACG 323

RESULT 10
AX258847
LOCUS      AX258847
DEFINITION Sequence 2346 from Patent WO0172771.
ACCESSION  AX258847
VERSION    AX258847.1  GI:16508400
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R.,
           Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Brandt,J.,
           Hansen,P.H., Ravera,M. and Hsiao,K.C.
TITLE      Insulin and igf-1 receptor agonists and antagonists
JOURNAL    Patent: WO 0172771-A 2346 04-OCT-2001;
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FEATURES   DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
   source  Location/Qualifiers
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           /db_xref="GI:16508401"
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           SQGISNYLAWYQQKPGKVPKLILIYAASTLQSGVPSRFSGSGSGTDFILTISSLQPEDV
           WYGAEDKWGQCPKVPGKVPKPQCPKVPKLILIYAASTLQSGVPSRFSGSGSGTDFILTISSLQPEDV
           ATYYCQKYNSAPFTFGPGTKVDIK"
BASE COUNT 177 a   196 c   217 g   162 t
ORIGIN

Query Match   90.3%;  Score 295.2;  DB 6;  Length 752;
Best Local Similarity  96.6%;  Pred. No. 3.3e-84;
Matches 313;  Conservative 0;  Mismatches 8;  Indels 3;  Gaps 1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db   424 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db   484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 603

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---TTCACTTTCGGC 720

Qy   301 CAAGGGACCAAGGCTGGAAATCAAA 324
           |||||||||||||||||||||||
Db   721 CCTGGGACCAAGGCTGGAGATATCAAA 744

RESULT 11
AX258851
LOCUS      AX258851
DEFINITION Sequence 2350 from Patent WO0172771.
ACCESSION  AX258851
VERSION    AX258851.1  GI:16508404
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
           Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
           Hansen,P.H., Ravera,M. and Hsiao,K.C.
TITLE      Insulin and igf-1 receptor agonists and antagonists
JOURNAL    Patent: WO 0172771-A 2350 04-OCT-2001;
           DGI Biotechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
FEATURES   Location/Qualifiers
   source  1..752
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           /db_xref="taxon:32630"
           /note="synthetic DNA"
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           /note="unnamed protein product"
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BASE COUNT    162 a    195 c    221 g    174 t
ORIGIN

Query Match          90.3%;    Score 295.2;  DB 6;  Length 752;
Best Local Similarity 96.6%;   Pred. No. 3.3e-84;
Matches 313;  Conservative  0;  Mismatches  8;  Indels  3;  Gaps  1;

Qy        1 GACATCCAGATGACCCAGTCTCCATCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      424 GACATCCAGATGACCCAGTCTCCATCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy       61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 543

Qy      121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATTCACCATCTCCATCT 180
            |||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db      544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATTCACCATCTCCATCT 603

Qy      181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy      241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
            |||||||||||||||||||||||||||||||||||||||        |||| ||||||||
Db      664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTATAACAGT GCCCCT---TACACTTTTGGC 720

Qy      301 CAAGGGACCAAGGTGGAAATCAAA 324
            |||||||||||||||||||||||
Db      721 CAGGGGACCAAGCTGGAGATCAAA 744


RESULT 12
AX258895
LOCUS       AX258895          761 bp   DNA     linear    PAT 26-OCT-2001
DEFINITION  Sequence 2394 from Patent WO0172771.
ACCESSION   AX258895
VERSION     AX258895.1  GI:16508408
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
            Hansen,P.H., Ravera,M. and Hsiao,K.C.
  TITLE     Insulin and igf-1 receptor agonists and antagonists
  JOURNAL   Patent: WO 0172771-A 2394 04-OCT-2001;
            DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
FEATURES             Location/Qualifiers
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                     /note="synthetic DNA"
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                     DVYDRDYDRWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT
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BASE COUNT    179 a    200 c    217 g    165 t
ORIGIN                      EDVATYYCQKYNSAPTTFGPGTKVDIK"

Query Match          90.3%;    Score 295.2;  DB 6;  Length 761;
Best Local Similarity 96.6%;   Pred. No. 3.3e-84;
Matches 313;  Conservative  0;  Mismatches  8;  Indels  3;  Gaps  1;

Qy        1 GACATCCAGATGACCCAGTCTCCATCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      433 GACATCCAGATGACCCAGTCTCCATCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 492

Qy       61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 552

Qy      121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGCAGTCCCATCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGCAGTCCCATCT 612

Qy      181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACCATCTCCACCATCAGCAGCCTGCAGCCT 240
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Db      613 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACCATCTCCACCATCAGCAGCCTGCAGCCT 672

Qy      241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db      673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TTCACTTTCGGC 729

Qy      301 CAAGGGACCAAGGTGGAAATCAAA 324
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Db      730 CCTGGGACCAAGTGGATATCAAA 753


RESULT 13
HUMIGHGU
LOCUS       HUMIGHGU          450 bp   mRNA     linear    PRI 03-MAY-2000
DEFINITION  Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
            (IGHV@) mRNA, partial cds.
ACCESSION   L03156
VERSION     L03156.1  GI:185391
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Collet,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.
            and Lerner,R.A.
  TITLE     A binary plasmid system for shuffling combinatorial antibody
            libraries
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
  MEDLINE   93066172
   PUBMED   1438192
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                     /dev_stage="adult"
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Best Local Similarity 96.6%; Pred. No. 1.4e-82;
Matches 308; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

Qy   8 AGATGACCAGTCTCCATCCTCCGTGTCTGCATCGTGTAGGAGACAGAGTCACCATCACTT 67
Db   2 AGCTCACCCAGTCTCCATCCTCCGTGTCTGCTTCTGTGTAGGAGACAGAGTCACCATCACTT 61

Qy   68 GCCGGCGGCGAGTCAGGGCCATTAGCAATTATTTAGCCTGGTATCAGCAGAAAACCAGGGAAAG 127
Db   62 GCCGGCGGCGAGTCAGGGCCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121

Qy 128 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCA 187
Db 122 TTCCTAGACTCCTGATCTATGCTGCATCCACTTTGCAACCAGGGGTCCCATCTCGGTTCA 181

Qy 188 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 247
Db 182 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 241

Qy 248 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGGGA 307
Db 242 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GGACGTTCGGCCAAGGGA 298

Qy 308 CCAAGGTGGAAATCAAACG 326
Db 299 CCAAGGTGGAAATCAAACG 317

RESULT 14
AF103772
LOCUS   AF103772   390 bp   mRNA   linear   PRI 03-NOV-1999
DEFINITION Homo sapiens clone B22 anti-phospholipid immunoglobulin light chain
            VL-J-C region mRNA, partial cds.
ACCESSION   AF103772
VERSION   AF103772.1 GI:6179863
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 390)
AUTHORS   Chukwuocha,R.U., Hfiao,E., Shaw,P., Witztum,J.L. and Chen,P.P.
TITLE   Isolation, characterization and sequence analysis of five IgG
            monoclonal anti-phospholipid Fab fragments generated by phage
            display
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 390)
AUTHORS   Chukwuocha,R.U., Hfiao,E., Shaw,P., Witztum,J.L. and Chen,P.P.
TITLE   Direct Submission
JOURNAL   Submitted (02-NOV-1998) Medicine/Rheumatology, UCLA, 32-59
            Rehabilitation Center, 1000 Veteran Avenue, Los Angeles, CA
            90095-1670, USA
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                     /db_xref="taxon:9606"
                     /clone="B22"
                     /cell_type="lymphocyte"
                     /tissue_type="blood"
                     /note="patient with oxidized low density lipoproteins"
     CDS   <1..>390
                     /codon_start=1
                     /product="anti-phospholipid immunoglobulin light chain
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                     /protein_id="AAF05689.1"

/db_xref="GI:6179864"
/translation="ELQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
NLLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYCQKYDSAPRTFGPGT
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BASE COUNT   93 a   111 c   91 g   95 t
ORIGIN

Query Match   88.4%;   Score 289.2; DB 9; Length 390;
Best Local Similarity 95.1%; Pred. No. 3e-82;
Matches 310; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
Db   1 GAGCCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
Db   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy 121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
Db 121 GGGAAAGTTCCTAACCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
Db 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy 241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
Db 241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATGACAGTGCCCCTC---GCACTTTCGGC 297

Qy 301 CAAGGGACCAAGGTGGAAATCAAACG 326
Db 298 CCTGGGACCAAAGTGGATATCAAACG 323

RESULT 15
AF193852
LOCUS   AF193852   316 bp   mRNA   linear   PRI 21-FEB-2000
DEFINITION Homo sapiens clone 11LC immunoglobulin light chain variable region
            mRNA, partial cds.
ACCESSION   AF193852
VERSION   AF193852.1 GI:7012709
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 316)
AUTHORS   Choi,I.H., Park,S.G., Chung,J.H., Kim,I.J. and Hong,H.J.
TITLE   Generation of human Fab monoclonal antibodies against preS1 of
            hepatitis B virus using repertoire cloning
JOURNAL   Hybridoma 17 (6), 535-540 (1998)
MEDLINE   99105715
PUBMED   9890709
REFERENCE   2 (bases 1 to 316)
AUTHORS   Choi,I.H., Park,S.G., Chung,J.H., Kim,I.J. and Hong,H.J.
TITLE   Direct Submission
JOURNAL   Submitted (12-OCT-1999) Microbiology, College of Medicine, INJE
            University, 633-165 Gaegum-Dong Jin-GU, Pusan 614-735, South Korea
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     CDS   <1..>316
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                     B virus"
                     /codon_start=1
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                    ETK"
BASE COUNT    80 a    88 c    76 g    72 t
ORIGIN

Query Match             88.4%;    Score 289; DB 9; Length 316;
Best Local Similarity   95.7%;    Pred. No. 3.5e-82;
Matches 311; Conservative    0; Mismatches    5; Indels    9; Gaps    1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAATCAGGGGTCCCATCT 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAATCAGGGGTCCCATCT 180

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         |||||||||||||||||||||||||||||||||||||||||||      |||||
Db   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC--------TCGGC 291

Qy   301 CAAGGGACCAAGGTGGAAATCAAAC 325
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Db   292 GGAGGGACCAAGGTGGAGACCAAAC 316


Search completed: July 18, 2003, 13:47:34
Job time : 917.261 secs
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                GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          July 18, 2003, 04:16:54 ; Search time 566.66 Seconds
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Title:           US-09-627-896B-25
Perfect score:   327
Sequence:        1 gacatccagatgacccagtc........ccaaggtggaaatcaaacgt 327

Scoring table:   IDENTITY.NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1615066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:     32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
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            2:   em_esthum:*
            3:   em_estin:*
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            6:   em_estpl:*
            7:   em_estro:*
            8:   em_htc:*
            9:   gb_est1:*
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           11:   gb_htc:*
           12:   gb_est3:*
           13:   gb_est4:*
           14:   gb_est5:*
           15:   em_estfun:*
           16:   em_estom:*
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           18:   em_gss_hum:*
           19:   em_gss_inv:*
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           26:   em_gss_pro:*
           27:   em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	302	92.4	826	12	BG684416	BG684416 602636169
2	302	92.4	957	12	BG341934	BG341934 602463276
3	302	92.4	959	12	BG341941	BG341941 602463283
4	290.8	88.9	888	14	BQ881840	BQ881840 AGENCOURT
5	286	87.5	626	13	BM509065	BM509065 ih16b08.x
6	278.2	85.1	358	10	AW404145	AW404145 UI-HF-BL0
7	276.4	84.5	935	12	BG342083	BG342083 602463029
8	274.8	84.0	773	13	BM007845	BM007845 603617528
9	271.6	83.1	928	14	BQ707369	BQ707369 AGENCOURT
10	270	82.6	493	10	AW405753	AW405753 UI-HF-BL0
11	268.4	82.1	422	10	AW407904	AW407904 UI-HF-BL0
12	268.4	82.1	921	12	BG758398	BG758398 602712592
13	265.2	81.1	422	10	AV733746	AV733746 AV733746
14	265.2	81.1	1153	13	BM543718	BM543718 AGENCOURT
15	263.6	80.6	391	10	AW404992	AW404992 UI-HF-BL0
16	263.6	80.6	608	10	AW406562	AW406562 UI-HF-BL0
17	263.6	80.6	891	12	BG540787	BG540787 602570674
18	263.6	80.6	1006	14	BQ706213	BQ706213 AGENCOURT
19	263.2	80.5	358	10	AW408194	AW408194 UI-HF-BL0
20	262	80.1	631	14	BM818943	BM818943 K-EST0086
21	262	80.1	742	12	BG756519	BG756519 602715662
22	262	80.1	776	12	BG684027	BG684027 602635634
23	262	80.1	923	14	BQ882857	BQ882857 AGENCOURT
24	262	80.1	945	14	BQ707400	BQ707400 AGENCOURT
25	261	79.8	768	12	BG685552	BG685552 602637525
26	260.8	79.8	378	10	AW405241	AW405241 UI-HF-BL0
27	260.4	79.6	867	12	BG754732	BG754732 602714301
28	258.8	79.1	417	10	AW406228	AW406228 UI-HF-BL0
29	258.8	79.1	471	10	AW406294	AW406294 UI-HF-BL0
30	258.8	79.1	686	12	BG686745	BG686745 602650714
31	258.8	79.1	886	12	BG756818	BG756818 602710291
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33	258.8	79.1	1100	12	BF663472	BF663472 602144635
34	257.2	78.7	426	10	AW405900	AW405900 UI-HF-BL0
35	257.2	78.7	903	12	BG756188	BG756188 602713490
36	257.2	78.7	943	14	BQ707106	BQ707106 AGENCOURT
37	256.2	78.3	813	12	BG431143	BG431143 602498773
38	256	78.3	655	10	AV731325	AV731325 AV731325
39	255.6	78.2	867	12	BG539961	BG539961 602567476
40	254.8	77.9	712	12	BG538665	BG538665 602566902
41	254.4	77.8	1011	14	BM914591	BM914591 AGENCOURT
42	254	77.7	418	10	AW404507	AW404507 UI-HF-BL0
43	254	77.7	431	10	AW406886	AW406886 UI-HF-BL0
44	254	77.7	447	10	AW405752	AW405752 UI-HF-BL0
45	254	77.7	453	10	AW383563	AW383563 PM4-HT034

                              ALIGNMENTS

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LOCUS        BG684416               826 bp    mRNA      linear   EST 01-MAY-2001
DEFINITION   602636169F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763993 5',
             mRNA sequence.
ACCESSION    BG684416
VERSION      BG684416.1  GI:13915813
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 826)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1620 row: i column: 18
             High quality sequence stop: 826.
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                     /tissue_type="primary B-cells from tonsils (cell line)"
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                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

High quality sequence stop: 673.

BASE COUNT     242 a    266 c    231 g    217 t
ORIGIN

Query Match        92.4%;    Score 302;    DB 12;    Length 957;
Best Local Similarity 97.5%;    Pred. No. 1.8e-86;
Matches 318;    Conservative 0;    Mismatches 5;    Indels 3;    Gaps 1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db    53 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 112

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
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Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db   173 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 232

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db   293 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC 349

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
         ||||||||||||||||||||||||||
Db   350 CAAGGGACCAAGGTGGAAATCAAACG 375


RESULT 3
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LOCUS       BG341941         959 bp    mRNA    linear    EST 27-FEB-2001
DEFINITION  602463283F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576124 5',
            mRNA sequence.
ACCESSION   BG341941
VERSION     BG341941.1    GI:13148379
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 959)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4763993"
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                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT     199 a    253 c    191 g    183 t
ORIGIN

Query Match        92.4%;    Score 302;    DB 12;    Length 826;
Best Local Similarity 97.5%;    Pred. No. 1.6e-86;
Matches 318;    Conservative 0;    Mismatches 5;    Indels 3;    Gaps 1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
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Db   114 ATCACTTGCCGGGCGAGTCAGGGCATTAACAATTTTTTAGCCTGGTATCAGCAGAAACTA 173

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db   174 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 233

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db   234 CGGTTCAGTGGCAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 293

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         |||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db   294 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC 350

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db   351 CAAGGGACCAAGGTGGAAATCAAACG 376


RESULT 2
BG341934
LOCUS       BG341934         957 bp    mRNA    linear    EST 27-FEB-2001
DEFINITION  602463276F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576170 5',
            mRNA sequence.
ACCESSION   BG341934
VERSION     BG341934.1    GI:13148372
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 957)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1288 row: g column: 19
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         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLCM2502 row: g  column: 22
         High quality sequence stop: 655.

FEATURES             Location/Qualifiers
    source           1..888
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6295725"
                     /clone_lib="NIH_MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Supserscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT       212 a    274 c    200 g    202 t
ORIGIN

Query Match            88.9%;  Score 290.8;  DB 14;  Length 888;
Best Local Similarity  95.4%;  Pred. No. 7.2e-83;
Matches 311; Conservative  0;  Mismatches 12; Indels  3; Gaps  1;

Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60
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Db   76 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC  135

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAAACCA  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  136 ATCACTTGCCGGGCGAGTCAGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAAACCA  195

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGTCCCATCT  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  196 GGTAAAGTTCCTAACCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT  255

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  256 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  315

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC  300
         |||||||||||||||||||||||||||||||||||||||||      ||||||  ||||
Db  316 GAAGATGTTGCAACTTATTATTGTCAAAAGTATAACAGTGCCCCTC---ACACTTTCGGC  372

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG  326
         ||||||||||||||||||||||||||
Db  373 CCTGGGACCAAGGTGGATATCAAACG  398


RESULT 5
BM509065
LOCUS       BM509065                 626 bp    mRNA     linear      EST 15-FEB-2002
DEFINITION  ih16b08.x1 Human insulinoma Homo sapiens cDNA 3' similar to
            SW:KV1W_HUMAN P04431 IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.;
            mRNA sequence.
ACCESSION   BM509065
VERSION     BM509065.1  GI:18680208
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 626)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Bistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
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         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLCM1288 row: e  column: 21
         High quality sequence stop: 616.

FEATURES             Location/Qualifiers
    source           1..959
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4576124"
                     /clone_lib="NIH_MGC 48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Supserscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT       244 a    265 c    232 g    218 t
ORIGIN

Query Match            92.4%;  Score 302;  DB 12;  Length 959;
Best Local Similarity  97.5%;  Pred. No. 1.8e-86;
Matches 318; Conservative  0;  Mismatches  5; Indels  3; Gaps  1;

Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60
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Db   54 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC  113

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAAACCA  120
         |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db  114 ATCACTTGCCGGGCGAGTCAGGGCATTAACAATTTTTAGCCTGGTATCAGCAGAAAACTA  173

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCATCTGATCCACTTTGCAATCAGGGGTCCCATCT  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  174 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCATCTGATCCACTTTGCAATCAGGGGTCCCATCT  233

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  234 CGGTTCAGTGGCAGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  293

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC  300
         |||||||||||||||||||||||||||||||||||||||||       ||||||||||
Db  294 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC  350

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG  326
         ||||||||||||||||||||||||||
Db  351 CAAGGGACCAAGGTGGAAATCAAACG  376


RESULT 4
BQ881840
LOCUS       BQ881840                 888 bp    mRNA     linear      EST 16-AUG-2002
DEFINITION  AGENCOURT_8642888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295725
            5', mRNA sequence.
ACCESSION   BQ881840
VERSION     BQ881840.1  GI:22273848
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
```

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TITLE          , Jackson,Y. and Bowers,Y.
JOURNAL        Endocrine Pancreas Consortium
COMMENT        Unpublished (2000)
               Other_ESTs: ih16b08.y1
               Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
               Endocrine Pancreas Consortium
               Harvard University, Howard Hughes Medical Institute
               Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
               MA 02138
               Tel: 617-495-1812
               Fax: 617-495-8557
               Email: dmelton@biohp.harvard.edu
               Library was constructed by Dr. J. Ferrer In vivo mass-excised to
               pBluescript SK- by Dr. H. Inoue DNA sequencing by Washington
               University Genome Sequencing Center For information on obtaining a
               clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
               Possible reversed clone: similarity on wrong strand
               Seq primer: -40UP from Gibco
               High quality sequence stop: 481.
FEATURES
     source    1..626
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="Human insulinoma"
               /tissue_type="insulinoma"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
               XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
               (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
               pBluescript SK- by Dr. H. Inoue following the Washington
               University protocol
               (http://genome.wustl.edu/est/lambda_protocol.shtml).
               Please contact Hiroshi Inoue, MD/PhD for further
               information on this library (Metabolism Division, Permutt
               Laboratory, Washington University School of Medicine, Box
               8127,660 S Euclid Ave, St. Louis, MO 63110). Note: this
               is a Washington University Pancreas EST project library. "
BASE COUNT
ORIGIN      156 a        183 c       153 g      134 t

Query Match          87.5%;     Score 286; DB 13; Length 626;
Best Local Similarity 94.5%;    Pred. No. 2.1e-81;
Matches 308;   Conservative   0;  Mismatches  15;  Indels   3;  Gaps    1;

Qy       1 GACATCCAGATGACCCAGTCTCCATCCTCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db      54 GACATCCAGATGACCCAGTCTCCATCCTCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 113

Qy      61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db     114 ATCACTTGCCGGGCGAGTCAGGGCATTAGAAATTATGTAGCCTGGTATCAGCAGAAACCA 173

Qy     121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     174 GGGCAAGTTCCTAAGGTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 233

Qy     181 CGGTTCAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 CGGTTCAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 293

Qy     241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACGTTCGGC 300
           |||||||||||||||||||||||||||||||| |||||||||
Db     294 GAAGATGTTGCAACTTATTACTGTCAAAAGTATGCCAGCGCCCCCCC---CACTTTCGGC 350

Qy     301 CAAGGGACCAAGGTGAAAATCAAAACG 326
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Db     351 GGAGGGACCAAGGTGAGATCAAAACG 376
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RESULT 6
AW404145
LOCUS      AW404145         358 bp    mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BLo-abu-e-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
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```
ACCESSION  IMAGE:3057865 5', mRNA sequence.
VERSION    AW404145
KEYWORDS   AW404145.1  GI:6923202
SOURCE     EST.
  ORGANISM human.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 358)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: M.B. Soares Lab
           cDNA Library Arrayed by: M.B. Soares Lab
           DNA Sequencing by: M.B. Soares Lab
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Seq primer: M13 Forward
FEATURES
     source 1..358
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3057865"
            /clone_lib="NIH_MGC_37"
            /tissue_type="lymph"
            /cell_type="germinal center B cells"
            /cell_line="MGC85"
            /lab_host="DH10B (LTI)"
            /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT       80 a       107 c        83 g       88 t
ORIGIN

Query Match          85.1%;    Score 278.2; DB 10; Length 358;
Best Local Similarity 97.3%;   Pred. No. 5e-79;
Matches 283;  Conservative   0;  Mismatches   8;  Indels  0;  Gaps   0;

Qy       1 GACATCCAGATGACCCAGTCTCCATCCTCCCGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db      64 GACATCCAGATGACCCAGTCTCCATCCTCCCGTCTGCATCTGTAGGAGACAGAGTCACC 123

Qy      61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGGTATCAGCAGAAACCA 183

Qy     121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCACTTTGCAATCAGGGGTCCCATCT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCACTTTGCAATCAGGGGTCCCATCT 243

Qy     181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 CGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCATCAGCAGCCTGCAGCCT 303

Qy     241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTTCCGAGT 291
           ||||||||||||||||||||||||||||||||||   | |
Db     304 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTATAACGTCCCGCTCACT 354
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RESULT 7
BG342083
LOCUS      BG342083         935 bp    mRNA     linear   EST 27-FEB-2001
           602463029F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575847 5',
DEFINITION mRNA sequence.
ACCESSION  BG342083
VERSION    BG342083.1  GI:13148509
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DEFINITION   AGENCOURT_8475108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301597
             5', mRNA sequence.
ACCESSION    BQ707369
VERSION      BQ707369.1  GI:21846268
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 928)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2517 row: 1 column: 14
             High quality sequence stop: 651.
FEATURES             Location/Qualifiers
     source          1..928
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301597"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT     219 a    284 c    224 g    201 t
ORIGIN

Query Match          83.1%;  Score 271.6;  DB 14;  Length 928;
Best Local Similarity 89.6%;  Pred. No. 1.2e-76;
Matches  292;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db    69 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAAC 128

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
           |||||||||||||||||||||||  |||||||||   |||||||||||||||||||||
Db   129 ATCACTTGCCGGGCGAGTCAGGTCAGGTCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA 188

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTCATGCTGGACACTTTGCAATCAGGGGTCCCATCT 180
           |||||| ||||||||||||||||  |||||||||||||||  ||||||||||||||||
Db   189 GGGAAAGCCCCTAAGCTCCTGATCTCGTCGTCCTACTCTGTCTGCATCCTGATCCATCC 248

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db   249 AGGTTCAGTGGCAGTGGATCTGGGACACTTATTACACTCTCACCATCAGCAGCCTGCAGCCT 308

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTCCCTCCGGACGTTCGGC 300
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Db   309 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGAACCCCTCGGCTCACTTTCGGC 368

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db   369 GGAGGGACCAAGGTGGAGATCAAACG 394

RESULT 10
AW405753
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LOCUS        AW405753                 493 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION   UI-HF-BL0-abp-a-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
             IMAGE:3057290 5', mRNA sequence.
ACCESSION    AW405753
VERSION      AW405753.1  GI:6924810
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 493)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Eco RI site is shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..493
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3057290"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT     117 a    138 c    119 g    119 t
ORIGIN

Query Match          82.6%;  Score 270;  DB 10;  Length 493;
Best Local Similarity 91.4%;  Pred. No. 2.7e-76;
Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 131

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
           ||||||||||||||||||||||| |||||||   ||   |||||||||||||||||||||
Db   132 ATCACTTGCCGGGCGAGTCAGGGCAAGTCAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 191

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGGACACTTTGCAATCAGGGGTCCCATCT 180
           |||||| |||||||||||||||||| |||||||| ||||||||||||||||||||||||
Db   192 GGGAAAGCCCTAAGCTCCTGATCTATGCTGGACAGATTTCACTCTCACCATCAGCAGTCTGGAT 251

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db   252 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 311

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTTCCCTCCGGACGTTCGGC 300
           ||||||| |||||||||||||||||||  |||||  |||| |||||||  |||||||
Db   312 GAAGATTTTGCAACTTACTTACTGTCAACAGAGTTTACAGTTACCCCCTC---GGACGTTCGGC 368

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
           |||||||||||||||||||||||||
Db   369 CAAGGGACCAAGGTGGAAATCAAACG 394

RESULT 11
```

AW407904
LOCUS   AW407904   422 bp   mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3061128 5', mRNA sequence.
ACCESSION   AW407904
VERSION   AW407904.1 GI:6926961
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 422)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
     source   1..422
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3061128"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   106 a   110 c   105 g   101 t
ORIGIN

Query Match   82.1%; Score 268.4; DB 10; Length 422;
  Best Local Similarity   91.1%; Pred. No. 8.2e-76;
  Matches   297; Conservative   0; Mismatches   26; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 82

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
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Db   83 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCATTAAATTGGTATCAGCAGAAACCA 142

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAACAGGGTCCCATCT 180
              |||||| | ||||||||||||||||||||||||||||| ||||||| | |||||||||
Db   143 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCA 202

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db   203 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCT 262

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||| ||||||||||| | | || | || || | |||||||||
Db   263 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CCGTGGACGTTCGGC 319

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||||||||||
Db   320 CAAGGGACCAAGGTGGAAATCAAACG 345

RESULT 12
BG758398
LOCUS   BG758398   921 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602712592F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852678 5',
            mRNA sequence.
ACCESSION   BG758398
VERSION   BG758398.1 GI:14069051
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 921)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI697 row: h column: 23
            High quality sequence stop: 848.
FEATURES   Location/Qualifiers
     source   1..921
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4852678"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="Primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT   236 a   264 c   219 g   202 t
ORIGIN

Query Match   82.1%; Score 268.4; DB 12; Length 921;
  Best Local Similarity   89.0%; Pred. No. 1.3e-75;
  Matches   290; Conservative   0; Mismatches   36; Indels   0; Gaps   0;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 146

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| ||||| ||||||||| ||| ||| |||||||||||||||||
Db   147 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCATTAAATTGGTATCAGCAGAAACCA 206

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAACAGGGTCCCATCT 180
              |||||| | ||||||||||||||||||||||||||||| ||||||| | |||||||||
Db   207 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCA 266

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   267 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCT 326

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||| ||||||||||| | | || | ||| ||||| | |||||||||
Db   327 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTATCCCTCCGGGACTTTCGGC 386

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||||||||||

Db   387 CCCGGGGACCAAACTGATATCAAACG 412

RESULT 13
AV733746
LOCUS   AV733746   422 bp   mRNA   linear   EST 17-OCT-2000
DEFINITION   AV733746 cdA Homo sapiens cDNA clone cdAATB08 5', mRNA sequence.
ACCESSION   AV733746
VERSION   AV733746.1 GI:10851291
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 422)
AUTHORS   Yang,Y., Song,H., Peng,Y., Gu,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
             Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
             ,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
             Chen,Z. and Han,Z.
TITLE   Homo sapiens cDNA cdA clones
JOURNAL   Unpublished (2000)
COMMENT   Contact: Zeguang Han
             Chinese National Human Genome Center at Shanghai
             351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
             201203, P.R. China
             Tel: 86-21-50801919(ex.45)
             Fax: 86-21-50801922
             Email: hanzg@chgc.sh.cn
             This clone is available at CHGC in Shanghai.
FEATURES   Location/Qualifiers
     source   1..422
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="cdAATB08"
                     /clone_lib="cdA"
                     /tissue_type="pheochromocytoma"
                     /dev_stage="Adult"
                     /lab_host="BM25.8"
                     /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
BASE COUNT   88 a   118 c   117 g   99 t
ORIGIN

Query Match   81.1%;   Score 265.2; DB 10; Length 422;
Best Local Similarity   89.6%;   Pred. No. 8.9e-75;
    Matches 285; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db   91 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 150

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||
Db   151 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAGTCTTTAGCCTGGTATCAGCAGAAACCA 210

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GGGAAAGCCCCTAAGCTCCTGGTGTCTATGTCATCCAGATTGGGAAGTGGGGTCCCAGCC 270

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db   271 AGGTTCAGTGGCAGTGGATCTGGGACGGACAGTCTCACAGTCTCTCCAGCCT 330

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGGAGTTCGGC 300
          ||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   331 GACGATTTTGCAATTTATTACTGTCAACAGTATATAGTTCCCCTCCGGTGACGTTCGGC 390

Qy   301 CAAGGGACCAAGGTGGAA 318
          |||||||||||||||||||
Db   391 CAAGGGACCAAGGTGGAA 408

RESULT 14
BM543718

Db   BM543718
DEFINITION AGENCOURT_6492277 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589037
           5', mRNA sequence.
ACCESSION BM543718
VERSION   BM543718.1 GI:18774347
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1153)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Invitrogen
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM12361 row: b column: 14
           High quality sequence start: 8
           High quality sequence stop: 539.
FEATURES   Location/Qualifiers
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                  /clone="IMAGE:5589037"
                  /clone_lib="NIH_MGC_125"
                  /lab_host="DH10B"
                  /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                  Site 1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                  of three ovaries, from females ranging in age from 38 to
                  49 yo. Library is oligo-dT primed and directionally cloned
                  (EcoRV site is destroyed upon cloning). Average insert
                  size 2.1 kb, insert size range 1-3.5 kb. Library is
                  normalized and enriched for full-length clones and was
                  constructed by C. Gruber (Invitrogen). Research Genetics
                  tracking code 036."
BASE COUNT   .295 a   334 c   272 g   246 t
ORIGIN

Query Match   81.1%;   Score 265.2; DB 13; Length 1153;
Best Local Similarity   88.3%;   Pred. No. 1.6e-74;
    Matches 288; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db   97 GGCATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 156

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTATTAGCCTGGTATCAGCAGAAACCA 120
          ||||||||||||||||| |||| ||||||||| ||||| |||||||||||||||||||
Db   157 ATCACTTGCCGGGCGAGTCAGGGCTTCGGCAACTATTTAAATTGGTATCAGCAGAAAACCA 216

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db   217 GGGAAAGCCCCCACCCTCCTGATCTACGAGGCATCCAATTTGCAACCAGGGGTCCCATCA 276

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db   277 AGGTTCAGTGGGAGTGGATCTGGGACAGATTTTACTTTACTTTCACCATCAGCAGCCTGCAGCCT 336

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGGAGTTCGGC 300
          |||||| ||||| |||||||||| |||||||||||| |||| ||| |||||||||||
Db   337 GAAGATATTGCAACATATTACTGTCAACAGTTTGATACTGTCCCCTCGTGACGTTCGGC 396

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db   397 CGAGGGACCAAGGTGGAAATCAAACG 422

Search completed: July 18, 2003, 09:26:04
Job time : 568.66 secs

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RESULT 15
AW404992
LOCUS        AW404992               391 bp    mRNA      linear    EST 16-FEB-2000
DEFINITION   UI-HF-BL0-abx-a-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
             IMAGE:3058060 5', mRNA sequence.
ACCESSION    AW404992
VERSION      AW404992.1  GI:6924049
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 391)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3058060"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA.
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT       98 a      108 c      94 g      91 t
ORIGIN

Query Match        80.6%;    Score 263.6;   DB 10;   Length 391;
Best Local Similarity  90.2%;   Pred. No. 2.8e-74;
Matches 294;   Conservative   0;   Mismatches  29;   Indels   3;   Gaps   1;

Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   65 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 124

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
          ||||||||||||||||||| ||||||| || ||||||||  |||||||||||||| | |
Db  125 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAATCA 184

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAATCAGGGGTCCCATCT 180
          ||||||  |||||| | ||||||||| || |||||||| ||||||||||| |||||||
Db  185 GGGAAAGCCCCTAAGCTCCTGATCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 244

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          |||||||||||||| |||||| ||||||||||||||||||||||| |||||||  ||  |
Db  245 AGGTTCAGTGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 304

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
          |||||  ||||| ||||| ||||||||| ||  | || || |||| |||||||||||||
Db  305 GAAGATTTTGCAATTTACTACTGTCAGCAGAGTTACAGTATCCCTCC---TACGTTCGGC 361

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG 326
          |||||||||||||||||||||||||
Db  362 CAAGGGACCAAGGTGGAAATCAAACG 387
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OM nucleic - nucleic search, using sw model

Copyright   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 18, 2003, 04:14:58 ; Search time 84.7713 Seconds
          (without alignments)
          8686.944 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	298.4	91.3	761	24	ABK47271	Insulin/insulin-li
3	295.2	90.3	752	24	ABK47272	Insulin/insulin-li
4	295.2	90.3	752	24	ABK47274	Insulin/insulin-li
5	295.2	90.3	761	24	ABK47276	Insulin/insulin-li
6	279.2	85.4	321	18	AAT88403	cDNA for anti-TNF-
7	278	85.0	632	24	ABK40186	Human/rabbit Ckapp
8	276.4	84.5	565	24	ABG58923	Human colon cancer
9	274.8	84.0	737	24	AAD31829	Human pancreatic t
10	274.4	83.9	306	24	AAB94230	CB2iE7 kappa light
11	271.6	83.1	936	21	AAA27390	Human IGFAM-10 imm
12	270	82.6	396	18	AAT75423	Human anti-tumour
13	270	82.6	720	20	AAX36070	DNA encoding a sin
14	270	82.6	729	21	AAA11630	Human immunoglobul
15	270	82.6	729	24	ABL46009	Humanised anti-Fas
16	270	82.6	917	21	AAA27381	Human IGFAM-1 immu
17	270	82.6	1106	24	ABQ54241	Human ovarian anti
18	269.6	82.4	318	19	AAV19745	Antibody LD1-117-v
19	269.4	82.4	324	22	AAH42395	Nucleotide sequenc
20	269	82.3	322	22	AAF55231	DNA sequence of li
21	269	82.3	322	22	AAF55238	TRO005 kappa chain
22	268.4	82.1	684	22	AAH30051	Sequence encoding
23	268.4	82.1	702	22	AAQ43773	Anti-murine CTLA-4
24	266.2	81.4	730	14	AAZ29000	Human monoclonal a
25	264.8	81.0	321	24	AAB06023	Coding sequence fo
26	263.6	80.7	341	18	AAT60117	Anti-human AILIM m
27	263.6	80.6	974	24	AAS99473	Human anti-Rh(D) c
28	263.4	80.6	324	22	AAH68646	Human anti-Rh(D) c
29	263.4	80.6	324	22	AAH68657	Insulin/insulin-li
30	263.2	80.5	758	24	ABK47277	TRO005 kappa chain
31	262	80.1	672	22	AAH30049	Human anti-Rh(D) c
32	261.8	80.1	324	22	AAH68655	Human anti-Rh(D) a
33	261.8	80.1	324	22	AAH68712	Nucleotide sequenc
34	261.4	79.9	333	22	AAH74684	Nucleotide sequenc
35	261.4	79.9	900	24	AAH74688	Light chain DNA fr
36	260.4	79.6	324	24	ABK41157	Human antibody CAT
37	260.4	79.6	326	22	AAD18149	Human cancer cell
38	260.4	79.6	333	15	AAX79686	Human coding seque
39	260.4	79.6	438	22	AAH41157	Human colon tumour
40	260.4	79.6	497	24	ABL38222	DNA encoding the k
41	260.4	79.6	714	21	AAA46899	Human endoglin (CD
42	260.2	79.6	321	24	AAL45699	Antibody ITA7 enco
43	260.2	79.6	723	20	AAX86938	Antibody ITA7 comp
44	260.2	79.6	723	20	AAX86939	Human endoglin (CD
45	260.2	79.6	921	24	AAL45702	

ALIGNMENTS

RESULT 1
ABK47275
ID   ABK47275 standard; DNA; 743 BP.
XX
AC   ABK47275;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #29.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI   Hansen PH, Ravera M, Hsiao K;

XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors -
XX
PS   Disclosure; Figure 39; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research reagents. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 743 BP; 163 A; 195 C; 218 G; 167 T; 0 other;

Query Match   93.2%; Score 304.8; DB 24; Length 743;
Best Local Similarity   98.5%; Pred. No. 4.5e-87;
Matches   319; Conservative   0; Mismatches   2; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   415 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 474

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 534

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 594

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   595 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 654

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   655 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TGGACGTTCGGC 711

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
              ||||||||||||||||||||||||
Db   712 CAAGGGACCAAGGTGGAAATCAAA 735

RESULT 2
ABK47271
ID   ABK47271 standard; DNA; 761 BP.
XX
AC   ABK47271;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #25.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.

XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI   Hansen PH, Ravera M, Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors -
XX
XX
PS   Example 1; Figure 19; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research reagents. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 761 BP; 179 A; 201 C; 219 G; 162 T; 0 other;

Query Match   91.3%; Score 298.4; DB 24; Length 761;
Best Local Similarity   97.2%; Pred. No. 5e-85;
Matches   315; Conservative   0; Mismatches   6; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 492

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 552

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 612

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 672

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---TCACTTTCGGC 729

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
              ||||||||||||||||| |||||
Db   730 GGAGGGACCAAGGTGGAGATCAAA 753

RESULT 3
ABK47272
ID   ABK47272 standard; DNA; 752 BP.
XX
AC   ABK47272;
XX

us-09-627-896b-25.rng

Sat Jul 19 10:01:58 2003

```
DT   18-JUN-2002 (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #26.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; tumour; prostate; breast;
KW   insulin-like growth factor-1; IGF-1; neurological diseases; stroke;
KW   diabetic retinopathy; gene; ss.
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
OS   WO200172771-A2.
PN
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528 LLC.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Ravera M, Hsiao K;
PI   Hansen PH, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
XX
DR   WPI; 2002-025774/03.
XX
XX   Modulating insulin activity in mammalian cells, comprises using peptides that bind to insulin
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors
XX
PS   Disclosure; Figure 36; 390pp; English.
CC
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian (IR). A composition containing Site 1 of IR and an insulin
CC   receptor therapy vectors that diabetes. Also, peptides that are
CC   from gene therapy for treating insulin-like growth factor-1 (IGF)-sensitive tumours
CC   agonists of treating insulin-like growth factor (IGF)-1 receptor are
CC   antagonists of ting insulin) and diabetic retinopathy, and diabetic neurological diseases, also useful in
CC   useful for prostate are useful for treating. The peptides are potential IR
CC   (e.g. of agonists and diabetic neuropathy or IGF-1 receptor) while IGF-1
CC   receptor stroke and diabetic bind to IR ABK4246-ABK4277 represent IR
CC   including for compounds reagents of the invention.
CC   screening for and research DNA sequences of the invention.
CC   therapeutics and research DNA sequences of the invention.
CC   and/or IGF-1 receptor DNA sequences that binds. ABK47246.
XX
SQ   Sequence 752 BP; 177 A; 196 C; 217 G; 162 T; 0 other;
```

Query Match Similarity 90.3%; Score 295.2; DB 24; Length 752;
Best Local Similarity 96.6%; Pred. 5.2e-84; Indels 8; Gaps 3;
Matches 313; Mismatches 0; Mismatches

```
Qy      1 GACATCCAGATGACCAGTTCCCATCCTCCCCTGTCTGCATCTGTGCATCTGTAGGAGACAGAGTCACC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GACATCCAGATGACCCAGTTCCCATCCTCCCCTGTCTGCATCTGTGCATCTGTAGGAGACAGAGTCACC 483

Qy     61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy    121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAATCAGGGGTCCCATCT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 GGGAAAGTTCCTAAGCTCCTGATCTGGGACAGATTTCACTCCTCACCATCAGCAGCCTGCAGCCT 603

Qy    181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 CGGTTCAGTGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy    241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCC 300
          |||||||||||||||
Db    664
```

```
Db    664 GAAGATGTTGCAACTTATTACTGTCAAAATCAAA 324
          |||||||||||||||| |||||||||| ||||
Qy    301 CAAGGACCAAGGTGGAAATCAAA 744
          |||||||||||||||
Db    721 CCTGGGACCAAAGTGGATATCAAA
```

```
RESULT 4
ABK47274
ID   ABK47274 standard; DNA; 752 BP.
XX
AC   ABK47274;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #28.
XX
KW   Cytostatic; antidiabetic; neuroprotective; receptor; gene; prostate; breast;
KW   ophthalmological; insulin; receptor-1; IGF-1; tumour; stroke;
KW   insulin retinopathy; gene; ss.
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
OS   WO200172771-A2.
PN
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528 LLC.
XX
PA   (DGIB-) DGI NOVO NORDISK AS.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI   Hansen PH, Ravera M, Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
XX   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors
XX
PS   Disclosure; Figure 38; 390pp; English.
CC   Modulating insulin activity in
CC   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors
PS   Disclosure; Figure 38; 390pp; English.
XX
XX   The invention relates to a method of modulating insulin binds the insulin activity in
PS   mammalian cells by administering a peptide, optionally and insulin
XX   The invention cells by administering containing Site 1 of peptides that are
XX   mammalian (IR). A composition binds to Also, peptides that an are
CC   receptor therapy vectors that diabetes. Also, peptides that optional insulin
CC   from gene therapy for insulin-like growth factor (IGF)-1 receptor tumours
CC   agonist are the insulin-like growth factor (IGF)-sensitive tumours
CC   antagonist are the insulin-like growth factor (IGF) while IGF-1
CC   useful of prostate are useful for treating. The peptides are potential IR
CC   (e.g. of agonists and diabetic bind to IR ABK47246-ABK47277.
CC   receptor stroke and diabetic bind to IR of IGF-1 receptor. to represent IR
CC   including for compounds reagents. ABK47246-ABK47277.
CC   screening and research reagents of the invention.
CC   therapeutics and research DNA sequences of the invention.
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 752 BP; 162 A; 195 C; 221 G; 174 T; 0 other;
```

Query Match Similarity 90.3%; Score 295.2; DB 24; Length 752;
Best Local Similarity 96.6%; Pred. No. 5.2e-84; Indels 8; Gaps 1;
Matches 313; Mismatches 0; Mismatches

```
Qy      1 GACATCCAGATGACCCAGTCTCCATCCTCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
Db    424 GACATCCAGATGACCCAGTCTCCATCCTCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy    424 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGGTATCAGCAGAAACCA 120

Db    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy    484 CGGTTCAGTGGCAGTGGATCTGGGACAGATTATTTAGCCTGTATCAGCAGAAACCA

Db    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGTATCAGCAGAAACCA

Qy    424 GACATCCAGATGACCCAGTGCCCAGTCTCCATCCTCCCCTGTCTGCATCTGTGCATCTGTAGGAGACAGAGTCACC 120
```

```
                |||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 ATCACTTGCCGGCCGAGTCAGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCAGGGGTCCCATCT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCAGGGGTCCCATCT 603

Qy   181 CGGTTCAGTGGCAGTGGATCGGGACAGATTTCACTCTCCACCATCAGCAGCCTGCAGCCT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 CGGTTCAGTGGCAGTGGATCGGGACAGATTTCACTCTCCACCATCAGCAGCCTGCAGCCT 663

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         |||||||||||||||||||||||||||||||||||||||||||||    |||| ||||||
Db   664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TACACTTTTGGC 720

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
         ||||| ||||||  ||||||||||
Db   721 CAGGGGACCAAGCTGGAGATCAAA 744
```

RESULT 5
ABK47276
ID   ABK47276 standard; DNA; 761 BP.
XX
AC   ABK47276;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #30.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI   Hansen PH, Ravera M, Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors -
XX
PS   Disclosure; Figure 57; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research reagents. ABK47246-ABK47277 represent IR

CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 761 BP; 179 A; 200 C; 217 G; 165 T; 0 other;

```
Query Match             90.3%;  Score 295.2;  DB 24;  Length 761;
Best Local Similarity   96.6%;  Pred. No. 5.2e-84;
Matches 313;  Conservative .0;  Mismatches 8;  Indels 3;  Gaps 1;

Qy     1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
         ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db   433 GACATCCAGATGACCCAGTCTCCATCCTCCCCGTGTGCATCTGTGTAGGAGACAGAGTCACC 492

Qy    61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
         |||||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||
Db   493 ATCACTTGCCGGCCGAGTCAGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 552

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCAGGGGTCCCATCT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCAGGGGTCCCATCT 612

Qy   181 CGGTTCAGTGGCAGTGGATCGGGACAGATTTCACTCTCCACCATCAGCAGCCTGCAGCCT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 CGGTTCAGTGGCAGTGGATCGGGACAGATTTCACTCTCCACCATCAGCAGCCTGCAGCCT 672

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         |||||||||||||||||||||||||||||||||||||||||||||    || |||||||
Db   673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCCT---TTCACTTTCGGC 729

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
         |  ||||||||| ||| ||||||
Db   730 CCTGGGACCAAGTGGATATCAAA 753
```

RESULT 6
AAT88403
ID   AAT88403 standard; cDNA; 321 BP.
XX
AC   AAT88403;
XX
DT   19-MAR-1998 (first entry)
XX
DE   cDNA for anti-TNF-alpha antibody light chain variable region.
XX
KW   Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
KW   light chain; variable region; inhibition;
KW   treatment; sepsis; disease; autoimmune disease; infectious disease;
KW   malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW   cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW   bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW   keloid formation; scar tissue formation; pyrexia; HUVEC;
KW   periodontal disease; obesity; radiation toxicity;
KW   endothelial cell leukocyte adhesion molecule-1;
KW   human umbilical vein endothelial cell; ds.
XX
OS   Homo sapiens.
XX
PN   WO9729131-A1.
XX
PD   14-AUG-1997.
XX
PF   10-FEB-1997; 97WO-US02219.
XX
PR   25-NOV-1996; 96US-0031476.
PR   09-FEB-1996; 96US-0599226.
XX
PA   (BADI) BASF AG.
XX
PI   Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B;
PI   Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P;
PI   Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
XX
DR   WPI; 1997-415302/38.
DR   P-PSDB; AAW27568.

XX
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
XX
PS Disclosure; Page 75; 102pp; English.
XX
CC The present sequence encodes a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
XX
SQ Sequence 321 BP; 85 A; 87 C; 74 G; 75 T; 0 other;

Query Match   85.4%;   Score 279.2; DB 18; Length 321;
Best Local Similarity 93.5%;   Pred. No. 4.8e-79;
Matches 303; Conservative   0; Mismatches 18; Indels 3; Gaps 1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   61 ATCACTTGTCGGGCAAGTCAGGGCATCAGAAATTACTTAGCCTGGTATCAGCAAAAACCA 120

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
          ||| ||| |||||||||||||||||| ||||||||||||| |||||||||||||||||||
Db   121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT 240

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAACAGTGCCCCTCCGAGTACGTTCGGC 300
          ||||||||||||||||||||||||| |||||||||| ||| ||||||||||||||||
Db   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACCGTG---CACCGTATACTTTTGGC 297

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
          || |||||||||||||||||||||
Db   298 CAGGGGACCAAGGTGGAAATCAAA 321

RESULT 7
ABK40186
ID ABK40186 standard; DNA; 632 BP.
XX
AC ABK40186;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human/rabbit Ckappa chimaeric DNA sequence.
XX
KW Antibody; Cgamma; Ckappa; Clambda2; ds; transgenic; vector;
KW infectious disease; malignancy; cancer; tumour; autoimmune disease;
KW humanised immunoglobulin; cytostatic; antibacterial; virucide;
KW fungicide; light chain variable region; heavy chain variable region;
KW Ig.
XX

XX
OS Chimeric - Oryctolagus cuniculus.
OS Chimeric - Homo sapiens.
XX
PN WO20021243 7-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-US24348.
XX
PR 03-AUG-2000; 2000US-222872P.
PR 15-MAR-2001; 2001US-276156P.
XX
PA (SCHO/) SCHOOTEN W.
PA (BUEL/) BUELOW R.
PA (PLAT/) PLATZER J.
PA (BUEL/) BUELOW J.
XX
PI Schooten W, Buelow R, Platzer J, Buelow J;
XX
DR WPI; 2002-217188/27.
XX
PT Novel humanised antibodies useful for treating diseases caused by
PT bacterial, viral, fungal infection and cancer, are derived from
PT transgenic non-human animals engineered to contain humanised
PT immunoglobulin loci -
XX
PS Claim 12; Fig 11; 81pp; English.
XX
CC The invention relates to a humanised immunoglobulin derived from a
CC transgenic animal, comprising a portion of a human immunoglobulin
CC polypeptide sequence (e.g. form immunoglobulin Cgamma, Ckappa or
CC Clambda). Also included are 1) nucleic acid molecules comprising the
CC 3' flanking regions of cow, sheep and rabbit Cgamma, the 3' flanking
CC region of rabbit Ckappa and the 5' flanking region of rabbit Cgamma,
CC 2) a recombination vector for replacing an Ig gene segment from
CC a non-human animal with a human immunoglobulin (Ig) gene segment,
CC comprising from 5' to 3', a 5' nucleotide sequence; the human Ig gene
CC segment, and a 3' nucleotide sequence, where the 5' and 3' nucleotide
CC sequences are homologous to the 5' and 3' flanking sequences of the Ig
CC gene segment from the non-human animal, 3) a transgenic vector comprising
CC a humanised Ig locus derived from an Ig locus or a portion of an Ig locus
CC of a non-human animal, where the locus comprises multiple Ig gene
CC segments, where at least one of the gene segments is a human Ig gene
CC segment, and the gene segments are juxtaposed in an unrearranged,
CC partially or fully rearranged configuration, and the locus is capable of
CC undergoing gene conversion and producing a repertoire of humanised Igs in
CC the non-human animal and 3) a transgenic animal comprising a humanised
CC Ig locus. The antibody is useful for treating a disease caused by
CC bacterial, fungal or viral infection, cancer or an autoimmune disease in
CC a human. The vector is useful for replacing rabbit light or heavy chain
CC constant or variable region gene, or a chicken light chain constant
CC region gene. The transgenic vector is useful for making a transgenic
CC non-human animal capable of producing a functional repertoire of
CC humanised antibodies, by introducing the construct into a recipient cell
CC of a non-human animal and integrating the humanised Ig loci in the
CC transgenic construct into the genome of the recipient cell. The animal
CC is rabbit having an impaired expression of endogenous Ig molecules, and
CC the recipient cell is a cell in an early embryo, or is a chicken and
CC the recipient cell is a fertilised egg. Alternatively, transgenic
CC non-human animals capable of producing a functional repertoire of
CC humanised heavy or light chains, respectively are mated and an
CC offspring is selected which produces both humanised heavy and light
CC chains. The Cgamma DNA is useful for creating a humanised Ig locus
CC and making transgenic animals capable of producing humanised Ig
CC molecules. The present sequence is a recombination vector of invention.
XX
SQ Sequence 632 BP; 149 A; 169 C; 143 G; 171 T; 0 other;

Query Match   85.0%;   Score 278; DB 24; Length 632;
Best Local Similarity 92.9%;   Pred. No. 1.5e-78;
Matches 303; Conservative   0; Mismatches 20; Indels 3; Gaps 1;

Qy   2 ACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCA 61

CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists.
XX
SQ   Sequence 565 BP; 128 A; 155 C; 142 G; 134 T; 6 other;

Query Match   84.5%;   Score 276.4;   DB 24;   Length 565;
Best Local Similarity   92.6%;   Pred. No. 4.6e-78;
Matches 302;   Conservative   0;   Mismatches 21;   Indels   3;   Gaps   1;

```
Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC    60
        ||||||||||||||||||||||||| |||||||||||  |||||||| |||||||||||||
Db  104 GACATCCAGATGACCCAGTCTCCATCTTTCCTGTCTGCATCTGTAGGAGACAGAGTCACC   163

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA   120
        ||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||||
Db  164 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCAATTATTTAGCCTGGTATCAGCAGAAACCA   223

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTGCAATCCACTTGCAATCCACATCT  180
        ||||||||||||||||||||||||||| |||| |||||||||||||||||| |||||||||
Db  224 GGGAAAGTTCCAAAGTCCTGATCTATGCTGCATCCACTTGCAAGCTGGGGTCCCATCT   283

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  240
        ||||||||||||||||||||  ||||||||||||||||||| |||||||||||||||||||
Db  284 CGGTTCAGTGGGCGGTGCTTCTGGGACAGAGTTCACTCTCACCATCAGTAGCCTGCAGCCT  343

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATATAACAGTGCCCCTCCGAGTACGTTCGGC  300
        |||||||||||||||||| |||||||||||||||||||||||| |||| ||| |||||||||
Db  344 GAAGATGCTGCCGCATTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC  400

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG  326
        |||||||||||||||||||||||||||
Db  401 CAGGGGACCAAGGTTGGAGATCAAACG  426
```

RESULT 9
AAD31829
ID   AAD31829 standard; cDNA; 737 BP.
XX
AC   AAD31829;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Human pancreatic tumour protein encoding cDNA clone 53796.2.
XX
KW   Human; pancreatic tumour protein; pancreatic cancer; therapy; diagnosis;
KW   cancer; vaccine; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO20212327-A2.
XX
PD   14-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US23969.
XX
PR   03-AUG-2000; 2000US-223102P.
PR   21-SEP-2000; 2000US-234451P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Pyle RA, Xu J;
XX
DR   WPI; 2002-241738/29.
XX
PT   New polynucleotides derived from pancreatic tumour cDNA library, useful
PT   as vaccines for preventing and treating pancreatic cancer, as well as
PT   for the diagnosis and monitoring of such cancers -
XX
PS   Claim 1; Page 107; 120pp; English.
XX
CC   The invention relates to polynucleotides derived from pancreatic tumour
CC   cDNA library, encoding pancreatic tumour proteins. The invention also

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Db  242 ACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTGGGAGACAGAGTCACCA   301

Qy   62 TCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCAG   121
        ||||||||| || ||||||||||||||||||| ||||||||||||||||||||||||||
Db  302 TCACTTGCCAGCCAGTCAGGGCATTAGCAATTACTTAGCCTGGTATCAGCAGAAACCAG   361

Qy  122 GGAAAGTTCCTAAGCTCCTGATCTGTGCATCCACTTGCAATCAGGGGGTCCCATCTC   181
        |||||||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db  362 GGAAGGTTCCCAAGCTCCTGATTTATGCTGCATCCACTTGCAATCTGGGGTCCCATCGC   421

Qy  182 GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG   241
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  422 GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG   481

Qy  242 AAGATGTTGCAACTTATTACTGTCAAAAGTATATAACAGTGCCCCTCCGAGTACGTTCGGCC   301
        ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  482 AAGATGTTGCCACCTATTACTGTCAAAAGTACAACAGTGCCCCTCACTT---TTCGGCG   538

Qy  302 AAGGGACCAAGGTGGAAATCAAACGT  327
        |||||||||||||||||||||||||
Db  539 GAGGGACCAAGGTGGAGATCAAACGT  564
```

RESULT 8
ABQ58923
ID   ABQ58923 standard; cDNA; 565 BP.
XX
AC   ABQ58923;
XX
DT   02-AUG-2002 (first entry)
XX
DE   Human colon cancer related nucleotide sequence SEQ ID NO:2618.
XX
KW   Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW   genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO20229086-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US30732.
XX
PR   02-OCT-2000; 2000US-237271P.
XX
PA   (FARB) BAYER CORP.
XX
PI   Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI   Thiaglingam A, Lewis ME;
XX
DR   WPI; 2002-426115/45.
XX
PT   New isolated nucleic acid that is differentially expressed in cancer
PT   tissues useful for determining the presence of colon cancer in a cell
PT   or tissue type, and in antisense therapy -
XX
PS   Claim 1; Fig 1; 796pp; English.
XX
CC   ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC   expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC   encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC   used in antisense therapy. An antibody immunoreactive with a polypeptide
CC   encoded by (I) is useful for detecting cancer in a patient sample, and
CC   for detecting the presence or absence of a polynucleotide encoded by a
CC   nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC   from (I) can be used for determining the presence of a nucleic acid which
CC   hybridises to (I), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (I) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence or
CC   state of other type of cancer, in antisense therapy, to generate
CC   macroarrays on a solid surface, to identify a chromosome on which the

CC relate; to therapy and diagnosis of cancer, such as pancreatic cancer.
CC The polypeptides and polynucleotides of the invention are useful as
CC vaccines and pharmaceutical compositions for preventing and treating
CC pancreatic cancer, as well as for the diagnosis and monitoring of such
CC cancers. The present sequence is human pancreatic tumour protein
CC encoding cDNA.
XX
SQ Sequence 737 BP; 188 A; 211 C; 181 G; 153 T; 4 other;

Query Match 84.0%; Score 274.8; DB 24; Length 737;
Best Local Similarity 90.2%; Pred. No. 1.7e-77;
Matches 294; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```
Qy    1 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   143

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA  120
         |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  144 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA  203

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTGCAATCAGGGGTCCCATCT  180
         ||||   |||||||||||| |  ||||||| ||||| |||||  ||| ||||||||||||
Db  204 GGGAGTGCCCCTAAGCTCCTACTCCATGCTGTATCCAACTTGGAAAGTGGGGTCCCATCC  263

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT  240
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  264 AGGTTCAGTGGCAGTGGATCTGGGACGGATTCACTCTCACCATCAGCAGCCTGCAGCCT  323

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC  300
         ||||| |||||||||||||||||||||  ||||  || |  || || ||  || |||||
Db  324 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTAACCCTCCGTCACTTTCGGC  383

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG  326
         |||||||||||||||| ||||||||
Db  384 GGAGGGACCAAGGTGGAGATCAAACG  409
```

RESULT 10
ABA94230
ID ABA94230 standard; DNA; 306 BP.
XX
AC ABA94230;
XX
DT 13-MAR-2002 (first entry)
XX
DE CB2iE7 kappa light chain variable region nucleotide sequence.
XX
KW Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..306
FT /*tag= a
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US14902.
XX
PR 10-MAY-2000; 2000US-0568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
DR P-PSDB; ABB07183.
XX

PT Novel neuromodulatory agent (a human IgM monoclonal antibody),
PT promoting neurite outgrowth, regeneration, remyelination and
PT neuroprotection in central nervous system, useful to treat
PT post-infectious encephalomyelitis -
XX
PS Claim 43; Fig 42; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating denvelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture.
CC (I) is also useful for stimulating remyelination of CNS axons. The
CC antibodies are useful for preventing infection by a bacterium, virus or
CC like pathogen that causes demyelination or other neurodegenerative
CC condition in a subject. Methods where (I) is administered to a patient
CC are useful for treating multiple sclerosis, Parkinson's disease,
CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
CC demyelinating disease, CNS diseases, and other conditions in the CNS
CC where nerves are damaged as by trauma. The present sequence represents
CC the CB2iE7 kappa light chain variable region nucleotide sequence.
XX
SQ Sequence 306 BP; 77 A; 84 C; 70 G; 75 T; 0 other;

Query Match 83.9%; Score 274.4; DB 24; Length 306;
Best Local Similarity 97.9%; Pred. No. 1.6e-77;
Matches 278; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy    1 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GACATCCAGATGACCCAGTCTCCATCCCCTGTCTGCATCTGTAGGAGACAGAGTCACC    60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA  120

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCCACTTTGCATCCCATCT  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCCACTTTGCATCCCATCT  180

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT  240

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTATAACAAGTGCCC  284
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTATAACAAGTGCCC  284
```

RESULT 11
AAA27390
ID AAA27390 standard; cDNA; 936 BP.
XX
AC AAA27390;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-10 immunoglobulin coding sequence.
XX
KW Human; immunoglobulin; IGFAM; IGFAM-10; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy; ss.
XX

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             19..732
FT                   /*tag=  a
FT                   /product= "IGFAM-10"
FT   sig_peptide     19..84
FT                   /*tag=  b
FT   mat_peptide     85..729
FT                   /*tag=  c
XX
PN   WO200029583-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US27566.
XX
PR   19-NOV-1998;   99US-0113635.
PR   22-DEC-1998;   98US-0113635.
PR   07-APR-1999;   99US-0128194.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Yue H,  Tang YT,  Corley NC,  Guegler KJ,  Gorgone GA,  Baughn MR;
PI   Lu DAM,  Lal P,  Hillman JL,  Yang J;
XX
DR   WPI; 2000-387796/33.
DR   P-PSDB; AAY96298.
XX
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders
PT   -
XX
PS   Claim 9; Page 99-100; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-10 gene, which was isolated from a cDNA library of colon
CC   tissue. It is expressed in reproductive, gastrointestinal and
CC   cardiovascular tissue, where cancer and inflammation are common. The
CC   gene, protein, its antibodies, agonists and antagonists are suitable for
CC   diagnosing and treating many diseases, including cancer, immune system
CC   disorders (such as inflammation, AIDS, allergies, anaemia,
CC   arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC   disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC   multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC   systemic lupus erythematosus and ulcerative colitis), complications of
CC   cancer, haemodialysis and extracorporeal circulation, trauma and
CC   haematopoietic cancer (such as leukaemia) and infections caused by
CC   bacteria, viruses, fungi or parasites.
XX
SQ   Sequence 936 BP; 239 A; 276 C; 214 G; 207 T; 0 other;

  Query Match            83.1%;  Score 271.6;  DB 21;  Length 936;
  Best Local Similarity  89.6%;  Pred. No. 1.9e-76;
  Matches  292;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 144

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        145 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 204

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||| |||||||   |||||||||||
Db        205 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 264

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        265 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 324
```

```
Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||  | ||||| |||||||||  || ||||||
Db        325 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGATCACCTTCGGC 384

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||     |||| || |||||
Db        385 CAAGGGACACGACTGGAGATTAAACG 410

RESULT 12
AAT75423
ID   AAT75423 standard; cDNA; 396 BP.
XX
AC   AAT75423;
XX
DT   12-SEP-1997  (first entry)
XX
DE   Human anti-tumour antigen antibody light chain variable region cDNA.
XX
KW   Human; tumour antigen; cancer; monoclonal; antibody; light chain;
KW   variable region; medicine; pharmacology; biochemistry; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..66
FT                   /*tag=  a
FT   mat_peptide     67..396
FT                   /*tag=  b
XX
PN   JP09100300-A.
XX
PD   15-APR-1997.
XX
PF   03-OCT-1995;   95JP-0278266.
XX
PR   03-OCT-1995;   95JP-0278266.
XX
PA   (HAGI/) HAGIWARA Y.
XX
DR   WPI; 1997-276726/25.
DR   P-PSDB; AAW22842.
XX
PT   Anticancer human monoclonal antibody variable region sequences - and
PT   related DNA and RNA
XX
PS   Claim 12; Page 11; 14pp; Japanese.
XX
CC   The present sequence encodes a human anti-tumour antigen
CC   monoclonal antibody (MAb) light chain variable region, useful in
CC   medicine, pharmacology and biochemistry. The isotype of a MAb
CC   secreted by the human/human hybridoma HT was determined to be mu
CC   and kappa. Human MAb was purified, and the antigen recognised by
CC   human MAb CLN"-IgM identified by western blotting.
XX
SQ   Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;

  Query Match            82.6%;  Score 270;  DB 18;  Length 396;
  Best Local Similarity  91.4%;  Pred. No. 4.5e-76;
  Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        127 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 186

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||| |||||||   |||||||||||
Db        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
```

```
Qy       1 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           ||||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||
Db     247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAACCT 306

Qy     241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
           ||||||| |||||||||||||| |||||||| | |||||| ||||||||||||||||||
Db     307 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCAG---ACGTTCGGC 363

Qy     301 CAAGGGACCAAGGTGGAAATCAAACG 326
           ||||||||||||||||||||||||||
Db     364 CAAGGGACCAAGGTGGAAATCAAACG 389
```

RESULT 13
AAX36070
ID   AAX36070 standard; DNA; 720 BP.
XX
AC   AAX36070;
XX
DT   15-JUL-1999 (first entry)
XX
DE   DNA encoding a single chain antibody (ScFv).
XX
KW   Screening; functional polypeptide; ligand; non-functional;
KW   enrichment; single chain antibody; ScFv; ss.
XX
OS   Unidentified.
XX
PN   WO992074-A1.
XX
PD   29-APR-1999.
XX
PF   20-OCT-1998; 98WO-GB03135.
XX
PR   21-NOV-1997; 97US-0066729.
PR   20-OCT-1997; 97GB-0022131.
PR   13-NOV-1997; 97US-0065428.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Tomlinson I, Winter G;
XX
DR   WPI; 1999-288302/24.
DR   P-PSDB; AAY02472.
XX
PT   Screening for functional polypeptides which bind a ligand
XX
PS   Disclosure; Fig 2; 67pp; English.
XX
CC   The specification describes a method for screening for functional
CC   polypeptides which bind a ligand. The method comprises contacting a
CC   repertoire of polypeptides with a generic ligand, and then screening
CC   selected functional polypeptides with a target ligand. The method
CC   permits the removal from a chosen repertoire of polypeptides, those
CC   which are non-functional, e.g. as a result of the introduction of
CC   frame-shift mutations, stop codons, folding mutants or expression
CC   mutants which would be or are incapable of binding to any target
CC   ligand. The method also permits the enrichment of a chosen repertoire
CC   of polypeptides for those polypeptides which are functional, well folded
CC   and highly expressed. The polypeptides obtained can be used in
CC   diagnostic, prophylactic and therapeutic procedures. The present
CC   sequence encodes the single chain antibody (ScFv) that forms the basis
CC   of a library according to the invention.
XX
SQ   Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;

Query Match   82.6%; Score 270; DB 20; Length 720;
Best Local Similarity 91.4%; Pred. No. 5.6e-76;
Matches 298; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456
```

```
Qy      61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTTGGTATCAGCAGAAACCA 120
           ||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||||
Db     457 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAGCATTAGCCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy     121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
           ||||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     517 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy     181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
           ||||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||
Db     577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy     241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
           ||||||| |||||||||||||| |||||||||||||||  ||||||||    |||||||||
Db     637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGAGTTACACGTACCCCT---AATACGTTCGGC 693

Qy     301 CAAGGGACCAAGGTGGAAATCAAACG 326
           ||||||||||||||||||||||||||
Db     694 CAAGGGACCAAGGTGGGAAATCAAACG 719
```

RESULT 14
AAA11630
ID   AAA11630 standard; DNA; 729 BP.
XX
AC   AAA11630;
XX
DT   08-AUG-2000 (first entry)
XX
DE   Human immunoglobulin light chain kappa region subgroup type I DNA.
XX
KW   Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW   anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
KW   dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW   nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW   hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW   Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW   Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW   Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW   insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
XX
OS   Homo sapiens.
XX
PN   EP990663-A2.
XX
PD   05-APR-2000.
XX
PF   29-SEP-1999; 99EP-0307711.
XX
PR   30-SEP-1998; 98JP-0276881.
PR   30-SEP-1998; 98JP-0276882.
XX
PA   (SANY) SANKYO CO LTD.
XX
PI   Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
DR   WPI; 2000-258930/23.
XX
PT   New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT   inflammatory or autoimmune disease, induces apoptosis selectively in
PT   cells with abnormal Fas-Fas ligand systems -
XX
PS   Example 2; Page 154; 263pp; English.
XX
CC   This invention describes a novel humanized anti-Fas antibody-like
CC   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC   ligand system, by binding to Fas on the cell surface, and prevents
CC   apoptosis in cells with a normal system, by inhibiting binding between
CC   Fas and its ligand. The products of the invention have anti-inflammatory,
CC   anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

RESULT 15
ABL46009
ID   ABL46009 standard; DNA; 729 BP.
XX
AC   ABL46009;
XX
DT   26-APR-2002 (first entry)
XX
DE   Humanised anti-Fas antibody related PCR primer SEQ ID NO 76.
XX
KW   Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW   light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW   autoimmune disease; allergy; atopic; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2001342148-A.
XX
PD   11-DEC-2002.
XX
PF   28-MAR-2001; 2001JP-0093106.
XX
PR   29-MAR-2000; 2000JP-0090918.
XX
PA   (SANY) SANKYO CO LTD.
XX
DR   WPI; 2002-145113/19.
XX
PT   Drug containing humanised anti-Fas antibody, used for preventing and
PT   treating autoimmune diseases, allergy, and atopy -
XX
PS   Example 15 (Preparatory); Page 40; 194pp; Japanese.
XX
CC   The invention relates to a preventive or treating agent for diseases
CC   caused by abnormality in Fas/Fas ligand system containing as the active
CC   component an antibody having as the light chain subunit a polypeptide
CC   containing residues 1-218 of one of 3,239 residue amino acid sequences,
CC   or residues 1-451 of one of 3,470 residue amino acid sequences, all
CC   fully defined in the specification and having an activity of combining
CC   specifically with mammalian Fas and an activity of inducing apoptosis
CC   in a cell expressing Fas. The agent has immunosuppressive and
CC   antiallergic activity and is used for preventing and treating autoimmune
CC   diseases, allergy, atopy and others. The present sequence is that of a
CC   PCR primer, useful to the invention.
XX
SQ   Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

Query Match   82.6%; Score 270; DB 24; Length 729;
Best Local Similarity   91.4%; Pred. No. 5.6e-76;
Matches   298; Conservative   0; Mismatches   25; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   73 GACATCCAGATGACCCAGTCCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 132

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
             |||||||||||||| ||||||| ||||||||| |||||||| |||||||||||||||||
Db   133 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACCA 192

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
             ||||||| ||||||||||||||||||||||||||| ||||||||||| || |||||||
Db   193 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 252

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
             ||||||||||||||||| |||||||||||||||||||||||||||||||| |||||||
Db   253 AGGTTCAGTGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 312

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTACCCCTCCGAGTACGTTCGGC 300
             ||||||| ||||||||| |||||||||| |||| |||||||||||||| |||||||||
Db   313 GAAGATTTTGCAACTTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC 369

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
             ||||||||||||||||||||||||||
Db   370 CAAGGGACCAAGGTGGAAATCAAACG 395

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 18, 2003, 06:19:39 ; Search time 79.0498 Seconds
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Perfect score: 327
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Scoring table: IDENTITY_NUC
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	294	89.9	514	15	US-10-066-543-2025	Sequence 2025, Ap
2	294	89.9	537	15	US-10-066-543-186	Sequence 186, App
3	279.2	85.4	321	12	US-09-801-185A-36	Sequence 36, Appl
4	278	85.0	490	12	US-09-918-995-37859	Sequence 37859, A
5	274.8	84.0	737	11	US-09-919-344-7	Sequence 7, Appli
6	274.8	84.0	819	11	US-10-158-646-65	Sequence 65, Appl
7	270	82.6	720	10	US-09-192-854-1	Sequence 1, Appli
8	270	82.6	729	11	US-09-968-561A-1	Sequence 1, Appli
9	270	82.6	715	15	US-10-216-484-125	Sequence 125, App
10	264.8	81.0	321	15	US-10-035-637-1	Sequence 1, Appli
11	263.6	80.6	974	11	US-09-859-053-29	Sequence 29, Appl
12	263.4	80.6	324	12	US-09-848-798-101	Sequence 101, App
13	263.4	80.6	324	12	US-09-848-798-112	Sequence 112, App
14	261.8	80.1	324	12	US-09-848-798-110	Sequence 110, App
15	261.8	80.1	324	12	US-09-848-798-210	Sequence 210, App
16	260.4	79.6	326	10	US-09-798-058-3	Sequence 3, Appli
17	260.4	79.6	494	11	US-09-878-178-1811	Sequence 1811, Ap
18	260.4	79.6	494	15	US-10-046-935-1811	Sequence 1811, Ap
19	260.4	79.6	494	15	US-10-146-502-1811	Sequence 1811, Ap
20	260.4	79.6	714	15	US-10-153-382-18	Sequence 18, Appl
21	259.8	79.4	728	11	US-09-844-684-15	Sequence 15, Appl
22	259.8	79.1	728	15	US-10-040-244-15	Sequence 15, Appl
23	258.6	79.1	324	12	US-09-848-798-220	Sequence 220, App
24	258.6	79.1	716	11	US-09-848-798-224	Sequence 224, App
25	258.2	79.0	716	11	US-09-844-684-13	Sequence 13, Appl
26	258.2	79.0	716	15	US-10-040-244-13	Sequence 13, Appl
27	257.2	78.7	324	15	US-10-067-800-65	Sequence 65, Appl
28	257	78.6	321	12	US-09-848-798-102	Sequence 102, App
29	257	78.6	321	12	US-09-848-798-218	Sequence 218, App
30	257	78.6	321	12	US-09-848-798-221	Sequence 221, App
31	257	78.6	321	12	US-09-848-798-222	Sequence 222, App
32	257	78.6	324	12	US-09-848-798-204	Sequence 204, App
33	256.8	78.5	321	15	US-10-073-644C-3	Sequence 3, Appli
34	256.8	78.5	387	12	US-09-019-441-3	Sequence 3, Appli
35	256.8	78.5	387	15	US-10-103-686-3	Sequence 3, Appli
36	256.2	78.3	384	10	US-09-905-243-20	Sequence 20, Appl
37	256	78.3	356	12	US-09-918-995-18784	Sequence 18784, A
38	255.6	78.2	390	10	US-09-905-243-57	Sequence 57, Appl
39	255.4	78.1	324	12	US-09-848-798-100	Sequence 100, App
40	255.4	78.1	324	12	US-09-848-798-206	Sequence 206, App
41	255.2	78.0	321	15	US-10-060-585-9	Sequence 9, Appli
42	255.2	78.0	321	15	US-10-172-317-3	Sequence 3, Appli
43	253.8	77.6	321	12	US-09-848-798-98	Sequence 98, Appl
44	253.8	77.6	321	12	US-09-848-798-107	Sequence 107, App
45	253.6	77.6	321	15	US-10-091-300-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-10-066-543-2025
; Sequence 2025, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2025
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-2025

  Query Match   89.9%; Score 294; DB 15; Length 514;
  Best Local Similarity   96.0%; Pred. No. 8.2e-92;
  Matches 313; Conservative   0; Mismatches   10; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db   78 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 137

Qy   61 ATCACTTGCCGGGCGAGTCAGTCAGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db  138 ATCACTTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 197
        ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
        ||||| ||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Db  198 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCTGGGGTCCCATCT 257
Qy  181 CGGTTCAGTGGCGCAGTGGATCTGGACAGATTTCACTCCACCATCAGCAGCCTGCAGCCT 240
        ||||||||||| |||||||||||||| ||||||||| |||||||| ||||||||||||||
Db  258 CGGTTCAGTGGCAGTGGATCTGGACACATTTCACTCTCACCATCCATCGGCAGCCTGCAGCCT 317
Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
        ||||||||||||||||||| |||||||||| |||||||||||   |||| |||||||||
Db  318 GAAGATGTTGCAACTTATTTCTGTCAAAAATATAACAGTGCC---CCCGGGACGTTCGGC 374

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG 326
        |||||||||||||||| |||||||||
Db  375 CAAGGGACCAAGGTGGACATCAAACG 400
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RESULT 2
US-10-066-543-186/c
; Sequence 186, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 529
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-186

Query Match   89.9%; Score -294; DB 15; Length 537;
Best Local Similarity 96.0%; Pred. No. 8.3e-92;
Matches   313; Conservative   0; Mismatches 10; Indels 10; Gaps 1;

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Qy    1 GACATCCAGATGACCCAGTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db  437 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 378
Qy   61 ATCACTTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  377 ATCACTTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 318
Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
        ||||| |||||||||||||||||||||||||||||| ||||||||||| |||||||||||
Db  317 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCCACTTTGCAATCTGGGGTCCCATCT 258
Qy  181 CGGTTCAGTGGCGCAGTGGATCTGGACAGATTTCACTCCACCATCAGCAGCCTGCAGCCT 240
        ||||||||||| |||||||||||||| ||||||||| |||||||| ||||||||||||||
Db  257 CGGTTCAGTGGCAGTGGATCTGGACACATTTCACTCTCACCATCCATCGGCAGCCTGCAGCCT 198
Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
        ||||||||||||||||||| |||||||||| ||||||||||   |||| |||||||||
Db  197 GAAGATGTTGCAACTTATTTCTGTCAAAAATATAACAGTGCC---CCCGGGACGTTCGGC 141
Qy  301 CAAGGGACCAAGGTGGAAATCAAACG 326
        |||||||||||||||| |||||||||
Db  140 CAAGGGACCAAGGTGGACATCAAACG 115
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RESULT 3
US-09-801-185A-36
; Sequence 36, Application US/09801185A
; Publication No. US2003009205941
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/801,185A
; FILING DATE: 07-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,226
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: US 60/031,476
; FILING DATE: 25-NOV-1996
; APPLICATION NUMBER: US 09/125,098
; FILING DATE: 07-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-801-185A-36

Query Match   85.4%; Score 279.2; DB 12; Length 321;
Best Local Similarity 93.5%; Pred. No. 9.4e-87;
Matches   303; Conservative   0; Mismatches 18; Indels 3; Gaps 1;

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Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
        |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    1 GACATCCAGATGACCCAGTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60
Qy   61 ATCACTTGCCGGGCGAGTCAGGCATTATTAGCCTGGTATCAGCAGAAAACCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACTTGTCGGGCAGTCAGGGCATCAGCAGAAAATTACTTAGCCTGGTATCAGCAGAAAAACCA 120
Qy  121 GGGAAAGTTCCTTAAGCTCCTGATCTATGCTGCATCCTATGCTGATCCACTTGCAATCACCACCTCCATCT 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGGAAAGCCCTAAGCTCCTGATCTATGCTCCTATGCTATCATGCATCATCAGCAGCCTCCATCT 180
Qy  181 CGGTTCAGTGGCAGTGGATCTGGGGACAGAGTCACGGGGATCTGGGTATCTGGGTATCTGGGGAGTTCGGC 240
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Db   181 CGGTTCAGTGGCAGTGCGGATCTCGGGACAGATTCACTCGTCACCATACAGCAGCCTACAGCCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
          |||||||||||||||||||||| ||| ||||||||||||||| ||| ||||

Db   241 GAAGATGTTGCAACTTATTACTGTCAAAGGTATAAACCGTG---CACCGTATACTTTTGGC 297

Qy   301 CAAGGGACCAAGGTGGAAATCAAA 324
          || |||||||||||||||||||||

Db   298 CAGGGGACCAAGGTGGAAATCAAA 321

RESULT 4
US-09-918-995-37859
; Sequence 37859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc.
;   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;   TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;   FILE REFERENCE: 20411-756
;   CURRENT APPLICATION NUMBER: US/09/918,995
;   CURRENT FILING DATE: 2001-07-30
;   PRIOR APPLICATION NUMBER: US/09/235,076
;   PRIOR FILING DATE: 1999-01-20
;   NUMBER OF SEQ ID NOS: 38054
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37859
;   LENGTH: 490
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(490)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37859

Query Match   85.0%; Score 278; DB 12; Length 490;
Best Local Similarity   92.9%; Pred. No. 2.9e-86;
Matches   303; Conservative   0; Mismatches   20; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCGATCTGAGGAGACAGAGTCACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||

Db   120 GACATCCAAATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGAGACACAGTCACC 179

Qy   61 ATCACTTGCCGGGCGAGTGCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||

Db   180 ATCACTTGCCGGGCGAGTGCAGGGCATTAGCAGTTACTTAGCCTGGTATCAGCAGAAACCA 239

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||

Db   240 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCTGTGCCTCCACTTTGCAATCAGGGGTCCCATCT 299

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   300 CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTACAGCCT 359

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
          |||||||||||||||||||||| ||| ||||||||||| |||||||||||||||||||

Db   360 GAAGATGTTGCAACCTATTACTGTCAAAATATAACAGTGCC---CCTGACACTTTTGGC 416

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
          || |||||||||||||||||||||||

Db   417 CAGGGGACCAAGGTGGAGATTAAACG 442

RESULT 5
US-09-919-344-7
; Sequence 7, Application US/09919344
; Patent No. US20020137911A1
; GENERAL INFORMATION:
;   APPLICANT: Pyle, Ruth A.
;   APPLICANT: Xu, Jiangchun

;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
;   FILE REFERENCE: 210121.543
;   CURRENT APPLICATION NUMBER: US/09/919,344
;   CURRENT FILING DATE: 2001-07-30
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 737
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 669_685, 718, 722
;   OTHER INFORMATION: n = A,T,C or G
US-09-919-344-7

Query Match   84.0%; Score 274.8; DB 11; Length 737;
Best Local Similarity   90.2%; Pred. No. 4.4e-85;
Matches   294; Conservative   0; Mismatches   32; Indels   0; Gaps   0;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCGATCTGTGGAGACAGAGTCACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   84 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCGATCTGTGGAGACAGAGTCACC 143

Qy   61 ATCACTTGCCGGGCGAGTGCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||| || |||||||||||||||||||||||

Db   144 ATCACTTGCCGGGCGAGTGCAGGGCATTAGCAATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA 203

Qy   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
          ||||| ||| ||||||||||| ||| ||||||||| || ||||||||||| |||||||

Db   204 GGGAGTGCCCCTAAGCTCCTGATCTATGCTGCATCGTGTATCCAACTTGGAAAGTGGGGTCCCATCC 263

Qy   181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          |||||||||||||| ||| ||||| |||||||||| |||||||||||||||||||||||

Db   264 AGGTTCAGTGGCAGTGGGACGGATCTGGGACGGATTCTCACCATCAGCAGCCTGCAGCCT 323

Qy   241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
          ||||| ||||||||||||| |||||| ||||| |||| |||||||||||||||||||||

Db   324 GAAGATTTGCAACTTATTACTGTCAACAGTATTATAGTAACCCTCCGGTCACTTTCGGC 383

Qy   301 CAAGGGACCAAGGTGGAAATCAAACG 326
          || |||||||||||||||||||||||

Db   384 GGAGGGACCAAGGTGGAGATCAAACG 409

RESULT 6
US-10-158-646-65
; Sequence 65, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
;   APPLICANT: Lasek, Amy K.W.
;   APPLICANT: Sornasse, Thierry
;   TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;   FILE REFERENCE: PA-0030-1 US
;   CURRENT APPLICATION NUMBER: US/10/158,646
;   CURRENT FILING DATE: 2002-05-29
;   PRIOR APPLICATION NUMBER: 60/295,239
;   PRIOR FILING DATE: 2001-05-31
;   NUMBER OF SEQ ID NOS: 78
;   SOFTWARE: PERL Program
; SEQ ID NO 65
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030073105A1 1329729.1
US-10-158-646-65

Query Match   84.0%; Score 274.8; DB 15; Length 819;
Best Local Similarity   92.3%; Pred. No. 4.6e-85;
Matches   301; Conservative   0; Mismatches   22; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   86 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAAAGTCACC 145

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
         |||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db 146 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAGCCT 205

Qy 121 GGGAAAGTTCCTAAGCTCCTGATCTATGCGCATCCACTTTGCAATCAGGGGTCCCATCT 180
         |||||| | ||||||||||||||||||||||| ||||||||||||||||
Db 206 GGGACAGCCCCTAACCTCCTGATCTATGCGCATCCACTTTGCAATCAGCTGTCCCATCT 265

Qy 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 266 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 325

Qy 241 GAAGATGTTGCAACTTACTGCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         |||||||||||||||||||||||||||||||||||||||| |||||||||
Db 326 GAAGATGTTGCAACTTATACTGCAAAAGTATAACAGTGCCCCTT---ATCACTTCGGC 382

Qy 301 CAAGGGACCAAGGTGGAAATCAAACG 326
         |||||||||||||||||||||||||
Db 383 CAAGGGACACGACGTGGAGATTAAACG 408

RESULT 7
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US2002006827 6A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

Query Match   82.6%; Score 270; DB 10; Length 720;
Best Local Similarity   91.4%; Pred. No. 2e-83;
Matches 298; Conservative 0; Mismatches 25; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAGAGTCACC 456

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
         |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 457 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy 121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCA 576

Qy 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
         |||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db 577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy 241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         ||||||||||||||||||||||||| ||||||||
Db 637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACAGTTACCCCT---AATACGTTCGGC 693

Qy 301 CAAGGGACCAAGGTGGAAATCAAACG 326
         |||||||||||||

Db 694 CAAGGGACCAAGGTGGAAATCAAACG 719

RESULT 8
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-561A-1

Query Match   82.6%; Score 270; DB 11; Length 720;
Best Local Similarity   91.4%; Pred. No. 2e-83;
Matches 298; Conservative 0; Mismatches 25; Indels   3; Gaps   1;

Qy   1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAGAGTCACC 456

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
         |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 457 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy 121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCA 576

Qy 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
         |||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db 577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy 241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
         ||||||||||||||||||||||||| ||||||||
Db 637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACAGTTACCCCT---AATACGTTCGGC 693

Qy 301 CAAGGGACCAAGGTGGAAATCAAACG 326
         ||||||||||||||||||||||||
Db 694 CAAGGGACCAAGGTGGAAATCAAACG 719

RESULT 9
US-10-216-484-125
; Sequence 125, Application US/10216484
; Publication No. US2003010 3976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US2003010 3976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG

Matches   294; Conservative   0; Mismatches   27; Indels   3; Gaps   1;

```
Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAAACCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACTTGTCGGGCGAGTCAGGGCATTAGCAGTGGTTAGCCTGGTATCAGCAGAAAACCA 120

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCATCCATCTGCATCCAGTTTGCAATCAGGGGGTCCCATCT 180
        |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGGAAAGCCCCTAAGTCCCTGATCTATGCTGCATCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAACAGTGCCCCTCCGAGTACGTTCGGC 300
        |||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db  241 GAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTACCCCTC--GGACGTTCGGC 297

Qy  301 CAAGGGACCAAGGTGGAAATCAAA 324
        |||||||||||||||||||||||
Db  298 CAAGGGACCAAGGTGGAAATCAAA 321
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RESULT 11
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658Aluaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match   80.6%; Score 263.6; DB 11; Length 974;
Best Local Similarity 90.2%; Pred. No. 3.8e-81;
Matches   294; Conservative   0; Mismatches   29; Indels   3; Gaps   1;

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Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  105 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 164

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAAACCA 120
        |||||||| ||||||||||||||||||||||    ||||||||||||||||||||||||||
Db  165 ATCACTTGTCGGGCGAGTCAGGGCATTAGCAGTGGTTAGCCTGGTATCAGCAGAAAACCA 224
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; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE:  2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-484-125
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Query Match   82.6%; Score 270; DB 15; Length 729;
Best Local Similarity 91.4%; Pred. No. 2e-83;
Matches   298; Conservative   0; Mismatches   25; Indels   3; Gaps   1;

```
Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   73 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 132

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAAACCA 120
        |||||||| |||||||||||||||||||||    ||||||||||||||||||||||||||
Db  133 ATCACTTGTCGGGCGAGTCAGGGCATTAGCAGTGGTTAGCCTGGTATCAGCAGAAAACCA 192

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTGCAATCAGGGGGTCCCATCT 180
        |||||||| ||||||||||||||||||||||       |||||||||||||||||||||
Db  193 GGGAAAGCCCCTAAGTCCCTGATCTATGCTGCATCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 252

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  253 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCT 312

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db  313 GAAGATTTTGCAACTTATTACTGTCAACAGAGTTACAGTAACCCCTC--GAACGTTCGGC 369

Qy  301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db  370 CAAGGGACCAAGGTGGAAATCAAACG 395
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RESULT 10
US-10-035-637-1
; Sequence 1, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(321)
US-10-035-637-1

Query Match   81.0%; Score 264.8; DB 15; Length 321;
Best Local Similarity 90.7%; Pred. No. 9.5e-82;

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Qy   121  GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT  180
          |||||||||||||||||||||||||||||||   ||||||||||||  |||||||||||||
Db   225  GGGAAAGCCCCTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA  284

Qy   181  CGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT  240
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  AGGTTCAGCGGCGCAGTGGATCTCGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  344

Qy   241  GAAGATGTGCAACTTATTACTGTCAAAAGTATTAACAGTGCCCCTCCGAGTACGTTCGGC  300
          ||||| |||||||||||||||| ||||||||||| || ||||||||  ||  |||||||||
Db   345  GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTC---CCGTGGACGTTCGGC  401

Qy   301  CAAGGGACCAAGGTGGAAATCAAACG  326
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Db   402  CAAGGGACCAAGGTGGAAATCAAACG  427


RESULT 12
US-09-848-798-101
; Sequence 101, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/848,798
;   CURRENT FILING DATE: 2001-05-04
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;   PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;   SOFTWARE: PatentIn Ver. 2.0
;   NUMBER OF SEQ ID NOS: 224
; SEQ ID NO 101
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-101

Query Match             80.6%;  Score 263.4;  DB 12;  Length 324;
Best Local Similarity   88.8%;  Pred. No. 2.9e-81;
Matches    285;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy    6  CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAGTCTGTAGGAGACAGAGTCACCATCAC  65
         ||||| |||||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db    3  CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC  62

Qy   66  TTGCCGGGCAGTCGGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCAGGGAA  125
         ||| ||||||||||||||||||||| || |||||||||| ||  ||||||||||||||||||||
Db   63  TTGCCGGGCAAGTCAGAGCATTAGCAGCATTAGCCTATTTAAATTGGTATCAGCAGAAACCAGGGAA  122

Qy  126  AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT  185
         || |||||||||||||||||||| ||||||||||||||| |||||||||||||||
Db  123  AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT  182

Qy  186  CAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA  245
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Db  183  CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCTGAAGA  242

Qy  246  TGTTGCAACTTATTACTGTCAAAAGTATTAACAGTGCCCCTCCGAGTACGTTCGGCCCAGG  305
         |||||||||||| |||| ||||| || ||||||||| ||||| |||||||| ||||||||
Db  243  TTTTGCAACTTACTACTGTCAACAGAGTTACAGAGTTACAGACCCCTCCGTACACTTTTGGCCAGGG  302

Qy  306  GACCAAGGTGGAAATCAAACG  326
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Db  303  GACCAAGCTGGAGATCAAACG  323


RESULT 13
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US-09-848-798-112
; Sequence 112, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/848,798
;   CURRENT FILING DATE: 2001-05-04
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;   PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;   SOFTWARE: PatentIn Ver. 2.0
;   NUMBER OF SEQ ID NOS: 224
; SEQ ID NO 112
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-112

Query Match             80.6%;  Score 263.4;  DB 12;  Length 324;
Best Local Similarity   88.8%;  Pred. No. 2.9e-81;
Matches    285;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy    6  CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAGTCTGTAGGAGACAGAGTCACCATCAC  65
         ||||| |||||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db    3  CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC  62

Qy   66  TTGCCGGGCAGTCGGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCAGGGAA  125
         ||| |||||||||||||||||||| || |||||||||| ||  ||||||||||||||||||||
Db   63  TTGCCGGGCAAGTCAGAGCATTAGCAGCATTAGCCTATTTAAATTGGTATCAGCAGAAACCAGGGAA  122

Qy  126  AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT  185
         || |||||||||||||||||||| ||||||||||||||| |||||||||||||||
Db  123  AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT  182

Qy  186  CAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA  245
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  183  CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCTGAAGA  242

Qy  246  TGTTGCAACTTATTACTGTCAAAAGTATTAACAGTGCCCCTCCGAGTACGTTCGGCCCAGG  305
         |||||||||||| |||| ||||| || ||||||||| ||||| |||||||| ||||||||
Db  243  TTTTGCAACTTACTACTGTCAACAGAGTTACAGAGTTACAGACCCCTCCGTACACTTTTGGCCAGGG  302

Qy  306  GACCAAGGTGGAAATCAAACG  326
         ||||| |||||||||||||||
Db  303  GACCAAGCTGGAGATCAAACG  323


RESULT 14
US-09-848-798-110
; Sequence 110, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/848,798
;   CURRENT FILING DATE: 2001-05-04
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;   PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;   SOFTWARE: PatentIn Ver. 2.0
;   NUMBER OF SEQ ID NOS: 224
; SEQ ID NO 110
;   LENGTH: 324
;   TYPE: DNA
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;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) chain I10
US-09-848-798-110

Query Match        80.1%;   Score 261.8;  DB 12;  Length 324;
Best Local Similarity   88.5%;   Pred. No. 1.1e-80;
Matches  284;  Conservative   0;  Mismatches   37;  Indels   0;  Gaps   0;

Qy      6 CCAGATGACCCAGTCTCCATCCCCGTCTGCATCCTGTGAGAGACAGAGTCACCATCAC 65
            |||||||| |||||||||||||  ||||| ||||||||| ||||||||| |||||||||
Db      3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCCTGTGAGGAGACAGAGTCACCATCAC 62

Qy     66 TTGCCGGGCGAGTCAGGGCAGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
            |||||| ||||||| ||||| |||||||||||||||||||||||||||||||||||||||||
Db     63 TTGCCGGGCAAGTCAGAACACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAATCAGGGGTCCCATCTCGGTT 185
            || ||||||||||||||||||||| |||||| |||||| ||||||| |||| ||||||||
Db    123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCTATCAAGGTT 182

Qy    186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy    246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
            |||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||
Db    243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCCCGTACACTTTTGGCCAGGG 302

Qy    306 GACCAAGGTGGAAATCAAACG 326
            ||||||||| ||||| |||||
Db    303 GACCAAGCTGGAGATCAAACG 323

RESULT 15
US-09-848-798-210
;    Sequence 210, Application US/09848798
;    Publication No. US20030040605A1
;    GENERAL INFORMATION:
;    APPLICANT: Siegel, Donald L.
;    TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;    TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;    FILE REFERENCE: 09596-42U2
;    CURRENT APPLICATION NUMBER: US/09/848,798
;    CURRENT FILING DATE:  2001-05-04
;    PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;    PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;    PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;    PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;    NUMBER OF SEQ ID NOS: 224
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 210
;    LENGTH: 324
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-848-798-210

Query Match        80.1%;   Score 261.8;  DB 12;  Length 324;
Best Local Similarity   88.5%;   Pred. No. 1.1e-80;
Matches  284;  Conservative   0;  Mismatches   37;  Indels   0;  Gaps   0;

Qy      6 CCAGATGACCCAGTCTCCATCCCCGTCTGCATCCTGTGAGAGACAGAGTCACCATCAC 65
            |||||||| |||||||||||||  ||||| ||||||||| ||||||||| |||||||||
Db      3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCCTGTGAGGAGACAGAGTCACCATCAC 62

Qy     66 TTGCCGGGCGAGTCAGGGCAGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
            |||||| ||||||| ||||| |||||||||||||||||||||||||||||||||||||||||
Db     63 TTGCCGGGCAAGTCAGAACACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAATCAGGGGTCCCATCTCGGTT 185
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Db   123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCTATCAAGGTT 182

Qy   186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
            |||||||||||||||||||||||||||||||||| |||||| |||||||||||||||||
Db   183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy   246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
            |||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||
Db   243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCCCGTACACTTTTGGCCAGGG 302

Qy   306 GACCAAGGTGGAAATCAAACG 326
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Db   303 GACCAAGCTGGAGATCAAACG 323

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Job time : 80.0498 secs

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             Copyright  GenCore version 5.1.6
             Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:      July 18, 2003, 09:26:19 ; Search time 17.3396 Seconds
                                        (without alignments)
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Title:          US-09-627-896B-25
Perfect score:  327
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Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:    882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                           SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279.2	85.4	321	3	US-08-599-226-36	Sequence 36, Appl
2	279.2	85.4	321	4	US-09-125-098-36	Sequence 36, Appl
3	263.4	80.6	324	4	US-09-240-274-101	Sequence 101, App
4	263.4	80.6	324	4	US-09-240-274-112	Sequence 112, App
5	261.8	80.1	324	4	US-09-240-274-110	Sequence 110, App
6	261.8	80.1	324	4	US-09-240-274-210	Sequence 210, App
7	260.4	79.6	324	2	US-08-378-939-31	Sequence 31, Appl
8	260.4	79.6	324	2	US-08-378-939-33	Sequence 33, Appl
9	259.8	79.4	19040	4	US-09-343-485A-3	Sequence 3, Appli
10	258.6	79.1	324	4	US-09-240-274-220	Sequence 220, App
11	258.6	79.1	324	4	US-09-240-274-224	Sequence 224, App
12	257	78.6	321	4	US-09-240-274-102	Sequence 102, App
13	257	78.6	324	4	US-09-240-274-218	Sequence 218, App
14	257	78.6	321	4	US-09-240-274-221	Sequence 221, App
15	257	78.6	321	4	US-09-240-274-222	Sequence 222, App
16	257	78.6	324	4	US-09-240-274-204	Sequence 204, App
17	256.8	78.5	387	3	US-08-803-085-3	Sequence 3, Appli
18	255.4	78.1	324	4	US-09-240-274-100	Sequence 100, App
19	255.4	78.1	324	4	US-09-240-274-206	Sequence 206, App
20	254	77.7	439	4	US-08-042-353-360	Sequence 360, App
21	254	77.7	439	4	US-08-758-417A-208	Sequence 208, App
22	254	77.7	642	1	US-08-157-101A-8	Sequence 8, Appli
23	254	77.7	1066	1	US-08-157-101A-4	Sequence 4, Appli
24	253.8	77.6	321	4	US-09-240-274-98	Sequence 98, Appl
25	253.8	77.6	321	4	US-09-240-274-107	Sequence 107, App
26	252.2	77.1	321	4	US-09-240-274-105	Sequence 105, App
27	252.2	77.1	321	4	US-09-240-274-216	Sequence 216, App
28	251.4	76.9	388	4	US-09-042-353-358	Sequence 358, App
29	251.4	76.9	388	4	US-08-758-417A-206	Sequence 206, App
30	250.6	76.6	321	4	US-09-240-274-201	Sequence 201, App
31	249	76.1	321	4	US-09-240-274-205	Sequence 205, App
32	249	76.1	321	4	US-09-240-274-211	Sequence 211, App
33	249	76.1	321	4	US-09-240-274-215	Sequence 215, App
34	249	76.1	321	4	US-09-240-274-217	Sequence 217, App
35	248.8	75.7	321	2	US-08-378-939-13	Sequence 13, Appl
36	247.4	75.7	324	2	US-08-378-939-23	Sequence 23, Appl
37	247.4	75.7	321	4	US-09-240-274-109	Sequence 109, App
38	247.4	75.7	321	4	US-09-240-274-113	Sequence 113, App
39	246.4	75.4	847	1	US-08-053-131-184	Sequence 184, App
40	246.4	75.4	847	1	US-08-096-762-184	Sequence 184, App
41	246.4	75.4	847	4	US-09-042-353-47	Sequence 47, Appl
42	246.4	75.4	847	4	US-08-758-417A-312	Sequence 312, App
43	246	75.2	324	2	US-08-378-939-17	Sequence 17, Appl
44	246	75.2	384	2	US-08-259-372A-13	Sequence 13, Appl
45	246	75.2	384	1	US-08-468-671-13	Sequence 13, Appl

                           ALIGNMENTS

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RESULT 1
US-08-599-226-36
; Sequence 36, Application US/0599226
Patent No. 6090382
GENERAL INFORMATION:
    APPLICANT: Salfeld, Jochen G.
    APPLICANT: Allen, Deborah J.
    APPLICANT: Hoogenboom, Hendricus R.J.M.
    APPLICANT: Kaymakcalan, Zehra
    APPLICANT: Labkovsky, Boris
    APPLICANT: Mankovich, John A.
    APPLICANT: McGuinness, Brian T.
    APPLICANT: Roberts, Andrew J.
    APPLICANT: Sakorafas, Paul
    APPLICANT: Schoenhaut, David
    APPLICANT: Vaughan, Tristan J.
    APPLICANT: White, Michael
    APPLICANT: Wilton, Andrew J.
    TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
    NUMBER OF SEQUENCES: 37
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: LAHIVE & COCKFIELD
        STREET:  60 State Street, suite 510
        CITY:  Boston
        STATE:  Massachusetts
        COUNTRY:  USA
        ZIP:  02109-1875
    COMPUTER READABLE FORM:
        MEDIUM TYPE:  Floppy disk
        COMPUTER:  IBM PC compatible
        OPERATING SYSTEM:  PC-DOS/MS-DOS
        SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/599,226
        FILING DATE: 08-FEB-1996
        CLASSIFICATION: 424
    ATTORNEY/AGENT INFORMATION:
        NAME: DeConti, Giulio A., Jr.
        REGISTRATION NUMBER: 31,503
        REFERENCE/DOCKET NUMBER: BBI-043
    TELECOMMUNICATION INFORMATION:
        TELEPHONE:  (617)227-7400
        TELEFAX:  (617)227-5941
INFORMATION FOR SEQ ID NO:      36:
    SEQUENCE CHARACTERISTICS:
        LENGTH:  321 base pairs
        TYPE:  nucleic acid
        STRANDEDNESS:  double
        TOPOLOGY:  linear
        MOLECULE TYPE:  cDNA
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US-08-599-226-36

Query Match   85.4%;   Score 279.2; DB 3; Length 321;
Best Local Similarity 93.5%;   Pred. No. 1e-81;
Matches 303; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

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Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60
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Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA  120
        ||||||| | |||||||||| | ||||   ||| || |||||||||||||||||| |||
Db   61 ATCACTTGTCTGGCAGTCAGCATCAGAAATTACTTAGCCTGGTATCAGCAGAAAACCA  120

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCGATCCACTTTGCAATCAGGGGTCCCATCT  180
        ||||||| | |||||||||||||||||  ||||| || |||||||||||||||||||||||||||
Db  121 GGGAAAGCCCCTAAGCTCCTGATCTATCCGATCCACTTTGCAATCAGGGGTCCCATCT  180

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT  240

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC  300
        |||||||||||||||||||||||||||||||||||||   ||  |  || |||| ||||
Db  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACCGTG---CACCGTATACTTTTGGC  297

Qy  301 CAAGGGACCAAGGTGGAAATCAAA  324
        || |||||||||||||||||||||
Db  298 CAGGGGACCAAGGTGGAAATCAAA  321
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RESULT 2
US-09-125-098-36
; Sequence 36, Application US/09125098
; Patent No. 6258562
; GENERAL INFORMATION:
;   APPLICANT: Salfeld, Jochen G.
;   APPLICANT: Allen, Deborah J.
;   APPLICANT: Hoogenboom, Hendricus R.J.M.
;   APPLICANT: Kaymakcalan, Zehra
;   APPLICANT: Labkovsky, Boris
;   APPLICANT: Mankovich, John A.
;   APPLICANT: McGuinness, Brian T.
;   APPLICANT: Roberts, Andrew J.
;   APPLICANT: Sakorafas, Paul
;   APPLICANT: Schoenhaut, David
;   APPLICANT: Vaughan, Tristan J.
;   APPLICANT: White, Michael
;   APPLICANT: Wilton, Andrew J.
;   TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 60 State Street, suite 510
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/125,098
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/599,226
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: DeConti, Giulio A., Jr.
;   REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)227-7400
;   TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-09-125-098-36

Query Match   85.4%;   Score 279.2; DB 4; Length 321;
Best Local Similarity 93.5%;   Pred. No. 1e-81;
Matches 303; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

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Qy    1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC   60
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Db    1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC   60

Qy   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA  120
        ||||||| | |||||||||| | ||||   ||| || |||||||||||||||||| |||
Db   61 ATCACTTGTCTGGCAGTCAGCATCAGAAATTACTTAGCCTGGTATCAGCAGAAAACCA  120

Qy  121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT  180
        ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT  180

Qy  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT  240

Qy  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC  300
        |||||||||||||||||||||||||||||||||||||   ||  |  || |||| ||||
Db  241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACCGTG---CACCGTATACTTTTGGC  297

Qy  301 CAAGGGACCAAGGTGGAAATCAAA  324
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Db  298 CAGGGGACCAAGGTGGAAATCAAA  321
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RESULT 3
US-09-240-274-101
; Sequence 101, Application US/09/240,274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 101
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-101

Query Match   80.6%;   Score 263.4; DB 4; Length 324;
Best Local Similarity 88.8%;   Pred. 1.4e-76;
Matches 285; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Qy    6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC   65
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Db   3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTGAGGACAGAGTCACCATCAC 62

Qy   66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTTGGTATCAGCAGAAACCAGGGAA 125
          |||||| ||||||||| |||||| || |||||||| ||||||||||||||||||||||
Db   63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy   126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
          ||||||| ||||||| ||||||||||||||| |||||||||||| ||||||||||||||
Db   123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy   186 CAGTGGCAGTGGGATCTGGGACAGAGTTCACTCACCATCAGCAGCCTGAAGA 245
          |||||| ||||||||||||||||||| || |||||| || ||||||||||||
Db   183 CAGTGGCAGTGGGATCTGGGACAGAGTTCACTCTCCACCATCAGCAGCCTGAAGA 242

Qy   246 TGTTGCAACTTATTACTGTCAAAAGTATAACGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
          ||||||||||||||||||| |||||||||||||||||||| || |||||||||||| ||
Db   243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy   306 GACCAAGGTGGAAATCAAACG 326
          |||||||||||||||||||||
Db   303 GACCAAGGTGGAGATCAAACG 323

RESULT 4
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112

Query Match   80.6%;   Score 263.4; DB 4; Length 324;
Best Local Similarity 88.8%;   Pred. No. 1.4e-76;
Matches 285; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy   6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGAGGACAGAGTCACCATCAC 65
          | |||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db   3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTGAGGACAGAGTCACCATCAC 62

Qy   66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTTGGTATCAGCAGAAACCAGGGAA 125
          |||||| ||||||| ||||||| || |||||||| ||||||||||||||||||||||
Db   63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy   126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
          ||||||| ||||||| ||||||||||||||| ||||||| || ||||||||||||||||
Db   123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy   186 CAGTGGCAGTGGGATCTGGGACAGAGTTCACTCACCATCAGCAGCCTGAAGA 245
          |||||| |||||||||||||||||||| || |||||| || ||||||||||||
Db   183 CAGTGGCAGTGGGATCTGGGACAGAGTTCACTCTCCACCATCAGCAGCCTGAAGA 242

Qy   246 TGTTGCAACTTATTACTGTCAAAAGTATAACGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
          ||||||||||||||||| ||||||||||||||||||||||| || |||||||||||| ||
Db   243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy   306 GACCAAGGTGGAAATCAAACG 326
          |||||||||||| |||||||||

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;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO.210
;    LENGTH: 324
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-240-274-210

Query Match          80.1%;  Score 261.8; DB 4;  Length 324;
Best Local Similarity 88.5%;  Pred. No. 4.7e-76;
Matches 284;  Conservative  0;  Mismatches 37;  Indels  0;  Gaps  0;

Qy      6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
            || || ||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy     66 TTGCCGGGCGGCAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGAA 125
            |||||||||  |||||||||||||||||||||||| |||||  ||||||||||||||||||
Db     63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCAATCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
            || ||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db    123 AGCCCTAAGCTCCTGATCTATGCTGCATCCGGTTTGCAAAGTGGGGTCCCATCAAAGGTT 182

Qy    186 CAGTGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 CAGTGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy    246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
            ||||| |||||||||||||||| |||||||||||||||| || || |||||||||||||
Db    243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCCCCGTACACTTTTGGCCAGGG 302

Qy    306 GACCAAGGTGGAAATCAAACG 326
            ||||||||||||||||||||||
Db    303 GACCAAGCTGGAGATCAAACG 323

RESULT 7
US-08-378-939-31
;  Sequence 31, Application US/08378939
;  Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT: CROWE, JAMES SCOTT
;    APPLICANT: LEWIS, ALAN PETER
;    TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES: 46
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
;    STREET: 555 THIRTEENTH ST. N.W.
;    CITY: WASHINGTON
;    STATE: D.C.
;    COUNTRY: U.S.
;    ZIP: 20004
;    COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/378,939
;    FILING DATE:
;    CLASSIFICATION: 435
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 07/952640
;    FILING DATE: 01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;    NAME: ERNST, BARBARA G
;    REGISTRATION NUMBER: 30,377
;    REFERENCE/DOCKET NUMBER: 1808-118
;    TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (202) 783-6040
```

```
;    TELEFAX: (202) 783-6031
;  INFORMATION FOR SEQ ID NO: 31;
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 324 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: both
;    TOPOLOGY: linear
;    MOLECULE TYPE: cDNA
;    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 1..324
US-08-378-939-31

Query Match          79.6%;  Score 260.4; DB 2;  Length 324;
Best Local Similarity 89.6%;  Pred. No. 1.3e-75;
Matches 292;  Conservative  0;  Mismatches 31;  Indels  3;  Gaps  1;

Qy      1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            |||||||| || ||| |||||||||||| || |||||||||||||||||||||||||||
Db      1 GACATTCAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACACAGTCACC 60

Qy     61 ATCACTTGCCGGGCGGAGTCAGGGCATTAGCAATTATTATTAGCCTGGTATCAGCAGAAACCA 120
            |||||||||||||| ||||||| |||||||| ||||| || |||||||||||||||||||
Db     61 ATCACTTGTCGGGCAAGTCAGGGCATTAGCAATAATTTTAGCCTGGTATCAGCAGAAACCA 120

Qy    121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCACTTTGCAATCACTTTGCAATCACTCT 180
            ||||||||||||| ||||||||||| |||||||| || ||||||||||||||||||||||
Db    121 GGGAAAGCTCCTAAGCCCTGATCTATGCTGCATCCTGGAAAGTGGGGTCCATCA 180

Qy    181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
            ||| |||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy    241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
            |||||| ||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db    241 GAAGATTTTGCAACTTATTACTGTCAACAGAGTAACAGT---TATCCTTTCACTTTCGGC 297

Qy    301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db    298 GGAGGGACCAAGCTGGAGATCAAACG 323

RESULT 8
US-08-378-939-33
;  Sequence 33, Application US/08378939
;  Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT: CROWE, JAMES SCOTT
;    APPLICANT: LEWIS, ALAN PETER
;    TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES: 46
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
;    STREET: 555 THIRTEENTH ST. N.W.
;    CITY: WASHINGTON
;    STATE: D.C.
;    COUNTRY: U.S.
;    ZIP: 20004
;    COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/378,939
;    FILING DATE:
;    CLASSIFICATION: 435
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 07/952640
;    FILING DATE: 01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
```

```
;   NAME: ERNST, BARBARA G
;   REGISTRATION NUMBER: 30,377
;   REFERENCE/DOCKET NUMBER: 1808-118
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 783-6040
;   TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 33:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 324 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..324
US-08-378-939-33

Query Match             79.6%;    Score 260.4;  DB 2;   Length 324;
Best Local Similarity   89.6%;    Pred. No. 1.3e-75;
Matches   292; Conservative    0; Mismatches   31; Indels    3; Gaps    1;

Qy      1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GACATTCAGCTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACACAGTCACC 60

Qy     61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
          ||||||||||| ||||| |||||||||||||||| ||||||||||||||||||||||||||
Db     61 ATCACTTGTCGGGCAAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120

Qy    121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
          || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAAAGCTCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAATCAGGGGTCCCATCA 180

Qy    181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy    241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
          ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db    241 GAAGATTTTGCGACTTATTACTGTCAACAGGATAACAGT--TATCCTTTCACTTTCGGC 297

Qy    301 CAAGGGACCAAGGTGGAAATCAAACG 326
          ||||||||||||||||||||||||||
Db    298 GGAGGGACCAAGGTGGAGATCAAACG 323

RESULT 9
US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

Query Match             79.4%;    Score 259.8;  DB 4;   Length 19040;
Best Local Similarity   89.3%;    Pred. No. 9.6e-75;
Matches   292; Conservative    0; Mismatches   32; Indels    3; Gaps    1;

Qy      1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7611 GACATTCAGCTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACC 7670

Qy     61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA 120
          ||||||||||| ||||| |||||||||||||||| ||||||||||||||||||||||||||
Db   7671 ATCACTTGCCAGGGCAAGTCAGGGCATTAGCAATTATTAAATTGGTATCAGCAGAAACCA 7730

Qy    121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
          || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7731 GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCCATCA 7790

Qy    181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7791 AGGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCT 7850

Qy    241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
          ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db   7851 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTC---GGACGTTCGGC 7907

Qy    301 CAAGGGACCAAGGTGGAAATCAAACGT 327
          |||||||||||||||||||||||||||
Db   7908 CAAGGGACCAAGGTGGAAATCAAACGT 7934

RESULT 10
US-09-240-274-220
; Sequence 220, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER APPLICATION FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER APPLICATION FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH51
US-09-240-274-220

Query Match             79.1%;    Score 258.6;  DB 4;   Length 324;
Best Local Similarity   87.9%;    Pred. No. 5.1e-75;
Matches   282; Conservative    0; Mismatches   39; Indels    0; Gaps    0;

Qy      6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 CGAGCTCACAGTCTCCATCCTTCCTGTCTGCATCTGTGAGGAGACAGAGTCACCATCAC 62

Qy     66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCAGGGAA 125
          ||||||||| ||||| ||||||||||||||| ||||||||||||||||||||||||||||
Db     63 TTGCCGGGCCAGTCAGGGCATAAGGAGTTATTTAGCCTGGTATCAGCAAAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
          ||  |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
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Db   123 AGCCCCTAAGCTCCTAATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy   186 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
           || ||||||||||||||||||||||||||| ||||||||||| |||| ||||||
Db   183 CAGCGGCAGTGGATCTGGGACAGAGAATTCACTCTCACAATCAGCAGCTCAGCCTGAAGA 242

Qy   246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
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Db   243 TTTTGCAACTTATTACTGTCAACAAGCTTAATAATTACCCCCCTTTCACTTTCGGCCCTGG 302

Qy   306 GACCAAGGTGGAAATCAAACG 326
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Db   303 GACCAAAGTGGAGATCAAACG 323

RESULT 11
US-09-240-274-224
; Sequence 224, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-224

Query Match   79.1%;   Score 258.6; DB 4; Length 324;
Best Local Similarity 87.9%;   Pred. No. 5.1e-75;
Matches 282;   Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy   6 CCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
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Db   3 CGAGCTCACCCAGTCTCCATCCTCCATCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy   66 TTGCCGGGCGAGTCAGGCATTAGCAATCATTAGCAGGTATTAAATTGGTATCAGCAGAAACCAGGGAA 125
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Db   63 TTGCCGGGCAAGTCAGGGCATTAGCAGTCAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy   126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACCTTTGCAATCAGGGGTCCCATCTCGGTT 185
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Qy   186 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
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Qy   246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
           | ||||||||||||||||||||||| |||| | |||||||| |||||||||||||
Db   243 TTTTGCAACTTACTACTGTCAACAGGGTTACAGTACCCCCTCCGTACCAGTTTTGGCCAGGG 302

Qy   306 GACCAAGGTGGAAATCAAACG 326
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Db   303 GACCAAGGTGGAGATCAAACG 323

RESULT 12
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455

;   GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query Match   78.6%;   Score 257; DB 4; Length 321;
Best Local Similarity 89.7%;   Pred. No. 1.7e-74;
Matches 288;   Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy   6 CCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3 CGAGCTCACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy   66 TTGCCGGGCGAGTCAGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
           |||||||||||||| ||||||||| |||||||||||||||||||||||||||||
Db   63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy   126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACCTTTGCAATCAGGGGTCCCATCTCGGTT 185
           ||||||||||||||||| |||||||||||||| |||||||||| ||||||||||||
Db   123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy   186 CAGTGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCTCCACAGTCAGCCTGAAGA 245
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Db   183 CAGTGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGTCTGCAACCTGAAGA 242

Qy   246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTATAACAGAGTTACAGTACC---CTGTGGACGTTCGGCCAAGG 305
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Db   243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CTGTGGACGTTCGGCCAAGG 299

Qy   306 GACCAAGGTGGAAATCAAACG 326
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RESULT 13
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERNCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49

US-09-240-274-218

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Query Match           78.6%;   Score 257;  DB 4;   Length 321;
Best Local Similarity 89.7%;   Pred. No. 1.7e-74;
Matches   288; Conservative   0; Mismatches   30; Indels   3;  Gaps   1;

Qy      6 CCAGATGACCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
            ||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||
Db      3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCAC 62

Qy     66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
            ||||||| ||||||||||||||||||| |||| ||||||||||||||||||||||||||
Db     63 TTGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
            ||||| |||||||||||||||||||||| |||||||||||||||||  ||||||| ||||
Db    123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy    186 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
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Db    183 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy    246 TGTTGCAACTTATTACTGTCAAAAGTATAACGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
            ||| ||||||| | |||||  |||||| ||||||   ||   ||||||||||||||||||
Db    243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CCGTGGACGTTCGGCCAAGG 299

Qy    306 GACCAAGGTGGAAATCAAACG 326
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Db    300 GACCAAGGTGGAAATCAAACG 320
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RESULT 14
US-09-240-274-221
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; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
;  LENGTH: 321
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match           78.6%;   Score 257;  DB 4;   Length 321;
Best Local Similarity 89.7%;   Pred. No. 1.7e-74;
Matches   288; Conservative   0; Mismatches   30; Indels   3;  Gaps   1;

Qy      6 CCAGATGACCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
            ||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||
Db      3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCAC 62

Qy     66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
            ||||||| ||||||||||||||||||| |||| ||||||||||||||||||||||||||
Db     63 TTGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
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Db    123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy    186 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
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RESULT 15
US-09-240-274-222
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; Sequence 222, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
;  LENGTH: 321
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match           78.6%;   Score 257;  DB 4;   Length 321;
Best Local Similarity 89.7%;   Pred. No. 1.7e-74;
Matches   288; Conservative   0; Mismatches   30; Indels   3;  Gaps   1;

Qy      6 CCAGATGACCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
            ||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||
Db      3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCAC 62

Qy     66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
            ||||||| ||||||||||||||||||| |||| ||||||||||||||||||||||||||
Db     63 TTGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy    126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
            ||||| |||||||||||||||||||||| |||||||||||||||||  ||||||| ||||
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Qy    186 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
            ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    183 CAGTGGCAGTGGATCTGGGACAGAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy    246 TGTTGCAACTTATTACTGTCAAAAGTATAACGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
            ||| ||||||| | |||||  |||||| ||||||   ||   ||||||||||||||||||
Db    243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CCGTGGACGTTCGGCCAAGG 299

Qy    306 GACCAAGGTGGAAATCAAACG 326
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Db    300 GACCAAGGTGGAAATCAAACG 320
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

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Perfect score: 339
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	327.8	96.7	619	6	E01735	E01735 Genomic DNA
4	326.2	96.2	341	6	E01737	E01737 Genomic DNA
5	326.2	96.2	355	9	HSU86791	U86791 Human Ig li
6	326.2	96.2	372	9	HUMIGLCDR	L11700 Human immun
7	321.4	94.8	339	9	HSIGKVBD	Z18328 H.sapiens m
8	321.4	94.8	342	6	AR058974	AR058974 Sequence
9	321.4	94.8	342	6	AR088798	AR088798 Sequence
10	321.4	94.8	342	6	AR088878	AR088878 Sequence
11	321.4	94.8	342	9	HUMIGKAW	E05868 DNA sequenc
12	321.4	94.8	405	9	S50732	M29467 Human Ig re
13	321.4	94.8	460	9	BC017870	S50732 immunoglobu
14	321.4	94.8	979	9	BC017870	BC017870 Homo sapi
15	319.8	94.3	342	9	AF455557	AF455557 Homo sapi
16	319.8	94.3	360	9	HSVKAP4	X83714 H.sapiens m
17	319.8	94.3	835	9	AB064111	AB064111 Homo sapi
18	319	94.1	360	6	I12039	I12039 Sequence 3
19	318.2	93.9	357	6	AX300034	AX300034 Sequence
20	315	92.9	339	9	AF099194	AF099194 Homo sapi
21	315	92.9	342	9	AB063957	AB063957 Homo sapi
22	315	92.9	813	9	AB064080	AB064080 Homo sapi
23	315	92.9	816	9	AB064075	AB064075 Homo sapi
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25	314	92.6	1330	6	A29530	A29530 Hum4 VL-CC4
26	314	92.6	1330	6	AR096955	AR096955 Sequence
27	314	92.6	1359	6	A29534	A29534 pSC49FLAG s
28	313.4	92.4	340	9	AY043136	AY043136 Homo sapi
29	313.4	92.4	342	6	A62121	A62121 Sequence 15
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31	313.4	92.4	402	9	HSBUD114L	Z46347 H.sapiens m
32	312.4	92.2	1027	6	AR096963	AR096963 Sequence
33	311.8	92.0	427	9	HSVKIVR	X02990 Human mRNA
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35	311.6	91.9	423	6	E37603	E37603 Monoclonal
36	310.4	91.6	388	9	HSIGKLV36	X72457 H.sapiens m
37	310.2	91.5	339	9	HSIGKVBE	Z18329 H.sapiens m
38	310.2	91.5	342	6	AX355947	AX355947 Sequence
39	310.2	91.5	342	9	HUMIGLVBC	L25536 Homo sapien
40	310.2	91.5	407	6	E05213	E05213 cDNA sequen
41	309.8	91.4	347	9	AF103492	AF103492 Homo sapi
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44	308.6	91.0	339	9	AF099195	AF099195 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS   HSVK4H2FG   339 bp   DNA   linear   PRI 17-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody light chain variable
            region,subgroup V(k)4 (H2F IgG line).
ACCESSION   X70465
VERSION   X70465.1 GI:38442
KEYWORDS   anti-DNA antibody; complementarity determining region; Ig kappa
            light chain; Ig light chain; Ig variable region; IgG;
            immunoglobulin; systemic lupus erythematosus.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 339)

Pred. No. is the number of results predicted by chance to have a

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AUTHORS    Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
           and Diamond,B.
TITLE      Molecular characteristics of antibodies bearing an
           anti-DNA-associated idiotype
JOURNAL    J. Exp. Med. 174 (6), 1639-1652 (1991)
MEDLINE    92078875
PUBMED     1660528
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     misc_feature    70..120
                     /note="complementarity determining region, CDR 1"
     misc_feature    166..186
                     /note="complementarity determining region, CDR 2"
     misc_feature    284..303
                     /note="complementarity determining region, CDR 3"
BASE COUNT     88 a     94 c     82 g     75 t
ORIGIN

Query Match       100.0%;  Score 339;  DB 9;  Length 339;
Best Local Similarity   100.0%;  Pred. No. 3.3e-100;
Matches 339;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120

Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy  181 GAATCCGGGGTCCCTGACCGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 2
E01736
LOCUS       E01736        400 bp     DNA       linear    PAT 29-SEP-1997
DEFINITION  Genomic DNA encoding V region of L-chain of monoclonal antibody
            against pseudomonas aeruginosa exotoxin.
ACCESSION   E01736
VERSION     E01736.1  GI:2169989
KEYWORDS    JP 1988267295-A/5.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
  TITLE     HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
  JOURNAL   Patent: JP 1988267295-A 5 04-NOV-1988;
            SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
  OS   Human
  PN , JP 198267295-A/5
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PD   04-NOV-1988
PF   26-NOV-1987 JP 1987298513
PR   03-DEC-1986 JP 86P  288340
PI   NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO, PI
     NOGUCHI HIROSHI
PC   C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00, (C12P21/02,
PC   C12R1:19),
PC   (C12P21/02,C12R1:91);
CC   strandedness: Double;
CC   topology: Linear;
CC   hypothetical: No;
CC   anti-sense: No;
FH   Key             Location/Qualifiers
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FT   sig_peptide     1..60
FT                   /product='signal peptide of V region of     FT
FT                   L-chain'
FT   mat_peptide     61..400
FT                   /product='mature peptide of V region of     FT
FT                   L-chain'
FEATURES             Location/Qualifiers
     source          1..400
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     93 a    110 c    100 g     97 t
ORIGIN

Query Match       96.7%;  Score 327.8;  DB 6;  Length 400;
Best Local Similarity   97.9%;  Pred. No. 1.6e-96;
Matches 332;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;

Qy    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db  121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAATAAGAACTACTTAGCT 180

Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db  181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240

Qy  181 GAATCCGGGGTCCCTGACCGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db  241 GAATTCGGGGTCCCTGACCGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 300

Qy  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db  301 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 399


RESULT 3
E01735
LOCUS       E01735             619 bp     DNA       linear    PAT 29-SEP-1997
DEFINITION  Genomic DNA encoding V region of L chain of monoclonal antibody
            against pseudomonas aeruginosa exotoxin.
ACCESSION   E01735
VERSION     E01735.1  GI:2169988
KEYWORDS    JP 1988267295-A/4.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
  TITLE     HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
  JOURNAL   Patent: JP 1988267295-A 4 04-NOV-1988;
            SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
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COMMENT
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         OS   Human
         PN   JP 198826 7295-A/4
         PD   04-NOV-1988
         PF   26-NOV-1987 JP 1987298513
         PR   03-DEC-1986 JP 86P    288340
         PI   NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO, PI
              NOGUCHI HIROSHI
         PC   C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00,(C12P21/02,
         PC   C12R1:19),
         PC   (C12P21/02,C12R1:91);
         CC   strandedness: Double;
         CC   topology: Linear;
         CC   hypothetical: No;
         CC   anti-sense: No;
         FH   Key            Location/Qualifiers
         FH
         FT   sig_peptide    join(1..49,269..279)
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         FT                  chain'
         FT   intron         50..268
         FT   mat_peptide    280..619
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         FT                  L-chain'
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         source         Location/Qualifiers
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                        /db_xref="taxon:9606"
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BASE COUNT   177 a   138 c   135 g   169 t
ORIGIN

Query Match   96.7%;   Score 327.8; DB 6; Length 619;
Best Local Similarity 97.9%; Pred. No. 1.7e-96;
Matches 332; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db 280 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 339

Qy  61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||||||| |||| ||||||||||||| ||| |||||||||
Db 340 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 399

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCTAAGCTCATTCATTTACTGGCATCTACCCGG 180
          |||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db 400 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 459

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 460 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 519

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 520 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 579

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 580 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 618
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RESULT 4
LOCUS   E01737   341 bp   DNA   linear   PAT 29-SEP-1997
DEFINITION   Genomic DNA encoding V region of L-chain of monoclonal antibody
               against pseudomonas aeruginosa exotoxin.
ACCESSION   E01737
VERSION   E01737.1 GI:2169990
KEYWORDS   JP 198826 7295-A/6.
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 341)
  AUTHORS   Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.

TITLE   HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
JOURNAL   Patent: JP 198826 7295-A 6 04-NOV-1988;
               SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
COMMENT
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         OS   Human
         PN   JP 198826 7295-A/6
         PD   04-NOV-1988
         PF   26-NOV-1987 JP 1987298513
         PR   03-DEC-1986 JP 86P    288340
         PI   NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO, PI
              NOGUCHI HIROSHI
         PC   C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00,(C12P21/02,
         PC   C12R1:19),
         PC   (C12P21/02,C12R1:91);
         CC   strandedness: Double;
         CC   topology: Linear;
         CC   hypothetical: No;
         CC   anti-sense: No;
         FH   Key            Location/Qualifiers
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         FT                  /product='mature peptide of V region of
         FT                  L-chain'.
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         source         Location/Qualifiers
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BASE COUNT   86 a   96 c   83 g   76 t
ORIGIN

Query Match   96.2%;   Score 326.2; DB 6; Length 341;
Best Local Similarity 97.6%; Pred. No. 5.4e-96;
Matches 331; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy  61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db  61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCTAAGCTGCTCATTTACTGGCATCTACCCGG 180
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Db 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 180

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 301 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 5
LOCUS   HSU86791   355 bp   mRNA   linear   PRI 04-MAR-1997
DEFINITION   Human Ig light chain gene variable domain (CLL-L1B) mRNA, partial
               cds.
ACCESSION   U86791
VERSION   U86791.1 GI:1864112
KEYWORDS   .
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 355)
  AUTHORS   Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magnac,C.,
               Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.

Column 1 (RESULT 6 — HUMIGLCDR)

TITLE   Restricted VH clan usage by siblings affected with Chronic
            Lymphocytic Leukemia
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 355)
AUTHORS   Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magnac,C.,
            Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.
TITLE   Direct Submission
JOURNAL   Submitted (24-JAN-1997) Unite d'Immunohematologie et
            d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
            75724
FEATURES   Location/Qualifiers
     source   1..355
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                     /chromosome="2"
                     /map="2p11-2"
                     /cell_type="B cells"
                     /note="patient with Chronic Lymphocytic Leukemia"
     gene   1..355
                     /gene="CLL-L1B"
     CDS   <1..>355
                     /gene="CLL-L1B"
                     /note="rearranged"
                     /codon_start=1
                     /product="Ig light chain variable domain"
                     /protein_id="AAB48604.1"
                     /db_xref="GI:1864113"
                     /translation="DIQMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQ
                     KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFLTISSLQAEDVAVYCQQYYSTPW
                     TFGQGTKVEIKRIRAR"
BASE COUNT   89 a   97 c   91 g   78 t
ORIGIN

Query Match   96.2%; Score 326.2; DB 9; Length 355;
Best Local Similarity   97.6%; Pred. No. 5.4e-96;
Matches   331; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Db    1 GACATCCAGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAATAAGAACTACTTAGCT 120
Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
Db  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
Qy  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGGACAGATTCACTCTCACC 240
Db  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGGACAGATTCACTCTCACC 240
Qy  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
Db  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
Db  301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 339
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RESULT 6
HUMIGLCDR
LOCUS   HUMIGLCDR   372 bp   mRNA   linear   PRI 08-MAR-1994
DEFINITION Human immunoglobulin light chain variable region complementarity
            determining region (CDR3) mRNA.
ACCESSION   L11700
VERSION   L11700.1   GI:436562
KEYWORDS   V-region; complementarity determining region; immunoglobulin light
            chain; monoclonal antibody.
SOURCE   Homo sapiens cDNA to mRNA.
ORGANISM   Home sapiens

Column 2 (RESULT 7 — HSIGKVBD)

            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 372)
AUTHORS   Hoon,D.S., Wang,Y., Sze,L., Kanda,H., Watanabe,T., Morrison,S.L.,
            Morton,D.L. and Irie,R.F.
TITLE   Molecular cloning of a human monoclonal antibody reactive to
            ganglioside GM3 antigen on human cancers
JOURNAL   Cancer Res. 53 (21), 5244-5250 (1993)
MEDLINE   94036806
PUBMED   7916649
FEATURES   Location/Qualifiers
     source   1..372
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                     /db_xref="taxon:9606"
                     /cell_line="L612 EBV transformed B-cell"
                     /cell_type="B-lymphocyte"
                     /tissue_type="blood"
     misc_feature   283..309
                     /standard_name="complementarity determining region 3
                     (CDR3)"
                     /note="putative"
BASE COUNT   91 a   105 c   90 g   86 t
ORIGIN

Query Match   96.2%; Score 326.2; DB 9; Length 372;
Best Local Similarity   97.6%; Pred. No. 5.4e-96;
Matches   331; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Qy    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
Db    1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAGCT 120
Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAATAAGAACTACTTAGCT 120
Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
Db  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
Qy  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGGACAGATTTCACTCTCACC 240
Db  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGGACAGATTTCACTCTCACC 240
Qy  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
Db  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
Db  301 CCTCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
```

RESULT 7
HSIGKVBD
LOCUS   HSIGKVBD   339 bp   mRNA   linear   PRI 02-FEB-1995
DEFINITION H.sapiens mRNA for immunoglobulin V-region of kappa chain.
ACCESSION   Z18328
VERSION   Z18328.1   GI:33300
KEYWORDS   anti-lamine antibody; cardiolipin/B2glycoprotein antibody;
            immunoglobulin light chain; kappa chain; monoclonal antibody;
            myelin-associated glycoprotein antibody; V-region.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 339)
AUTHORS   Mariette,X., Tsapis,A. and Brouet,J.C.
TITLE   Nucleocidic Sequence Analysis Of The Variable Domains Of Four Human
            Monoclonal IgM With An Antibody Activity To Myelin-Associated
            Glycoprotein
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 339)

AUTHORS   Mariette,X.
TITLE   Direct Submission
JOURNAL   Submitted (29-OCT-1992) Xavier Mariette, Laboratoire d'
          Immunopathologie, Hopital, Saint-Louis, 1, avenue Claude Vellefaux,
          Paris, 75010, France
FEATURES   Location/Qualifiers
     source   1..339
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="Epstein-Barr transformed lymphoblastoid cell
                     line"
                     /tissue_type="blood"
     V_region   1..339
                     /product="kappa chain"
                     /note="VK IV family"
     V_segment   1..314
     J_segment   315..339
BASE COUNT   85 a   93 c   86 g   75 t
ORIGIN

Query Match   94.8%; Score 321.4; DB 9; Length 339;
Best Local Similarity 96.8%; Pred. No. 2e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACATAAGAAATACTTAGCT 120

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          |||||||||||||||||||||||||||||||||||||||
Db 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

RESULT 8
AR058974
LOCUS   AR058974   342 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5837845.
ACCESSION   AR058974
VERSION   AR058974.1 GI:5984551
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unclassified.
REFERENCE   1 (bases 1 to 342)
  AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
  TITLE   Human monoclonal antibody specifically binding to surface antigen
            of cancer cell membrane
  JOURNAL   Patent: US 5837845-A 4 17-NOV-1998;
FEATURES   Location/Qualifiers
     source   1..342
                     /organism="unknown"
BASE COUNT   88 a   92 c   87 g   75 t
ORIGIN

Query Match   94.8%; Score 321.4; DB 6; Length 342;
Best Local Similarity 96.8%; Pred. No. 2e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACACAAGAATTACTTAACT 120
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Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

RESULT 9
AR088798
LOCUS   AR088798   342 bp   DNA   linear   PAT 07-SEP-2000
DEFINITION Sequence 4 from patent US 5990287.
ACCESSION   AR088798
VERSION   AR088798.1 GI:10015561
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unclassified.
REFERENCE   1 (bases 1 to 342)
  AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
  TITLE   Human monoclonal antibody specifically binding to surface antigen
            of cancer cell membrane
  JOURNAL   Patent: US 5990287-A 4 23-NOV-1999;
FEATURES   Location/Qualifiers
     source   1..342
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BASE COUNT   88 a   92 c   87 g   75 t
ORIGIN

Query Match   94.8%; Score 321.4; DB 6; Length 342;
Best Local Similarity 96.8%; Pred. No. 2e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACATAAGAAATACTTAGCT 120

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

Db   301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

RESULT 10
AR088878
LOCUS   AR088878   342 bp   DNA   linear   PAT 07-SEP-2000
DEFINITION Sequence 4 from patent US 5990297.
ACCESSION   AR088878
VERSION   AR088878.1 GI:10015639
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 342)
AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
TITLE   Human monoclonal antibody specifically binding to surface antigen
            of cancer cell membrane
JOURNAL   Patent: US 5990297-A 4 23-NOV-1999;
FEATURES   Location/Qualifiers
   source   1..342
            /organism="unknown"
BASE COUNT   88 a   92 c   87 g   75 t
ORIGIN

Query Match   94.8%; Score 321.4; DB 6; Length 342;
Best Local Similarity 96.8%; Pred. No. 2e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

RESULT 11
E05868
LOCUS   E05868   342 bp   RNA   linear   PAT 29-SEP-1997
DEFINITION DNA sequence coding monoclonal antibody.
ACCESSION   E05868
VERSION   E05868.1 GI:2174055
KEYWORDS   JP 1993304987-A/4.
SOURCE   Unidentified.
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 342)
AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
TITLE   HUMAN TYPE MONOCLONAL ANTIBODY AND GENE CODING THE SAME, HYBRIDOMA
            AND ANTITUMOR AGENT
JOURNAL   Patent: JP 1993304987-A 4 19-NOV-1993;
            MITSUBISHI KASEI CORP
COMMENT   PN   JP 1993304987-A/4
            PD   19-NOV-1993
            PF   22-JUN-1992 JP 1992162849
            PR   28-JUN-1991 JP 91P 158859, 28-JUN-1991 JP 91P 158860, PR

            28-JUN-1991 JP 91P 158861
            PI   HOSOKAWA SEIKO, TAGAWA TOSHIAKI, HIRAKAWA YOKO, ITO NORIHIKO,
            PI   NAGAIKE KAZUHIRO
            PC   C12P21/08,A61K39/395,C12N5/28,C12N15/13//A61B10/00,C12N15/08,
            PC   G01N33/577,
            PC   (C12P21/08,C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   *source: tissue_type=human antibody GAH hybridoma.
FEATURES   Location/Qualifiers
   source   1..342
            /organism="synthetic construct"
            /db_xref="taxon:32630"
BASE COUNT   88 a   92 c   87 g   75 t
ORIGIN

Query Match   94.8%; Score 321.4; DB 6; Length 342;
Best Local Similarity 96.8%; Pred. No. 2e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

RESULT 12
HUMIGKAW
LOCUS   HUMIGKAW   405 bp   mRNA   linear   PRI 04-JAN-1995
DEFINITION Human Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5,
            5' end.
ACCESSION   M29467
VERSION   M29467.1 GI:185920
KEYWORDS   J-region; V-region; immunoglobulin-kappa; processed gene; variable
            region subgroup VK-IV
SOURCE   Human (patient POP) hybridoma AE6-5 DNA, clone pHuUCVK, derived
            from B-CLL cell line UC729-6.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 405)
AUTHORS   Spatz,L.A., Wong,K.K., Williams,M., Desai,R., Golier,J.,
            Berman,J.E., Alt,F.W. and Latov,N.
TITLE   Cloning and sequence analysis of the VH and VL regions of an
            anti-myelin/DNA antibody from a patient with peripheral neuropathy
            and chronic lymphocytic leukemia
JOURNAL   J. Immunol. 144 (7), 2821-2828 (1990)
MEDLINE   90203623
PUBMED   2156935
COMMENT   Draft entry and printed sequence for [1] kindly submitted by
            L.A.Spatz, 26-OCT-1989, for release after publication. Columbia
            University, Department of Neurology BB-322, 630 W. 168th street,
            New York, NY 10032.
FEATURES   Location/Qualifiers

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CDS              1..>405
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                 /db_xref="GDB:G00-119-341"
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mat_peptide      61..>405
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BASE COUNT       95 a      110 c      101 g       99 t
ORIGIN

Query Match             94.8%;  Score 321.4;  DB 9;  Length 405;
Best Local Similarity   96.8%;  Pred. No. 2.1e-94;
Matches  328;  Conservative  0;  Mismatches  11;  Indels  0;  Gaps  0;

Qy      1  GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db     61  GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy     61  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db    121  ATCAACTGCAAGTCAGCCAGAGTCTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180

Qy    121  TGGTACCAGCAGAAACCAGGACAGCAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTGGG 180
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Db    181  TGGTACCAGCAGAAACCAGGACAGCAGCCCTCCTAAGTTGCTCATTTGCTGGGCATCTGGG 240

Qy    181  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    241  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 300

Qy    241  ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db    301  ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 360

Qy    301  CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db    361  CCTCCGATGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 399
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RESULT 13
S50732
LOCUS       S50732            460 bp  mRNA    linear   PRI 08-MAY-1993
DEFINITION  immunoglobulin M light chain V region=anti-lipid A antibody [human,
            hybridoma cell line HR78, mRNA Partial, 460 nt].
ACCESSION   S50732
VERSION     S50732.1  GI:261239
KEYWORDS    .
SOURCE      Homo sapiens hybridoma cell line HR78.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Dorai,H., Bubbers,J.E. and Gillies,S.D.
  TITLE     Cloning and reexpression of a functional human IgM anti-lipid A
            antibody
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JOURNAL   Hybridoma 11 (5), 667-675 (1992)
MEDLINE   93093632
PUBMED    1459589
REMARK    GenBank staff at the National Library of Medicine created this
          entry [NCBI gibbsq 120606] from the original journal article.
          This sequence comes from Fig. 3A.
FEATURES             Location/Qualifiers
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BASE COUNT      107 a      124 c      120 g      109 t
ORIGIN

Query Match             94.8%;  Score 321.4;  DB 9;  Length 460;
Best Local Similarity   96.8%;  Pred. No. 2.1e-94;
Matches  328;  Conservative  0;  Mismatches  11;  Indels  0;  Gaps  0;

Qy      1  GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db     98  GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC 157

Qy     61  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db    158  ATCAACTGCAAGTCAGCCAGAGTCTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 217

Qy    121  TGGTACCAGCAGAAACCAGGACAGCAGCCCTCATTTACTGCTCATTTACTGGGCATCCCGG 180
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Db    218  TGGTACCAGCAGAAACCAGGACAGCAGCCCTCCTAAGTTGCTCATTTGCTGGGCATCCCGG 277

Qy    181  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db    278  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 337

Qy    241  ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db    338  ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 397

Qy    301  CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db    398  CCTCCGATGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 436
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RESULT 14
BC017870
LOCUS       BC017870            979 bp  mRNA    linear   PRI 06-DEC-2001
DEFINITION  Homo sapiens, Similar to immunoglobulin kappa constant, clone
            MGC:22669 IMAGE:4274551, mRNA, complete cds.
ACCESSION   BC017870
VERSION     BC017870.1  GI:17389701
KEYWORDS    MGC.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2001) National Institutes of Health, Mammalian
```

REMARK   Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
COMMENT   NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: CLONTECH
          cDNA Library Preparation: CLONTECH Laboratories, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Sequencing Group at the Stanford Human Genome
          Center, Stanford University School of Medicine, Stanford, CA 94305
          Web site: http://www-shgc.stanford.edu
          Contact: (Dickson, Mark) mcd@paxil.stanford.edu
          Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
          R. M.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 35 Row: i Column: 15
          This clone was selected for full length sequencing because it
          passed the following selection criteria: GenomeScan gene
          prediction, similarity but not identity to protein.
FEATURES   Location/Qualifiers
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                   LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
                   ACEVTHQGLSSPVTKSFNRGEC"
BASE COUNT   261 a   275 c   230 g   213 t
ORIGIN

Query Match   94.8%; Score 321.4; DB 9; Length 979;
Best Local Similarity 96.8%; Pred. No. 2.3e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy   331 ATCAGCAGCCTGCAGGCTGAAGATGTGCAGTTTATTACTGTCAGCAATATTATAGTACT 390

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db   391 CCTCAGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 429

RESULT 15
AF455557
LOCUS   AF455557   342 bp   mRNA   linear   PRI 09-JAN-2002
DEFINITION Homo sapiens clone RIZMVL6 anti-cardiolipin immunoglobulin light
            chain mRNA, partial cds.
ACCESSION   AF455557
VERSION   AF455557.1   GI:18092613
KEYWORDS   .
SOURCE   Homo sapiens.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 342)
  AUTHORS   Lieby,P., Soley,A., Cerutti,M., Freyssinet,J.M., Pasquali,J.L. and
            Martin,T.
  TITLE   Anticardiolipin antibodies in normal individuals
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 342)
  AUTHORS   Lieby,P., Soley,A., Cerutti,M., Freyssinet,J.M., Pasquali,J.L. and
            Martin,T.
  TITLE   Direct Submission
  JOURNAL   Submitted (05-DEC-2001) Laboratoire d'immunopathologie, Institut
            d'immunologie et d'Hematologie, 1 place de l'Hopital, Strasbourg
            67091, France
FEATURES   Location/Qualifiers
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BASE COUNT   86 a   93 c   88 g   75 t
ORIGIN

Query Match   94.3%; Score 319.8; DB 9; Length 342;
Best Local Similarity 96.5%; Pred. No. 6.9e-94;
Matches 327; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAATAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db   241 ATCAGCAGCCTGCGGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAATACT 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Search completed: July 18, 2003, 13:47:35
Job time : 949.849 secs

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          GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      July 18, 2003, 04:16:54 ; Search time 587.455 Seconds
                          (without alignments)
                          9345.860 Million cell updates/sec

Title:        US-09-627-896B-26
Perfect score: 339
Sequence:    1 gacatccagttgacccagtc.........ggaccaaggtggaaatcaaa 339

Scoring table: IDENTITY_NUC
          Gapop 10.0 , Gapext 1.0

Searched:    1615406 seqs, 809774376 residues

Total number of hits satisfying chosen parameters:    32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
          Listing first 45 summaries

Database :    EST:*
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          2:  em_esthum:*
          3:  em_estin:*
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          5:  em_estcov:*
          6:  em_estpl:*
          7:  em_estro:*
          8:  em_htc:*
          9:  gb_est1:*
          10: gb_est2:*
          11: gb_htc:*
          12: gb_est3:*
          13: gb_est4:*
          14: gb_est5:*
          15: em_estfun:*
          16: em_estom:*
          17: gb_gss:*
          18: em_gss_hum:*
          19: em_gss_inv:*
          20: em_gss_pln:*
          21: em_gss_vrt:*
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          23: em_gss_mam:*
          24: em_gss_mus:*
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          26: em_gss_pro:*
          27: em_gss_rod:*

                  SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1	323	95.3	964	12	BG757678	BG757678 602711268
2	321.4	94.4	886	12	BF674779	BF674779 602137932
3	319.8	94.3	641	10	AW405821	AW405821 UI-HF-BLO
4	318.2	93.9	533	10	AW802126	AW802126 IL5-UM007
5	311.8	92.0	935	12	BG398034	BG398034 602439564
6	310.2	91.5	643	10	AW390292	AW390292 CM2-ST018

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 7  310.2  91.5  691  12  BF128999  BF128999 601811318
 8  305.4  90.1  508  10  AW406572  AW406572 UI-HF-BLO
 9  305.4  90.1  550  10  AW404610  AW404610 UI-HF-BLO
10  305.4  90.1  904  14  BQ711273  BQ711273 AGENCOURT
11  303.8  89.6  630  10  AW406512  AW406512 UI-HF-BLO
12  303.8  89.2  798  12  BG426036  BG426036 602492715
13  302.4  89.2  921  12  BG569993  BG569993 602590249
14  302.2  89.1  553  12  BF870122  BF870122 IL3-ET011
15  299.4  88.3  757  12  BG484518  BG484518 602205173
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18    297   87.6  388  10  AW951579  AW951579 EST63649
19  296.4  87.4  573  12  BF128829  BF128829 601811013
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22  296.4  87.4  887  12  BF663188  BF663188 602144432
23  295.8  87.3  761  12  BG536372  BG536372 602564763
24  295.6  87.2  957  12  BG756233  BG756233 602713544
25  294.2  86.8  473  12  BQ083970  BQ083970 K-EST0147
26  294.2  86.8  661  14  BM831430  BM831430 K-EST0105
27  294.2  86.8 1057  12  BG539525  BG539525 602558157
28  292.6  86.3  495  14  BQ082810  BQ082810 K-EST0144
29  292.6  86.3  665  14  BM768906  BM768906 K-EST0051
30  292.6  86.3  876  12  BG397563  BG397563 602438602
31  292.6  86.3  984  14  BQ707260  BQ707260 AGENCOURT
32  291.4  86.3  769  12  BG534966  BG534966 602554155
33  291.8  86.1  473  12  BG685769  BG685769 602637868
34  291.8  86.1  826  12  BG758298  BG758298 602712482
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37    291   85.8  767  12  BG541967  BG541967 602569470
38    290   85.5  328  10  AW406484  AW406484 UI-HF-BLO
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42  289.4  85.4  541  12  BG547312  BG547312 602574731
43  289.4  85.4  649  14  BM769427  BM769427 K-EST0052
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                       ALIGNMENTS

RESULT 1
BG757678
LOCUS         BG757678             964 bp    mRNA    linear  EST 15-MAY-2001
DEFINITION    602711268F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851521 5',
              mRNA sequence.
ACCESSION     BG757678
VERSION       BG757678.1  GI:14068331
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 964)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1694 row: h column: 18
              High quality sequence stop: 784.
FEATURES             Location/Qualifiers
     source          1 ..964
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High quality sequence stop: 576.

FEATURES   Location/Qualifiers
source   1..886
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4274551"
                     /clone_lib="NIH_MGC_83"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site 1: SfiI (ggccgcctcggcc); Site 2: SfiI (ggccattatggcc
                     ); 5' and 3' adaptors were used in cloning as follows:5'
                     adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence: 5'-ATTCTAGAGGCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T). Average
                     insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
                     contained inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."

BASE COUNT   218 a   214 c   245 g   209 t
ORIGIN

Query Match
Best Local Similarity   94.8%;   Score 321.4;   DB 12;   Length 886;
                        96.8%;   Pred. No. 2.1e-87;
Matches 328;   Conservative 0;   Mismatches 11;   Indels 0;   Gaps 0;

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Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db  91 GACATCGTGATGACCCAGTCTCCAGATTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 150

Qy  61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
       |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||| | |
Db 151 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTTTCT 210

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db 211 TGGTACCAGCAGAAACCAGGACAGCCGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 270

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 330

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 331 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 390

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
       |||| ||||||||||||||||||||||||||||||||||
Db 391 CCTCAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 429
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RESULT 3
AW405821
LOCUS   AW405821   641 bp   mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BL0-abp-h-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3057636 5', mRNA sequence.
ACCESSION   AW405821
VERSION   AW405821.1   GI:6924878
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 641)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab

                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4851521"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT   236 a   280 c   238 g   210 t
ORIGIN

Query Match
Best Local Similarity   95.3%;   Score 323;   DB 12;   Length 964;
Conservative   97.1%;   Pred. No. 7.2e-88;
Matches 329;   Conservative 0;   Mismatches 10;   Indels 0;   Gaps 0;

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Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db  59 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 118

Qy  61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db 119 ATCAACTGCAAGTCCAGCCAGAGTGTTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 178

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db 179 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 238

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db 239 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 298

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 299 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 358

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db 359 CCAAAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 397
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RESULT 2
BF674779
LOCUS   BF674779   886 bp   mRNA   linear   EST 21-DEC-2000
DEFINITION 602137932F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274551 5',
            mRNA sequence.
ACCESSION   BF674779
VERSION   BF674779.1   GI:11948674
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 886)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Place: LLCM1091 row: p column: 08

COMMENT   Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward.

FEATURES   Location/Qualifiers
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                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT   159 a   178 c   163 g   141 t
ORIGIN

Query Match   94.3%;   Score 319.8; DB 10; Length 641;
Best Local Similarity   96.5%;   Pred. No. 5.9e-87;
Matches 327;   Conservative   0; Mismatches 12; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTCATTTACTGGCCATCTACCACCGG 180
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Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db   293 ATCAGCAGCCTGCAGGCTGAGGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 352

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           |||||||||||||||||||||||||||||||||||||||
Db   353 CCTCGGACGTTCGGCCAGGGGACCAAGGTGGAAATCAAA 391

RESULT 4
AW802126
LOCUS   AW802126   533 bp   mRNA   linear   EST 16-MAY-2000
DEFINITION IL5-UM0071-120400-065-d06 UM0071 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW802126
VERSION   AW802126.1 GI:7853996
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 533)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   MEDLINE   20202663

COMMENT   Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5-UM0071-120
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             Seg primer: puc 18 forward
             High quality sequence stop: 419.

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="UM0071"
                     /dev_stage="Adult"
                     /note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2:
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."

BASE COUNT   131 a   145 c   137 g   120 t
ORIGIN

Query Match   93.9%;   Score 318.2; DB 10; Length 533;
Best Local Similarity   96.2%;   Pred. No. 1.7e-86;
Matches 326;   Conservative   0; Mismatches 13; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db   135 TGGTATCAGCAGAAACCAGGGCAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 194

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db   195 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 254

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGCAAGTTTATTACTGTGTCAGCAATATTATAGTACT 300
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Db   255 ATCAGCAGCCTGCAGGCTGAAGATGTGCAAGTTTATTACTGTGTCAGCAATATTATAGTACT 314

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           ||| |||||||| ||||||||||||||||||||||||||
Db   315 CCCCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA 353

RESULT 5
BG398034
LOCUS   BG398034   935 bp   mRNA   linear   EST 12-MAR-2001
DEFINITION 602439564F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565991 5',
            mRNA sequence.
ACCESSION   BG398034
VERSION   BG398034.1 GI:13291482
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 935)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1283   row: o   column: 16
             High quality sequence stop: 764.

FEATURES   Location/Qualifiers
     source   1..935
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:4565991"
              /clone_lib="NIH_MGC_48"
              /tissue_type="primary B-cells from tonsils (cell line)"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
              Site 2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Size-selected >500bp
              for average insert size 1.8kb. Library constructed by Ling
              Hong in the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

BASE COUNT   231 a   249 c   234 g   221 t
ORIGIN

Query Match   92.0%;   Score 311.8;   DB 12;   Length 935;
Best Local Similarity   95.0%;   Pred. No. 1.9e-84;
Matches 322;   Conservative   0;   Mismatches   17;   Indels   0;   Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC   60
            |||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||
Db   66 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 125

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
            |||||||||||||||||||||||||||| ||| |||||||||| |||||||||||| |||
Db   126 ATCAACTGCAAGTCCAGCCAGACTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 185

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGACATCTACCCGG 180
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||
Db   186 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGACATCTACCCGG 245

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   246 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 305

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   306 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATACTACT 365

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
            |||||||| ||||||||||||||||||||||||||||||
Db   366 CCTATCACTTTCGGCCCTGGGACCCAAGTGGATATCAAA 404

RESULT 6
AW390292
LOCUS   AW390292   643 bp   mRNA   linear   EST 04-FEB-2000
DEFINITION   CM2-ST0182-221099-023-F04 ST0182 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW390292
VERSION   AW390292.1   GI:6894951
KEYWORDS   EST.
SOURCE   human.
             Homo sapiens
  ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 643)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE   The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM2&t2=CM2-ST0182-
             221099-023-f04&t3=1999-10-22&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 7
             High quality sequence stop: 641.

FEATURES   Location/Qualifiers
     source   1..643
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_lib="ST0182"
              /dev_stage="Adult"
              /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
              Site 2: SmaI; A mini-library was made by cloning products
              derived from ORESTES PCR (U.S. Letters-Patent application
              No. 196,716 - Ludwig Institute for Cancer Research)
              profiles into the pUC 18 vector. Reverse transcription of
              tissue mRNA and cDNA amplification were performed under
              low stringency conditions."

BASE COUNT   162 a   173 c   162 g   146 t
ORIGIN

Query Match   91.5%;   Score 310.2;   DB 10;   Length 643;
Best Local Similarity   94.7%;   Pred. No. 5.1e-84;
Matches 321;   Conservative   0;   Mismatches   18;   Indels   0;   Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC   60
            |||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db   69 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 128

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
            |||||||||||||||||||||||||||| ||| |||||||||| |||||||||||| |||
Db   129 ATCAACTGCAAGTCCAGCCAGACTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 188

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGACATCTACCCGG 180
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||
Db   189 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCGTCTTTTACTGGGACATCTACCCGG 248

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
            |||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   249 AAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 308

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   309 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTTTAGTCAT 368

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
            |||||||| |||||||||||||||||||||||||||||
Db   369 CCTCAAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 407

RESULT 7
BF128999
LOCUS   BF128999   691 bp   mRNA   linear   EST 24-OCT-2000
DEFINITION   601811318F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054205 5',
             mRNA sequence.
ACCESSION   BF128999
VERSION   BF128999.1   GI:10968039
KEYWORDS   EST.
SOURCE   human.

ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 691)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished.(1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Ling Hong/Rubin Laboratory
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM894 row: c column: 06
          High quality sequence stop: 682.
FEATURES   Location/Qualifiers
     source   1..691
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone_lib="NIH_MGC_48"
                   /clone="IMAGE:4054205"
                   /tissue_type="primary B-cells from tonsils (cell line)"
                   /lab_host="DH10B (phage-resistant)"
                   /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                   Site_2: EcoRI; cDNA made by oligo-dT priming,
                   Directionally cloned into EcoRI/XhoI sites using the
                   following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                   for average insert size 1.8kb. Library constructed by Ling
                   Hong in the laboratory of Gerald M. Rubin (University of
                   California, Berkeley) using ZAP-cDNA synthesis kit
                   (Stratagene) and Superscript II RT (Life Technologies)..
                   Note: this is a NIH_MGC library."
BASE COUNT   160 a   175 c   178 g   176 t   2 others
ORIGIN

Query Match   91.5%; Score 310.2; DB 12; Length 691;
Best Local Similarity 96.8%; Pred. No. 5.2e-84;
Matches 328; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTCTCGGCGAGAGGGCCACC 60
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   230 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTCTCGGCGAGAGGGCCACC 289

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAACAAGAATTACTTAACT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 349

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 409

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGACACAGATTTCACTCTCACC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGACACAGATTTCACTCTCACC 469

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   470 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTA-- 527

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           ||| |||||||||||||||||||||||||||||||||||
Db   528 -CTGGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 565

RESULT 8
AW406572
LOCUS   AW406572   508 bp mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BLo-acu-g-10-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3060307 5', mRNA sequence.
ACCESSION   AW406572

VERSION   AW406572.1 GI:6925629
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 508)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
     source   1..508
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:3060307"
                   /clone_lib="NIH_MGC_37"
                   /tissue_type="lymph"
                   /cell_type="germinal center B cells"
                   /cell_line="MGC85"
                   /lab_host="DH10B (LN1)"
                   /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                   Constructed from size fractionated cytoplasmic mRNA
                   (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                   M. Staudt, Ph.D. Library preparation by Maria de Fatima
                   Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   115 a   139 c   126 g   128 t
ORIGIN

Query Match   90.1%; Score 305.4; DB 10; Length 508;
Best Local Similarity 93.8%; Pred. No. 1.4e-82;
Matches 318; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAACAAGAATTACTTAACT 120
           |||||||||||||||||||||||||||||||||||||||| || || |||||||| ||| ||
Db   121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTCCTTAACT 180

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGATGATCATTTACTGGCATCTCCCCGG 240

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGACAGATTTCACTCTCACC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGACAGATTTCACTCTCACC 300

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATCATAGTATT 360

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           ||| |||||||||||||||||||||| ||||
Db   361 CCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 399

RESULT 9
AW404610
LOCUS   AW404610   550 bp mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BLo-acc-a-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3058451 5', mRNA sequence.

ACCESSION   AW404610
VERSION   AW404610.1 GI:6923667
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 550)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
     source   1..550
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3058451"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LfTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   140 a   150 c   139 g   121 t
ORIGIN

Query Match
Best Local Similarity   90.1%;   Score 305.4;   DB 10;   Length 550;
Matches 318;   Conservative   0; Mismatches   21; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGAGGGCCACC 60
          |||||||||||| |||||||||||||||||||||| |||||||||||||||||| |||||
Db   22 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGAGGGCCACC 81

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   82 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 141

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   142 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAACTGCTCATTTACCGGGGCATCTACCCGG 201

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 261

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   262 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTATTGTCAGCAATATTATAGTACT 321

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          || ||||||||||||||||||||||||||||||||||
Db   322 CCCATCACCTTCGGCCAAGGGACACGGACTGGAGATTAAA 360

RESULT 10
BQ711273
LOCUS   BQ711273
DEFINITION AGENCOURT_B353747 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278306
            904 bp   mRNA   linear   EST 16-JUL-2002

ACCESSION   BQ711273
VERSION   BQ711273.1 GI:21850172
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 904)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2466 row: b column: 03
             High quality sequence stop: 679.
FEATURES   Location/Qualifiers
     source   1..904
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278306"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT   208 a   264 c   219 g   212 t
ORIGIN

Query Match
Best Local Similarity   90.1%;   Score 305.4;   DB 14;   Length 904;
Matches 318;   Conservative   0; Mismatches   21; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGAGGGCCACC 60
          |||||||||||| |||||||||||||||||||||| |||||||||||||||||| |||||
Db   63 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGAGGGCCACC 122

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   123 TTCAACTGCAAGTCCAGCCAGAGTGTTTTATACACAGTCCAACAATAAGAACTCCTTAGCT 182

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
          |||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db   183 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGCTGCTCATTTTCTGGGCATCTACCCGG 242

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 GAATCTGGGGTCCCTGACCGCTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 302

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db   303 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTAGT 362

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          ||||||||| ||||||||||||||||||||||||||||
Db   363 CCTCCGACTTTTGGCCAGGGGACCAAGTCTGGAGATCAGA 401

RESULT 11
AW406512
LOCUS   AW406512   630 bp   mRNA   linear   EST 16-FEB-2000

LOCUS   BG426036   798 bp   mRNA   linear   EST 14-MAR-2001
DEFINITION   602492715F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4606658 5',
                mRNA sequence.
ACCESSION   BG426036
VERSION   BG426036.1 GI:13332542
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 798)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: CLONTECH Laboratories, Inc.
                cDNA Library Preparation: CLONTECH Laboratories, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLCM1345 row: n column: 03
                High quality sequence stop: 542.
FEATURES   Location/Qualifiers
     source   1..798
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4606658"
                     /clone_lib="NIH_MGC_75"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC library."
BASE COUNT   192 a   213 c   212 g   181 t
ORIGIN

Query Match   89.6%; Score 303.8; DB 12; Length 798;
Best Local Similarity   93.5%; Pred. No. 5e-82;
Matches 317; Conservative   0; Mismatches 22; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||||||||||||||||||||||| |||| ||| ||||||||||||||||||||||
Db   91 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 150

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACACAAGAATTACTTAACT 120
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   151 ATCAACTGCAAGTCCAGCCAGAGTGTTTTGTCCAGCTCCAACATAAGAACTACTTAGTT 210

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 TGGTACCAGCACAAACCAGGACAGCCCTCCTAAACTGCTCATTTCCTGGGACAGATTCACC 270

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGCAGCAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGCAGCAGATTTCACTCTCACC 330

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 ATCAGCAGTCTGCAGGCTGCAGATGTGGCAGTTTATTACTGTCAGCAATGTTATAGTGCT 390

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||||||| |||||||||||||||||||||||||||
Db   391 CCTTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA 429

RESULT 12
BG426036

DEFINITION   UI-HF-BL0-acu-a-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
                IMAGE:3060017 5', mRNA sequence.
ACCESSION   AW406512
VERSION   AW406512.1 GI:6925569
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 630)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Eco RI site shown at the beginning of the sequence.
                Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                cDNA Library Preparation: M.B. Soares Lab
                cDNA Library Arrayed by: M.B. Soares Lab
                DNA Sequencing by: M.B. Soares Lab
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html
                Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
     source   1..630
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3060017"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LITI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb) Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   162 a   178 c   156 g   134 t
ORIGIN

Query Match   89.6%; Score 303.8; DB 10; Length 630;
Best Local Similarity   93.5%; Pred. No. 4.6e-82;
Matches 317; Conservative   0; Mismatches 22; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||||||||||||||||||||||| |||| ||| ||||||||||||||||||||||
Db   20 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 79

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACACAAGAATTACTTAACT 120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   80 ATCAACTGCAAGTCCAGCCAGAGTCTTTTATACAGCTCCAACATAAGAATTCTTAGTT 139

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140 TGGTACCAGCAGAAACCAGGACAGCCCTCCTAAGCTGCTCATTTCCTGGGCATCTACCCGG 199

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGCAGCAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGCAGCAGATTTCACTCTCACC 259

Qy   241 ATCAGCAGCCTGCAGGCTGAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   260 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTATT 319

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||||| |||||||||||||||||||||||||||
Db   320 CCCTTCACTTTCGGCCAAGGGACCACGACGACTGGAGATTAAA 358

RESULT 13
BG569993
LOCUS   BG569993   921 bp   mRNA   linear   EST 10-APR-2001
DEFINITION   602590249F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4716948 5',
               mRNA sequence.
ACCESSION   BG569993
VERSION   BG569993.1   GI:13577646
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 921)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: CLONTECH Laboratories, Inc.
               cDNA Library Preparation: CLONTECH Laboratories, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM1566 row: a   column: 13
               High quality sequence stop: 596.
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     source   1..921
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:4716948"
               /clone_lib="NIH_MGC_77"
               /lab_host="DH10B (T1 phage-resistant)"
               /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
               SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
               3' adaptors were used in cloning as follows: 5' adaptor
               sequence: 5'-CACGGCGCCATTATGGCC-3' and 3' adaptor sequence:
               5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
               C, or G and N = A, C, G, or T). Average insert size 1.9
               kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
               by PCR. This library was enriched for full-length clones
               and was constructed by Clontech Laboratories (Palo Alto,
               CA). Note: this is a NIH MGC Library."
BASE COUNT   269 a   251 c   238 g   163 t
ORIGIN

Query Match   89.2%; Score 302.4; DB 12; Length 921;
Best Local Similarity 95.0%; Pred. No. 1.4e-81;
Matches 323; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 149

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   150 ATCAACTGCAAGTCCAGCCAGAGTGTTTTTATACAGCTCCAATAATAAGAACTACTTAACT 209

Qy   121 TGGTACCAGCAGAAACCAGGACAGC-CTCCTAAGCTGCTCATTTACTGGGCATCTACCCG 179
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   210 TGGTACCAGCAGAAACCAGGACAGCACTCCTAAGCTGCTCATTTACTGGGCATCTACCCG 269

Qy   180 GGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 GGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 329

Qy   240 CATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTAC 299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 CATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATTACTAC 389

Qy   300 TGCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 339

RESULT 14
BF870122/c
LOCUS   BF870122   553 bp   mRNA   linear   EST 17-JAN-2001
DEFINITION   IL3-ET0116-281000-308-H01 ET0116 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF870122
VERSION   BF870122.1   GI:12260252
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 553)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
               Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
               ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3-ET0116-
               281000-308-H01&t3=2000-10-28&t4=1)
               Seq primer: puc 18 forward
               High quality sequence start: 46
               High quality sequence stop: 99.
FEATURES   Location/Qualifiers
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               /db_xref="taxon:9606"
               /clone_lib="ET0116"
               /dev_stage="Adult"
               /note="Organ: lung-tumor; Vector: puc18; Site_1: SmaI;
               Site_2: SmaI; A mini-library was made by cloning products
               derived from ORESTPS PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
BASE COUNT   125 a   140 c   150 g   138 t
ORIGIN

Query Match   89.1%; Score 302.2; DB 12; Length 553;
Best Local Similarity 93.2%; Pred. No. 1.3e-81;
Matches 316; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 492

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||||||||||||||||||||||||| |||| |||||||
Db   491 ATCAACTGCAAGTCCAGCCAGAGTGTTTTTATACAGCTTAAACAATTGAACTACATAGCT 432

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTGCTCATTTACTGGGCATCTACCCGG 180
          |||||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||
Db   431 TGGTACCAGCAGAAAGCCGGACCAGCCTCCTAAGTTACTCATTTACTTGGGCATCTACCCGG 372

Db   390 TCCCTACACTTTTGGCCCAGGGGACCAAGCTGGAGATCAAA 429
          ||| ||| |||| |||||| |||||||||| |||||| ||||||

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Qy   181 GAATCCGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTCGGACAGATTTCACTCTCACC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 GAATCCGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTCGGACAGATTTCACTCTCACC 312

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTATTACTGTCAGCAATATTATGCAACT 300
             |||||||||||||||||||||||||||| |||| ||||||||||||||| |||| ||
Db   311 ATCAGCAGCCTGCAGGCAGAGATGTGGCAGTTTATTACTGTCAGCAACATTATGCAACT 252

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
             |||| |||||||||||||||||||||||||||||||||
Db   251 CCTCGGACGTTCGGCCAAGGGGCCAAGGTGGAAATCAAA 213
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RESULT 15
BG484518

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LOCUS       BG484518                 757 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602505173F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4618290 5',
            mRNA sequence.
ACCESSION   BG484518
VERSION     BG484518.1   GI:13416797
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1376 row: b column: 19
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
     source          1..757
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4618290"
                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
                     SfiI (ggccgcctcggcc); Site 2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA). Note: this is a NIH MGC Library."
BASE COUNT      195 a    202 c    203 g    157 t
ORIGIN
```

```
Query Match       88.3%;   Score 299.4;  DB 12;  Length 757;
Best Local Similarity 95.0%;  Pred. No. 1.1e-80;
Matches  322;  Conservative  0;  Mismatches  11;  Indels  6;  Gaps  1;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGGAGAGGGCCACC 60
           ||||||||||||||| ||||||||||| |||||||| ||| ||||||||||||| ||
Db    92 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGGGAGGGCCACC 151

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
           ||||| |||||||||||||||||||||||| |||||  |||||||||||||||||||||
Db   152 ATCAACTGCAAGTCCAGCCAGAGTGTTTTTTATACAGCTC------CACGAATTACTTAGCT 205

Qy   121 TGGTACCAGCAGAAACCAGGACAGCGCCTCCTAAGCTGCTGCTTCATTTACTGGGCATCTACCCGG 180
```

```
Db   206 TGGTACCAGCAGAAACCAGGACAGCGCCTCCTAAACTGCTCATTTATTGGGCATCTACCCGG 265

Qy   181 GAATCCGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTCGGACAGATTTCACTCTCACC 240

Db   266 GAATCCGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTCGGACAGATTTCACTCTCACC 325

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTATTACTGTCAGCAATATTATGCAACT 300

Db   326 ATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATGCAACT 385

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

Db   386 CCTCCAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 424
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Search completed: July 18, 2003, 09:26:08
Job time : 591.455 secs
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 18, 2003, 04:14:58 ; Search time 87.8822 Seconds
(without alignments)
8606.944 Million cell updates/sec

Title: US-09-627-896b-26
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Score	Query Match	Length	DB	ID	Description
1	327.8	96.7	400	9	AAN80499	Encodes V region o
2	327.8	96.7	1373	9	AAN80941	Encodes Vchi regio
3	326.2	96.2	619	9	AAN80498	Encodes V region o
4	321.4	94.8	342	14	AAQ33032	MAb GAH variable r
5	319	94.1	360	15	AAQ71718	Monoclonal antibod
6	318.2	93.9	357	24	ABA94219	ebvHigM MSI19D10 l
7	315.2	93.0	463	21	AAC98443	Human colon cancer
8	315	92.9	360	22	AAH47729	Nucleotide sequenc
9	314	92.6	1028	14	AAQ45606	Sequence of pATDFL

10	314	92.6	1028	20	AAZ39437	DNA sequence of Hu
11	314	92.6	1028	20	AAZ23975	Plasmid pATDFLAG F
12	314	92.6	1330	14	AAZ45605	Sequence of Hum4 V
13	314	92.6	1330	20	AAZ39436	DNA sequence of Hu
14	314	92.6	1330	20	AAZ23974	Human Hum4L-CC49 V
15	314	92.6	1359	14	AAQ45607	Sequence of pSC49F
16	314	92.6	1359	20	AAZ39438	DNA sequence of pS
17	314	92.6	1359	20	AAZ23976	Plasmid pSC49FLAG
18	313.4	92.4	1048	20	AAZ23970	Human Hum4 VL ClaI
19	313.4	92.4	1088	20	AAZ39432	Nucleotide sequenc
20	311.8	92.0	792	20	ABQ56219	Human ovarian anti
21	311.8	92.0	1003	22	AAS00145	Human cDNA clone H
22	311.8	92.0	1088	15	AAQ56735	Sequence of Hum4VL
23	311.6	91.9	339	20	AAX90025	Nucleotide sequenc
24	311.6	91.9	423	20	AAX90025	Human monoclonal a
25	310.8	91.7	1361	15	AAQ56740	Sequence of plasmi
26	310.2	91.5	342	18	AAT60383	Anti-TGF beta-1 sc
27	310.2	91.5	342	24	ABK24413	Light chain DNA fr
28	310.2	91.5	407	13	AAQ26047	V-region of L-chai
29	310.2	91.5	804	24	ABQ56211	Human ovarian anti
30	310	91.4	339	21	AAA96134	Nucleotide sequenc
31	310	91.4	339	21	AAA96150	Nucleotide sequenc
32	309	91.2	339	21	AAA96158	Nucleotide sequenc
33	306.8	90.5	339	21	AAA96138	Nucleotide sequenc
34	306.8	90.5	339	21	AAA96140	Nucleotide sequenc
35	305.4	90.1	342	22	AAF29082	Human HIV-1 monocl
36	305.4	90.1	660	20	AAX77410	JP1127855 Seq ID
37	305.4	90.1	1097	14	AAQ45602	Sequence of the Hu
38	301.6	89.0	836	14	AAQ45604	Nucleotide sequenc
39	301.6	89.0	836	20	AAZ39435	Human SCFV1 DNA.
40	301.6	89.0	836	20	AAZ23973	IgM antibody CEM 1
41	300.8	88.7	447	20	AAZ20412	LNBOTDC vector #2.
42	300.4	88.6	9511	24	AAD28297	LNBOTDC vector #2.
43	300.4	88.6	9511	24	AAD28332	Nucleotide sequenc
44	298.8	88.1	339	21	AAA96132	Nucleotide sequenc
45	298.8	88.1	339	21	AAA96148	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAN80499
ID   AAN80499 standard; DNA; 400 BP.
XX
AC   AAN80499;
XX
DT   03-DEC-1990 (first entry)
XX
DE   Encodes V region of L chain of anti-P.aeruginosa exotoxin Ab #2.
XX
KW   Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   sig_peptide   1..20
FT   /*tag= a
XX
PN   EP270077-A.
XX
PD   08-JUN-1988.
XX
PF   01-DEC-1987; 87EP-0117760.
XX
PR   03-DEC-1986; 86JP-0288340.
PR   26-NOV-1987; 87JP-0298513.
XX
PA   (SUMO) SUMITOMO CHEM IND KK.
XX
PI   Nakatani T, Nomura N, Horigome K, Noguchi H;
XX

DR   WPI; 1988-156310/23.
DR   P-PSDB; AAP80894.
XX
PT   New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT   plus recombinant vectors and host cells, useful for treating
PT   infections.
XX
PS   Claim 5; page 27; 39pp; English.
XX
CC   Sequence encodes variable region of light chain of anti-exotoxin
CC   antibody. It encodes the same protein sequence as AAN80498 except
CC   that the signal sequence of AAN80498 contains an intron.
CC   See also AAN80495-N80496, AAN80498 and AAN80941-2.
XX
SQ   Sequence 400 BP; 93 A; 109 C; 101 G; 97 T; 0 other;

Query Match   96.7%; Score 327.8; DB 9; Length 400;
Best Local Similarity   97.9%; Pred. No. 2.4e-95;
Matches 332;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC   60
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
         |||||||||||||||||||||||||||||||||| ||||||||| |||| |||||| ||
Db 121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240

Qy 181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 300

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 360

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
         ||||| |||||||||||||||||||||||||||||||
Db 361 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 399

RESULT 2
AAN80941
ID   AAN80941 standard; DNA; 1373 BP.
XX
AC   AAN80941;
XX
DT   03-DEC-1990 (first entry)
XX
DE   Encodes Vchi region of FK-001 from lambda gFK1.
XX
KW   Pseudomonas aeruginosa; anti-exotoxin antibody; FK-001;
KW   lambda gFK1; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS.   532..882
FT   /*tag= a
FT   /product=V region
XX
PN   EP270077-A.
XX
PD   08-JUN-1988.
XX
PF   01-DEC-1987; 87EP-0117760.
XX
PR   03-DEC-1986; 86JP-0288340;
PR   26-NOV-1987; 87JP-0298513.

XX
PA   (SUMO) SUMITOMO CHEM IND KK.
XX
PI   Nakatani T, Nomura N, Horigome K, Noguchi H;
XX
DR   WPI; 1988-156310/23.
XX
PT   New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT   plus recombinant vectors and host cells, useful for treating
PT   infections.
XX
PS   Disclosure; ; p; English.
XX
CC   Genomic DNA was isolated from the Epstein Barr virus-transformed
CC   human cell line FK001, fragmented and a gene library constructed.
CC   The library was screened with H or L chain probes and positive
CC   clones were identified including lambda gFK1. This clone contained
CC   an 11.5kb insert encoding the V and C regions of kappa chain.
CC   EcoRI digested vector pSV2neo was end-filled and then blunt-end
CC   ligated to a SalI linker to form pSV2neoSalI. This plasmid and
CC   gFK1 were both digested with SalI and ligated together to form
CC   pSV2neogFK1 which was itself digested with PvuI. The plasmid
CC   pSV2dhfr was likewise digested with PvuI and a mixture of the two
CC   was used to transform mouse myeloma cells which then expressed
CC   the antibody.
CC   See also AAN80495-N80496, AAN80499 and AAN80942.
XX
SQ   Sequence 1373 BP; 396 A; 264 C; 306 G; 407 T; 0 other;

Query Match   96.7%; Score 327.8; DB 9; Length 1373;
Best Local Similarity   97.9%; Pred. No. 4e-95;
Matches 332;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC   60
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 543 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 602

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
         |||||||||||||||||||||||||||||||||| ||||||||| |||| |||||| ||
Db 603 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 662

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 663 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 722

Qy 181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 723 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 782

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 783 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 842

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
         ||||| |||||||||||||||||||||||||||||||
Db 843 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 881

RESULT 3
AAN80498
ID   AAN80498 standard; DNA; 619 BP.
XX
AC   AAN80498;
XX
DT   03-DEC-1990 (first entry)
XX
DE   Encodes V.region of L chain of anti-P.aeruginosa exotoxin Ab #1.
XX
KW   Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
KW   ds.
XX
OS   Homo sapiens.
XX

FH   Key   Location/Qualifiers
FT   sig_peptide   1..49
FT   /*tag= a
FT   sig_peptide   269..279
FT   /*tag= b
FT   intron   50..268
FT   /*tag= c
XX
PN   EP270077-A.
XX
PD   08-JUN-1988.
XX
PF   01-DEC-1987; 87EP-0117760.
XX
PR   03-DEC-1986; 86JP-0288340.
PR   26-NOV-1987; 87JP-0298513.
XX
PA   (SUMO) SUMITOMO CHEM IND KK.
XX
PI   Nakatani T, Nomura N, Horigome K, Noguchi H;
XX
DR   WPI; 1988-156310/23.
DR   P-PSDB; AAP80894.
XX
PT   New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT   plus recombinant vectors and host cells, useful for treating
PT   infections.
XX
PS   Claim 5; page 26; 39pp; English.
XX
CC   Sequence encodes variable region of light chain of anti-exotoxin
CC   antibody. The signal sequence contains an intron which is spliced
CC   out prior to translation.
CC   See also AAN80495-N80496, AAN80499 and AAN80941-2.
XX
SQ   Sequence 619 BP; 177 A; 139 C; 134 G; 169 T; 0 other;

Query Match   96.2%; Score 326.2; DB 9; Length 619;
Best Local Similarity   97.7%; Pred. No. 9.3e-95;
Matches 331; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
            |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   280 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 339

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
            ||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||||||
Db   340 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTGTTTATACAGAACATTAGTAGCT 399

Qy   121 TGGTACCAGCAGAAACCAGGACAGCAGCCTCCTCAAGCTGCTCATTTCACTGGCATCTACCCGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   400 TGGTACCAGCAGAAACCAGGACAGCAGCCTCCTCAAGCTGCTCATTTCACTGGGCATCTACCCGG 459

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   460 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 519

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   520 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 579

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
            ||||| |||||||||||||||||||||||||||||||||
Db   580 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 618

RESULT 4
AAQ33032
ID   AAQ33032 standard; cDNA; 342 BP.
XX
AC   AAQ33032;
XX
DT   06-MAY-1993 (first entry)

XX
DE   MAb GAH variable region of light chain.
XX
KW   Monoclonal antibody; hybridoma; PCR; variable region;
KW   constant region; heavy chain; light chain; ss.
XX
OS   Synthetic.
XX
PN   EP520499-A.
XX
PD   30-DEC-1992.
XX
PF   26-JUN-1992; 92EP-0110841.
XX
PR   28-JUN-1991; 91JP-0158859.
PR   28-JUN-1991; 91JP-0158860.
PR   28-JUN-1991; 91JP-0158861.
XX
PA   (MITU) MITSUBISHI KASEI CORP.
XX
PI   Hirakawa Y, Hosokawa S, Ito N, Nagaike K, Tagawa T;
XX
DR   WPI; 1993-001328/01.
DR   P-PSDB; AAR30144.
XX
PT   Human monoclonal antibody specific for a cancer cell membrane
PT   surface antigen - prepd. from a hybridoma obtd. by cell fusion
PT   between human lymphocytes derived from cancer patients and mouse
PT   myeloma cells
XX
PS   Claim 13; Page 31 + 15; 37pp; English.
XX
CC   A human MAb specifically binding to a surface antigen of cancer
CC   cell membrane comprises variable regions of the heavy and light
CC   chains having the amino acid sequences of AAR30143-44 respectively,
CC   encoded by DNA sequences AAQ38670 and AAQ33032 respectively.
XX
SQ   Sequence 342 BP; 88 A; 92 C; 87 G; 75 T; 0 other;

Query Match   94.8%; Score 321.4; DB 14; Length 342;
Best Local Similarity   96.8%; Pred. No. 2.5e-93;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
            |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
            ||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTGTTTATACAACATAAGAAATTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCAGCCTCCTCAAGCTGCTCATTTCACTGGGCATCTACCCGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGTACCAGCAGAAACCAGGACAGCAGCCTCCTCAAGCTGCTCATTTCACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGAAGATGTGGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   241 ATCAGCAGCCTGAAGATGTGGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
            || ||||||||||||||||||||||||||||||||||
Db   301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339

RESULT 5
AAQ71718
ID   AAQ71718 standard; cDNA; 360 BP.
XX
AC   AAQ71718;

```
XX
DT   13-APR-1995 (first entry)
XX
DE   Monoclonal antibody L612 light chain variable region.
XX
KW   Immunoglobulin; L612; light chain; variable region;
KW   monoclonal antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key          Location/Qualifiers
FT   CDS          1..360
FT                /*tag= a
FT   misc_feature 58..108
FT                /*tag= b
FT                /label= CDR 1
FT   misc_feature 154..174
FT                /*tag= c
FT                /label= CDR 2
FT   misc_feature 271..297
FT                /*tag= d
FT                /label= CDR 3
XX
PN   WO9419457-A.
XX
PD   01-SEP-1994.
XX
PF   09-FEB-1994;   94WO-US01469.
XX
PR   26-FEB-1993;   93US-0026320.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Irie RF;
XX
DR   WPI; 1994-294324/36.
DR   P-PSDB; AAR61240.
XX
PT   New transformed human B lymphoblastoid cell line - producing
PT   monoclonal antibody reactive with GM3 and GM4 ganglioside(s), for
PT   treating.tumours, esp. melanoma
XX
PS   Disclosure; Page 31-32; 39pp; English.
XX
CC   Lymphocytes were sepd. from regional lymph nodes of a patient who had
CC   undergone mastectomy for breast cancer. The B lymphocyte fraction
CC   was incubated for 20 hrs with Epstein-Barr virus, then cloned by
CC   limiting dilution and tested for immunoadherence. Clones producing
CC   antibodies reactive with the UCLA-SO-M12 melanoma cell line were
CC   recloned 7 times in serum-free medium contg. growth factors. The
CC   resulting L612 is a B-lymphoblastoid cell line transformed by the
CC   Epstein-Barr virus. It is deposited at the ATCC under CRL 10724.
CC   HuMab L612 binds to renal cell carcinomas. The DNA sequence of the L612
CC   variable regions for both the light and heavy chains of the L612
CC   antibody were determined by PCR and are given in AAQ71718 and AAQ71717
CC   respectively.
XX
SQ   Sequence 360 BP; 88 A; 104 C; 85 G; 83 T; 0 other;

Query Match     94.1%;   Score 319;  DB 15;  Length 360;
Best Local Similarity   98.5%;   Pred. No. 1.5e-92;
Matches  322;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;

Qy          13 ACCCAGTCTCCAGACTCCCCTGGCTGTGTCTCTGGGCGGGAGAGGGCCACCATCAACTGCAAG 72
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGAGGGCCACCATCAACTGCAAG 60

Qy          73 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG 132
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACATAAGAACTACTTACCTTGGTACCAGCAG 120

Qy         133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCCTCCGGGAATCCGGGGTC 192
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCCTCCGGGAATCCGGGGTC 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy         193 CCTGACCGATTCAGTGGCAGCGGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 252
               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         181 CCTGACCGATTCAGTGGCAGCGGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 240
Qy         253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCGCAATATAATTATAGTACTCCTCGAACGTTC 312
               |||||||||||||||||||| |||||||||||||| ||||||||||||||||  ||||||
Db         241 CAGGCTGAAGATGTGGCAGTTTATTACTGTCGCAATATAATTATAGTACTCCTCCGACGTTC 300
Qy         313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
               |||||||||||||||||||||||||||
Db         301 GGCCAAGGGACCAAGGTGGAAATCAAA 327

RESULT 6
ABA94219
ID   ABA94219 standard; DNA; 357 BP.
XX
AC   ABA94219;
XX
DT   13-MAR-2002 (first entry)
XX
DE   ebvHigM MS19D10 light chain variable region nucleotide sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHigM22; LYM 22; AKJR4;
KW   ebvHigM MsI19D10; ebv HiGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
XX
OS   Homo sapiens.
XX
FH   Key          Location/Qualifiers
FT   CDS          1..357
FT                /*tag= a
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US14902.
XX
PR   10-MAY-2000; 2000US-0568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M, Miller DJ, Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   P-PSDB; ABB07172.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody),
PT   promoting neurite outgrowth, regeneration, remyelination and
PT   neuroprotection in central nervous system, useful to treat
PT   post-infectious encephalomyelitis -
XX
PS   Claim 43; Fig 20; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHigM22 (LYM 22), ebvHigM MsI19Dp10, ebv HigM
CC   CB2bG8, AKJR4, CB2iEI2, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture.
```

CC   (I) is also useful for stimulating remyelination of CNS axons. The
CC   antibodies are useful for preventing infection by a bacterium, virus or
CC   like pathogen that causes demyelination or other neurodegenerative
CC   condition in a subject. Methods where (I) is administered to a patient
CC   are useful for treating multiple sclerosis, Parkinson's disease,
CC   Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
CC   demyelinating disease, CNS diseases, and other conditions in the CNS
CC   where nerves are damaged as by trauma. The present sequence represents
CC   the ebvHigM MSI1D10 light chain variable region nucleotide sequence.
XX
SQ   Sequence 357 BP; 88 A; 101 C; 86 G; 82 T; 0 other;

Query Match   93.9%; Score 318.2; DB 24; Length 357;
Best Local Similarity   96.2%; Pred. No. 2.8e-92;
Matches 326; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||| ||||||||||||||||||||| |||||| |||||
Db   61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATCCAGTGGCAGCGGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGTCCCTGACCGATCCAGTGGCAGCGGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          |||||| |||| |||||||||||||||||||||||||||
Db   301 CCTCTCACTTTCGGCCCTGGGACCAAAGTGGAAATCAAA 339

RESULT 7
AAC98443
ID AAC98443 standard; cDNA; 463 BP.
XX
AC AAC98443;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:453.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200055351-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX

DR WPI; 2000-587534/55.
DR P-PSDB; AAB53686.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
PS Claim 1; Page 935; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular,
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 463 BP; 106 A; 126 C; 113 G; 112 T; 6 other;

Query Match   93.0%; Score 315.2; DB 21; Length 463;
Best Local Similarity   95.3%; Pred. No. 2.8e-91;
Matches 323; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Db   67 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 126

Qy   61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||| ||||||||||||||||||||| |||||| |||||
Db   127 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAACT 186

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   187 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCCTTTACTGGGCATCTACCCGG 246

Qy   181 GAATCCGGGGTCCCTGACCGATCCAGTGGCAGCGGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   247 GAATCCGGGGTCCCTGACCGATCCAGTGGCAGCGGGGTCTGGGACAGATTTCACTCTCACC 306

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   307 ATCAGCAGNCTGCAGNCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATACTACT 366

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          |||||| |||| ||||||||||||||||||||||||||
Db   367 CCTGGACGTTCGGCCACTGGACCAANGTGGAAATCANA 405

RESULT 8
AAH47729
ID AAH47729 standard; DNA; 360 BP.
XX
AC AAH47729;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of seq Id No. 72.
XX
KW Gene library; immunoglobulin; antibody library; human; ds.
XX
OS Homo sapiens.
XX
PN WO200162907-A1.
XX

PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-JP01298.
PR   22-FEB-2000; 2000JP-0050543.
XX
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI   Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI   Okuno Y, Shiraki K;
XX
DR   WPI; 2001-565420/63.
DR   P-PSDB; AAG65565.
XX
PT   Producing gene libraries and antibody libraries, involves selecting a
PT   light chain that binds to a heavy chain product to produce a functional
PT   formation, and producing a gene library of the light chain variable
PT   regions -
XX
PS   Examples; p 147-148; 181pp; Japanese.
XX
CC   The invention relates to producing gene libraries, comprising
CC   immunoglobulin light and heavy variable region. The method involves
CC   selecting light chain that binds with the heavy chain product to produce
CC   a functional conformation, producing a gene library comprising a
CC   collection of these light chain variable genes, and combining with gene
CC   library of heavy chain variable genes. The method is used for production
CC   of gene and antibody libraries.
XX
SQ   Sequence 360 BP; 89 A; 100 C; 89 G; 82 T; 0 other;

Query Match   92.9%; Score 315; DB 22; Length 360;
Best Local Similarity   95.6%; Pred. No. 3e-91;
Matches   324; Conservative   0; Mismatches 15; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTCGGCGAGAGGGCCACC 60
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTCGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
           |||||||||||||||||||||||||||||||||||||| |||| |||||||||| |||||
Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           |||| |||||||||||||||||||||||||||||||||||
Db   301 CCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 339

RESULT 9
AAQ45606
ID   AAQ45606 standard; DNA; 1028 BP.
XX
AC   AAQ45606;
XX
DT   04-DEC-1993 (first entry)
XX
DE   Sequence of pATDFLAG encoding signal peptide, H4VL, linker and
DE   FLAG adapter.
XX
KW   Single chain antibody; SCFV1; human subgroup 4 germline antibody;
KW   variable light; ss.

XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   293..775
FT   /*tag= a
FT   /note= "ENCODES SIGNAL,H4VL,LINKER
FT   see AAR38320 FT"
FT   CDS   784..816
FT   /*tag= c
FT   /product= flag peptide
XX
PN   WO9312231-A.
XX
PD   24-JUN-1993.
XX
PF   13-DEC-1991; 91WO-AU00583.
XX
PR   13-DEC-1991; 91WO-AU00583.
XX
PA   (DOWC) DOW CHEM AUSTRALIA LTD.
XX
PI   Johnson KS, Mezes PS, Richard RA;
XX
DR   WPI; 1993-214173/26.
DR   P-PSDB; AAR38320, AAR40753.
XX
PT   New composite antibody binding to tumour associated TAG-72
PT   antigen - includes light chain variable region from human
PT   subgroup 4 germline gene, useful, opt. as conjugate, for
PT   diagnosis or treatment of cancer
XX
PS   Example; Figure 28; 150pp; English.
XX
CC   The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605)
CC   to incorporate a flag-coating sequence 3' to any human VH gene
CC   to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG,
CC   when digested with XhoI and Nhe I and purified becomes the human
CC   CH discovery plasmid contg. Hum4 VL in this SCFV format. pSC49FLAG
CC   contains murine antibody CC49VH inserted into sites of XhoI - NheI
CC   of pATDFLAG. It was evaluated for biological activity with the
CC   purpose of serving as a positive control for the FLAG assay
CC   system to detect binding to TAG-72.
XX
SQ   Sequence 1028 BP; 289 A; 226 C; 244 G; 269 T; 0 other;

Query Match   92.6%; Score 314; DB 14; Length 1028;
Best Local Similarity   95.6%; Pred. No. 9.7e-91;
Matches   323; Conservative   0; Mismatches 15; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTCGGCGAGAGGGCCACC 60
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTCGGCGAGAGGGCCACC 418

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
           |||||||||||||||||||||||||||||||||||||| |||| |||||||||| |||||
Db   419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy   181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
           |||| ||||||||||||||||||||||||||||||| ||
Db   659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696

RESULT 10

```
AAZ39437
ID   AAZ39437 standard; DNA; 1028 BP.
XX
AC   AAZ39437;
XX
DT   29-FEB-2000  (first entry)
XX
DE   DNA sequence of Hum4 VL-UNIHOPE linker-FLAG peptide of pATDFLAG.
XX
KW   Tumor associated sialylated glycoprotein; TAG-72; cancer antigen;
KW   carcinoma lesion; diagnostic; cancer; antibody;
KW   anti-mouse antibody hypersensitivity reaction; ss.
XX
OS   Synthetic.
XX
PN   US5976845-A.
XX
PD   02-NOV-1999.
XX
PF   07-JUN-1995;  95US-0487743.
XX
PR   16-JUN-1994;  94US-0261354.
PR   19-APR-1990;  90US-0510697.
PR   20-OCT-1992;  92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS,  Richard RA,  Mezes PS;
XX
DR   WPI; 1999-619651/53.
DR   P-PSDB; AAY57184.
XX
PT   Production of humanized anti-TAG-72 antibodies, used for the detection,
PT   in vivo imaging and treatment of cancers  -
XX
PS   Example 5; Fig 28A-C; 85pp; English.
XX
CC   The invention relates to producing humanized anti-tumor associated
CC   sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies
CC   have binding specificity for the cancer antigen TAG-72. These antibodies
CC   have variable regions with VL segments derived from human subgroup IV
CC   germline gene and a VH segment (encoded by the VHalphaTAG germline gene)
CC   which is capable of combining with the VL to form a threee dimensional
CC   structure having the ability to bind TAG-72. They can be used for the in
CC   vivo detection of carcinoma lesions. They can also be used for in vitro
CC   diagnostics. They can also be modified with therapeutic agents e.g. a
CC   radionuclide, drug, biological response modifier, toxin or another
CC   antibody for the treatment of cancers. The humanized anti-TAG-72
CC   antibodies can reduce harmful anti-mouse antibody hypersensitivity
CC   reactions.
XX
SQ   Sequence 1028 BP; 289 A; 227 C; 243 G; 269 T; 0 other;

Query Match       92.6%;  Score 314;  DB 20;  Length 1028;
Best Local Similarity  95.6%;  Pred. No. 9.7e-91;
Matches  323;  Conservative   0;  Mismatches  15;  Indels   0;  Gaps   0;

Qy      1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 GACATCGTGATGACCCAGTCTCCAGCCACCCTGTCTGTCTCTGGGCGAGAGGGCCACC 418

Qy     61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          ||||||||||||||||||||||||||||| |||||||||||| ||||||||||||| |||
Db    419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy    121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTACCCGG 538

Qy    181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCGGGACAGATTTCACTCTCACC 240
```

RESULT 11

```
AAZ23975
ID   AAZ23975 standard; DNA; 1028 BP.
XX
AC   AAZ23975;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Plasmid pATDFLAG FLAG DNA adapter.
XX
KW   Human; antibody; humanized; anti-tumor; sialylated glycoprotein antibody;
KW   TAG-72; cytostatic; cancer antigen; detection; carcinoma lesion;
KW   diagnostic; treatment; ss.
XX
OS   Synthetic.
XX
PN   US5976531-A.
XX
PD   02-NOV-1999.
XX
PF   16-JUN-1994;  94US-0261354.
XX
PR   19-APR-1990;  90US-0510697.
PR   20-OCT-1992;  92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS,  Mezes PS,  Richard RA;
XX
DR   WPI; 1999-632731/54.
DR   P-PSDB; AAY50693.
XX
PT   New humanized anti-TAG-72 antibodies, used for the detection, in vivo
PT   imaging and treatment of cancers --
XX
PS   Example 5; Figure 28A-C; 83pp; English.
XX
CC   This invention describes novel humanized anti-tumor associated
CC   sialylated glycoprotein antibodies (TAG-72) which have cytostatic
CC   activity. The antibodies have binding specificity for the cancer antigen
CC   TAG-72. They can be used for the in vivo detection of carcinoma lesions.
CC   They can also be used for in vitro diagnostics. They can also be modified
CC   with therapeutic agents e.g. a radionuclide, drug, biological response
CC   modifier, toxin or another antibody for the treatment of cancers. The
CC   humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
CC   hypersensitivity reactions.
XX
SQ   Sequence 1028 BP; 289 A; 227 C; 243 G; 269 T; 0 other;

Query Match       92.6%;  Score 314;  DB 20;  Length 1028;
Best Local Similarity  95.6%;  Pred. No. 9.7e-91;
Matches  323;  Conservative   0;  Mismatches  15;  Indels   0;  Gaps   0;

Qy      1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 GACATCGTGATGACCCAGTCTCCAGCCACCCTGTCTGTCTCTGGGCGAGAGGGCCACC 418

Qy     61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          ||||||||||||||||||||||||||||| |||||||||||| ||||||||||||| |||
Db    419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478
```

```
Db    539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy    241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Db    599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy    301 CCTCGAACGTTCGGCCAGGGACCAAGGTGGAAATCAA 338

Db    659 CCTCTCACTTTCGGCGAGGGACCAAGGTGGTGATCAA 696
```

```
Matches   323;  Conservative   0;  Mismatches   15;  Indels   0;  Gaps   0;

Qy      1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC    60
          ||||| ||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC   418

Qy     61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT   120
          ||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||| ||
Db    419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT   478

Qy    121 TGGTACCAGCAGAAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG   180
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    479 TGGTACCAGCAGAAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG   538

Qy    181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC   598

Qy    241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT   658

Qy    301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA   338
          |||||||||||||||||||||||||||||||| |||||
Db    659 CCTCCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA   696
```

RESULT 13
AAZ39436
ID   AAZ39436 standard; DNA; 1330 BP.
XX
AC   AAZ39436;
XX
DT   29-FEB-2000 (first entry)
XX
DE   DNA sequence of Hum4 VL-CC49VH SCFV present in pSCFVUIII.
XX
KW   Tumor associated sialylated glycoprotein; TAG-72; cancer antigen;
KW   carcinoma lesion; diagnostic; cancer; antibody; SCFV;
KW   anti-mouse antibody hypersensitivity reaction; ss.
XX
OS   Synthetic.
XX
PN   US5976845-A.
XX
PD   02-NOV-1999.
XX
PF   07-JUN-1995; 95US-0487743.
XX
PR   16-JUN-1994; 94US-0261354.
PR   19-APR-1990; 90US-0510697.
PR   20-OCT-1992; 92US-0964536.
XX
PA   (DOWC) DOW CHEM CO.
XX
PI   Johnson KS, Richard RA, Mezes PS;
XX
DR   WPI; 1999-619651/53.
DR   P-PSDB; AAY57183.
XX
PT   Production of humanized anti-TAG-72 antibodies, used for the detection,
PT   in vivo imaging and treatment of cancers -
XX
PS   Example 4; Fig 26A-D; 85pp; English.
XX
CC   The invention relates to producing humanized anti-tumor associated
CC   sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies
CC   have binding specificity for the cancer antigen TAG-72. These antibodies
CC   have variable regions with VL segments derived from human subgroup IV
CC   germline gene and a VH segment (encoded by the VHalphaTAG germline gene)
CC   which is capable of combining with the VL to form a threee dimensional
CC   structure having the ability to bind TAG-72. They can be used for the in
CC   vivo detection of carcinoma lesions. They can also be used for in vitro

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```
Qy    121 TGGTACCAGCAGAAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 TGGTACCAGCAGAAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG   538

Qy    181 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 GAATCCGGGGTCCCTGACCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC   598

Qy    241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||| ||
Db    599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT   658

Qy    301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA   338
          |||||||||||||||||||||||||||||||| |||||
Db    659 CCTCCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA   696
```

RESULT 12
AAQ45605
ID   AAQ45605 standard; DNA; 1330 BP.
XX
AC   AAQ45605;
XX
DT   04-DEC-1993 (first entry)
XX
DE   Sequence of Hum4 VL-CC49VH SCFV present in pSCFVUHH.
XX
KW   Single chain antibody; SCFV1; human subgroup 4 germline antibody;
KW   variable heavy; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   293..1117
FT   /*tag= a
FT   /note= "ENCODES SIGNAL,H4VL,LINKER,CC49VH (SEE
FT   AAR38819 FT)"
XX
PN   WO9312231-A.
XX
PD   24-JUN-1993.
XX
PF   13-DEC-1991; 91WO-AU00583.
XX
PR   13-DEC-1991; 91WO-AU00583.
XX
PA   (DOWC) DOW CHEM AUSTRALIA LTD.
XX
PI   Johnson KS, Mezes PS, Richard RA;
XX
DR   WPI; 1993-214173/26.
DR   P-PSDB; AAR38319.
XX
PT   New composite antibody binding to tumour associated TAG-72
PT   antigen - includes light chain variable region from human
PT   subgroup 4 germline gene, useful, opt. as conjugate, for
PT   diagnosis or treatment of cancer
XX
PS   Example; Figure 26; 150pp; English.
XX
CC   Plasmid pSCFV UHH expresses a biologically active, TAG-72 binding
CC   SCFV consisting of the Hum4 VL and CC49 VH. The expression plasmid
CC   utilises the beta-lactamase penP promoter, pectate lyase pelB
CC   signal sequence and the penP terminator region. Different Ig light
CC   chain variable regions can be inserted in the NcoI-HindIII sites,
CC   different SCFV linkers can be inserted in the HindIII-XhoI sites,
CC   and different Ig heavy chain variable regions can be inserted in
CC   the XhoI-NheI sites.
XX
SQ   Sequence 1330 BP; 362 A; 300 C; 319 G; 349 T; 0 other;

Query Match   92.6%; Score 314; DB 14; Length 1330;
Best Local Similarity   95.6%; Pred. No. 1.1e-90;

Left column

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CC   diagnostics. They can also be modified with therapeutic agents e.g. a
CC   radionuclide, drug, biological response modifier, toxin or another
CC   antibody for the treatment of cancers. The humanized anti-TAG-72
CC   antibodies can reduce harmful anti-mouse antibody hypersensitivity
CC   reactions.
XX
SQ   Sequence 1330 BP; 362 A; 302 C; 317 G; 349 T; 0 other;

Query Match             92.6%; Score 314; DB 20; Length 1330;
Best Local Similarity   95.6%; Pred. No. 1.1e-90;
Matches  323; Conservative    0; Mismatches   15; Indels    0; Gaps    0;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db   479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCCACCCGG 538

Qy   181 GAATCCGGGGTCCCTGACCGGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db   539 GAATCCGGGGTCCCTGACCGGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
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Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
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RESULT 14
AAZ23974
ID   AAZ23974 standard; DNA; 1330 BP.
XX
AC   AAZ23974;
XX
DT   09-FEB-2000 (first entry)
XX
DE   Human Hum4L-CC49 VH SCVF DNA.
XX
KW   Human; antibody; humanized; anti-tumor; sialylated glycoprotein antibody;
KW   TAG-72; cytostatic; cancer antigen; detection; carcinoma lesion;
KW   diagnostic; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   US5976531-A.
XX
PD   02-NOV-1999.
XX
PF   16-JUN-1994;   94US-0261354.
XX
PR   19-APR-1990;   90US-0510697.
PR   20-OCT-1992;   92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS, Mezes PS, Richard RA;
XX
PR   WPI; 1999-632731/54.
DR   P-PSDB; AAY50692.
XX
PT   New humanized anti-TAG-72 antibodies, used for the detection, in vivo
PT   imaging and treatment of cancers -
XX
PS   Example 4; Figure 26A-D; 83pp; English.
```

Right column

```
XX
CC   This invention describes novel humanized anti-tumor associated
CC   sialylated glycoprotein antibodies (TAG-72) which have cytostatic
CC   activity. The antibodies have binding specificity for the cancer antigen
CC   TAG-72. They can be used for the in vivo detection of carcinoma lesions.
CC   They can also be used for in vitro diagnostics. They can also be modified
CC   with therapeutic agents e.g. a radionuclide, drug, biological response
CC   modifier, toxin or another antibody for the treatment of cancers. The
CC   humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
CC   hypersensitivity reactions.
XX
SQ   Sequence 1330 BP; 362 A; 302 C; 317 G; 349 T; 0 other;

Query Match             92.6%; Score 314; DB 20; Length 1330;
Best Local Similarity   95.6%; Pred. No. 1.1e-90;
Matches  323; Conservative    0; Mismatches   15; Indels    0; Gaps    0;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
          |||||||||||||||||||||||||||||| ||||||||||||| || |||||||| ||||
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Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCCACCCGG 180
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Db   479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCCACCCGG 538

Qy   181 GAATCCGGGGTCCCTGACCGGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
          |||| || ||||||||| |||||| |||||
Db   659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696
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RESULT 15
AAQ45607
ID   AAQ45607 standard; DNA; 1359 BP.
XX
AC   AAQ45607;
XX
DT   04-DEC-1993 (first entry)
XX
DE   Sequence of pSC49FLAG.
XX
KW   Single chain antibody; SCFV1; human subgroup 4 germline antibody;
KW   variable heavy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             293..1147
FT                   /tag= a
FT                   /note= "ENCODES SIGNAL,HV4L,LINKER,CC49VH,FLAG
FT                         - SEE AAR38321 FT"
XX
PN   WO9312231-A.
XX
PD   24-JUN-1993.
XX
PR   13-DEC-1991;   91WO-AU00583.
XX
PR   13-DEC-1991;   91WO-AU00583.
XX
PA   (DOWC ) DOW CHEM AUSTRALIA LTD.
XX
```

PI   Johnson KS, Mezes PS, Richard RA;
XX
DR   WPI; 1993-214173/26.
DR   N-PSDB; AAQ44607.
XX
PT   New composite antibody binding to tumour associated TAG-72
PT   antigen - includes light chain variable region from human
PT   subgroup 4 germline gene, useful, opt. as conjugate, for
PT   diagnosis or treatment of cancer
XX
PS   Example; Figure 30; 150pp; English.
XX
CC   The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605)
CC   to incorporate a flag-coating sequence 3' to any human VH gene
CC   to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG,
CC   when digested with XhoI and Nhe I and purified becomes the human
CC   CH discovery plasmid contg. Hum4 VL in this SCFV format. pSC49FLAG
CC   contains murine antibody CC49VH inserted into sites of XhoI - NheI
CC   of pATDFLAG. It was evaluated for biological activity with the
CC   purpose of serving as a positive control for the FLAG assay
CC   system to detect binding to TAG-72.
XX
SQ   Sequence 1359 BP; 374 A; 308 C; 325 G; 352 T; 0 other;

Query Match   92.6%;   Score 314; DB 14;   Length 1359;
Best Local Similarity 95.6%;   Pred. No. 1.1e-90;
Matches 323; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
         ||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||| |
Db 419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db 599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy 301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
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Db 659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696

Search completed: July 18, 2003, 06:44:05
Job time : 88.8822 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 18, 2003, 06:19:39 ; Search time 81.9507 Seconds
(without alignments)
8533.875 Million cell updates/sec

Title: US-09-627-896b-26
Perfect score: 339
Sequence: 1 gacatccagttgacccagtc.........ggaccaaggtggaaatcaaa 339

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1439767 seqs, 103150376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	315.2	93.0	463	10	US-09-925-299-453	Sequence 453, App
2	315.2	93.0	463	12	US-09-925-299-453	Sequence 453, App
3	311.8	92.0	1033	10	US-09-799-514-2	Sequence 2, Appli
4	305.2	90.0	788	15	US-10-158-646-58	Sequence 58, Appl
5	303	89.4	463	11	US-09-187-693-26	Sequence 26, Appl
6	300.4	88.6	9511	11	US-09-897-006-34	Sequence 34, Appl
7	300.4	88.6	9511	12	US-09-897-511A-34	Sequence 34, Appl
8	294.4	86.8	305	12	US-09-995-529-5	Sequence 1, Appli
9	292.6	86.3	342	11	US-09-274-163E-1	Sequence 1, Appli
10	291	85.8	343	11	US-09-274-163E-3	Sequence 3, Appli
11	291	85.8	343	11	US-09-274-163E-5	Sequence 5, Appli
12	288	85.0	1230	15	US-10-158-646-59	Sequence 59, Appl
13	280.2	82.7	460	11	US-09-187-693-22	Sequence 22, Appl
14	279	82.3	456	11	US-09-187-693-24	Sequence 24, Appl
15	276.4	81.5	476	11	US-09-187-693-30	Sequence 30, Appl
16	273.4	80.6	384	10	US-09-905-243-54	Sequence 54, Appl
17	272.6	80.4	453	11	US-09-187-693-28	Sequence 28, Appl
18	268.4	79.2	327	11	US-09-828-708-112	Sequence 112, App
19	268.4	79.2	327	11	US-09-828-708-115	Sequence 115, App
20	251.6	74.2	266	10	US-09-604-287A-409	Sequence 409, App
21	251.6	74.2	266	12	US-09-551-621-409	Sequence 409, App
22	251.6	74.2	266	15	US-10-007-805-409	Sequence 409, App
23	251.6	74.2	266	15	US-10-076-622-409	Sequence 409, App
24	246.2	72.6	339	15	US-10-121-464-5	Sequence 5, Appli
25	244.6	72.2	339	15	US-10-121-464-1	Sequence 1, Appli
26	241.4	71.2	339	15	US-10-121-464-3	Sequence 3, Appli
27	233.8	69.0	1045	15	US-10-198-846-13629	Sequence 13629, A
28	228	67.3	962	15	US-10-198-846-10845	Sequence 10845, A
29	225.8	66.6	393	11	US-09-879-461-13	Sequence 13, Appl
30	225.8	66.6	393	11	US-09-879-461-57	Sequence 57, Appl
31	225.4	66.5	347	11	US-09-998-831-8	Sequence 8, Appli
32	225.4	66.5	396	11	US-09-249-011A-7	Sequence 7, Appli
33	223.8	66.0	390	15	US-10-146-305-5	Sequence 21, Appl
34	223.8	66.0	1960	11	US-09-249-011A-21	Sequence 21, Appl
35	223.8	66.0	3344	15	US-10-176-380-17	Sequence 17, Appl
36	222.2	65.5	4661	11	US-09-897-006-10	Sequence 10, Appl
37	222.2	65.5	4661	12	US-09-897-511A-10	Sequence 10, Appl
38	220.6	65.1	660	11	US-09-995-693-3	Sequence 3, Appli
39	220.6	65.1	660	15	US-10-232-408-3	Sequence 5, Appli
40	220.6	65.1	723	10	US-09-791-578-5	Sequence 5, Appli
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42	220.6	65.1	758	11	US-09-956-086-1	Sequence 1, Appli
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44	220.6	65.1	782	10	US-09-791-578-3	Sequence 3, Appli
45	220.6	65.1	782	10	US-09-791-540-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-925-299-453
; Sequence 453, Application US/09925299
; Patent No. US2002005527A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS:1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (393)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (404)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (426)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (453)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-299-453

Best Local Similarity   93.0%;   Score 315.2;   DB 10;   Length 463;
Matches 323;   Conservative   0;   Mismatches 16;   Indels   0;   Gaps   0;

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Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db 187 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 246

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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RESULT 2
US-09-925-299-453
; Sequence 453, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (393)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (404)
; OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (453)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-453

Query Match   93.0%;   Score 315.2;   DB 12;   Length 463;

Best Local Similarity   95.3%;   Pred. No. 2.8e-98;
Matches 323;   Conservative   0;   Mismatches 16;   Indels   0;   Gaps   0;

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Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy 241 ATCAGCAGCCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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RESULT 3
US-09-799-514
; Sequence 2, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ant...
; FILE REFERENCE: PT015P1
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-514-2

Query Match   92.0%;   Score 311.8;   DB 10;   Length 1033;
Best Local Similarity   95.0%;   Pred. No. 5.9e-97;
Matches 322;   Conservative   0;   Mismatches 17;   Indels   0;   Gaps   0;
US-09-799-514-2

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Qy  61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 190 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 249

Qy 181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 250 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 309

Qy 241 ATCAGCAGCCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 310 ATCAGCAGCCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 369
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Qy    301 CCTCGAACGTTCGCGCCAAGGGACCAAGGTGGAAATCAAA 339
          |||||| |||| |||||||||||||||||||||||||||
Db    370 CCGTACAGTTTTGGCCAGGGGACCAAGCTGGAAATCAAA 408


RESULT 4
US-10-158-646-58
; Sequence 58, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
;    APPLICANT: Lasek, Amy K.W.
;    APPLICANT: Sornasse, Thierry
;    TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;    FILE REFERENCE: PA-0030-1 US
;    CURRENT APPLICATION NUMBER: US/10/158,646
;    CURRENT FILING DATE: 2002-05-29
;    PRIOR APPLICATION NUMBER: 60/295,239
;    PRIOR FILING DATE: 2001-05-31
;    NUMBER OF SEQ ID NOS: 78
;    SOFTWARE: PERL Program
; SEQ ID NO 58
;    LENGTH: 788
;    TYPE: DNA
;    ORGANISM: Homo sapiens
; FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No. US2003007310A1 1101440.8
US-10-158-646-58

Query Match             90.0%;  Score 305.2;  DB 15;  Length 788;
Best Local Similarity   95.3%;  Pred. No. 9.8e-95;
Matches 326;  Conservative  0;  Mismatches  13;  Indels  3;  Gaps  1;

Qy      1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     82 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 141

Qy     61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGTCCAACACAGAATTACTTAACT 120
          ||||||| |||||||||||||| |||||||||||| |||||||||||||||||||
Db    142 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGTCCAACAATATAGAATTACTTAGCT 201

Qy    121 TGGTACCAGCAGAAACCAGGACAGCGCCTCCTAAGCTGCTCATTTGGGCATCTACCCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 TGGTACCAGCAGAAACCAGGACAGCGCCTCCTAAGCTGCTCATTTGGGCATCTACCCGG 261

Qy    181 GAATCCGGGGTCCCTGACGGGTCTGGGCACGGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||| ||||||||||||||| |||||||||||||||||||||||||||
Db    262 GAATCCGGGGTCCCTGACCGGTCAGTGCGACGGGGTCTGGGACAGATTTCACTCTCACC 321

Qy    241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    322 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 381

Qy    301 C--CTCGAACGTTCGCGCCAAGGGACCAAGGTGGAAATCAAA 339
          |      ||| |||||||| ||||||||||||||||||
Db    382 CTCGCGCTCACTTTCGGCGGGAGGGACCAAGGTGGAGATCAAA 423


RESULT 5
US-09-187-693-26
; Sequence 26, Application US/09187693
; Patent No. US2002017362A1
; GENERAL INFORMATION:
;    APPLICANT: Jakobovits, Aya
;    APPLICANT: Yang, Xiao-Dong
;    APPLICANT: Gallo, Michael
;    APPLICANT: Jia, Xiao-Chi
;    TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;    TITLE OF INVENTION: Growth Factor Receptor
;    FILE REFERENCE: Cell 4.20 CIP2
;    CURRENT APPLICATION NUMBER: US/09/187,693
;    CURRENT FILING DATE: 1998-11-05
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;    PRIOR APPLICATION NUMBER: 09/162,280
;    PRIOR FILING DATE: 1998-09-29
;    PRIOR APPLICATION NUMBER: 08/851,362
;    PRIOR FILING DATE: 1997-05-05
;    NUMBER OF SEQ ID NOS: 75
;    SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;    LENGTH: 463
;    TYPE: DNA
;    ORGANISM: human
; FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)..(463)
;    OTHER INFORMATION: n = A,T,C or G
US-09-187-693-26

Query Match             89.4%;  Score 303;  DB 11;  Length 463;
Best Local Similarity   95.4%;  Pred. No. 4.4e-94;
Matches 312;  Conservative  0;  Mismatches  15;  Indels  0;  Gaps  0;

Qy     13 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 72
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 60

Qy     73 TCCAGCCAGAGTGTTTTATACAGCTCCAACACAGAATTACTTAACTTGGTACCAGCAG 132
          |||||||||||||||||||||| ||||||||||||||| |||||||||||||||||
Db     61 TCCAGCCAGAGTGTTTTATACGGCTCCAAGAATCAGAACTACTTGTTGGTACCAGCAG 120

Qy    133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGGAATCCGGGGTC 192
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGGAATCCGGGGTC 180

Qy    193 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 252
          |||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db    181 CCTGACCGATTCAGGGGCAGCGGGTCTAGGACAGATTTCACTCTCACCATCAGCAGCCTG 240

Qy    253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTC 312
          |||||||||||||||||||||||||||||||||||||||||||||| | |||| ||||
Db    241 CAGGCTGAAGATGTGGCAGTTTACTTTGGTCACCAATATTATAGTACTCCGTGACGTTC 300

Qy    313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
          |||||||||||||||||||||||||
Db    301 GGCCAAGGGACCAAGGTGGAAATCAAA 327


RESULT 6
US-09-897-006-34
; Sequence 34, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
;    APPLICANT: Bleck, Gregory
;    TITLE OF INVENTION: Expression Vectors
;    FILE REFERENCE: GALA-06415
;    CURRENT APPLICATION NUMBER: US/09/897,006
;    CURRENT FILING DATE: 2001-06-29
;    PRIOR APPLICATION NUMBER: 60/215,851
;    PRIOR FILING DATE: 2000-07-03
;    NUMBER OF SEQ ID NOS: 36
;    SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
;    LENGTH: 9511
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
; FEATURE:
;    OTHER INFORMATION: Synthetic
US-09-897-006-34

Query Match             88.6%;  Score 300.4;  DB 11;  Length 9511;
Best Local Similarity   95.8%;  Pred. No. 1.4e-92;
Matches 320;  Conservative  0;  Mismatches  11;  Indels  3;  Gaps  1;

Qy      6 CCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAA 65
          || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   6000 GACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 6033

RESULT 8
US-09-995-529-5
; Sequence 5, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
;   APPLICANT: Watkins, Jeffry D.
;   APPLICANT: Huse, William D.
;   APPLICANT: Tang, Ying
;   TITLE OF INVENTION: Humanized Collagen Antibodies and
;   TITLE OF INVENTION: Related Methods
;   FILE REFERENCE: P-IX 4976
;   CURRENT APPLICATION NUMBER: US/09/995,529
;   CURRENT FILING DATE: 2001-11-26
;   NUMBER OF SEQ ID NOS: 358
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-995-529-5

Query Match   86.8%;   Score 294.4; DB 12; Length 305;
Best Local Similarity 98.0%; Pred. No. 3.4e-91;
Matches 298; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 60
          ||||||| ||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Db   1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACACAAGAATTACTTAACT 120
          |||||||| |||||||||||||||||||||| |||||||||||| ||||| |||||||
Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   *121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGCCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCAGCAGCCTGCAGCCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy   301 CCTC 304
          ||||
Db   301 CCTC 304

RESULT 9
US-09-274-163E-1
; Sequence 1, Application US/09274163E
; Patent No. US2020137897A1
; GENERAL INFORMATION:
;   APPLICANT: STEVENS, Fred J.
;   APPLICANT: WILKINS STEVENS, Priscilla
;   APPLICANT: RAFFEN, Rosemarie
;   APPLICANT: SCHIFFER, Marianne
;   TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
;   FILE REFERENCE: 051583/0224
;   CURRENT APPLICATION NUMBER: US/09/274,163E
;   CURRENT FILING DATE: 1999-03-22
;   PRIOR APPLICATION NUMBER: US 08/373,380
;   PRIOR FILING DATE: 1995-01-17
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 342
;   TYPE: DNA

Db   5703 CGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAA 5762

Qy   66 CTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACACAAGAATTACTTAACTTGGTA 125
          |||||||| ||||||| |||||||||||| ||||||||||| ||||| ||||||||
Db   5763 CTGCAAGTCCAGCCAGAGTGTTTGTACAGCTCCAACAATAAGAACTATTTAGCTTGGTA 5822

Qy   126 CCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 185
          ||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   5823 TCAGCAGAAACCAGGACAGCCGGGTCTGGGACAGTCAGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 5882

Qy   186 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 245
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5883 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 5942

Qy   246 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCG 305
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||| |||
Db   5943 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTA---CTCA 5999

Qy   306 AACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          ||||||||||||||||||||||||||||||||||
Db   6000 GACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 6033

RESULT 7
US-09-897-511A-34
; Sequence 34, Application US/09897511A
; Publication No. US2003009288A1
; GENERAL INFORMATION:
;   APPLICANT: Bremel, Robert
;   APPLICANT: Miller, Linda
;   APPLICANT: Bleck, Gregory
;   TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
;   FILE REFERENCE: GALA-06416
;   CURRENT APPLICATION NUMBER: US/09/897,511A
;   CURRENT FILING DATE: 2001-06-29
;   PRIOR APPLICATION NUMBER: 60/215,925
;   PRIOR FILING DATE: 2000-07-03
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
;   LENGTH: 9511
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-897-511A-34

Query Match   88.6%;   Score 300.4; DB 12; Length 9511;
Best Local Similarity 95.8%; Pred. No. 1.4e-92;
Matches 320; Conservative   0; Mismatches 11; Indels   3; Gaps   3;

Qy   6 CCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAA 65
          ||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db   5703 CGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAA 5762

Qy   66 CTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACACAAGAATTACTTAACTTGGTA 125
          |||||||| ||||||| |||||||| ||||||||||| ||||| |||||||
Db   5763 CTGCAAGTCCAGCCAGAGTGTTTGTACAGCTCCAACAATAAGAACTATTTAGCTTGGTA 5822

Qy   126 CCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 185
          ||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   5823 TCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 5882

Qy   186 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 245
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   5883 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 5942

Qy   246 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCG 305
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||| |||
Db   5943 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTA---CTCA 5999

Qy   306 AACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
          ||||||||||||||||||||||||||||||||||

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;   ORGANISM:  Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(342)
;   OTHER INFORMATION:
US-09-274-163E-1

Query Match        86.3%;    Score 292.6;   DB 11;   Length 342;
Best Local Similarity   91.4%;   Pred. No. 1.5e-90;
Matches  310;   Conservative   0;   Mismatches  29;   Indels  0;   Gaps  0;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTCTCTGGGGGAGAGGGCCACC 60
           ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTCTCTGGGGGAGAGGGCCACC 60

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
           ||||||||||||||||||||||||||||||||||||||||||    || || ||
Db    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
           ||||| ||| |||||||||||||||||||||||||||||||||||||
Db   121 TGGTATCAGGACAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACTACTCCACC 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           || |||||||||||| ||| ||||||||||||||||
Db   301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339


RESULT 10
US-09-274-163E-3
;   Sequence 3, Application US/09274163E
;   Patent No. US20020137897A1
;   GENERAL INFORMATION:
;   APPLICANT: STEVENS, Fred J.
;   APPLICANT: WILKINS STEVENS, Priscilla
;   APPLICANT: RAFFEN, Rosemarie
;   APPLICANT: SCHIFFER, Marianne
;   TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
;   FILE REFERENCE: 051583/0224
;   CURRENT APPLICATION NUMBER: US/09/274,163E
;   CURRENT FILING DATE: 1999-03-22
;   PRIOR APPLICATION NUMBER: US 08/373,380
;   PRIOR FILING DATE: 1995-01-17
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
;   LENGTH: 343
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(342)
;   OTHER INFORMATION:
US-09-274-163E-3

Query Match        85.8%;    Score 291;   DB 11;   Length 343;
Best Local Similarity   91.2%;   Pred. No. 5.3e-90;
Matches  309;   Conservative   0;   Mismatches  30;   Indels  0;   Gaps  0;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTCTCTGGGGGAGAGGGCCACC 60
           ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTCTCTGGGGGAGAGGGCCACC 60

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
           ||||| ||
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Db    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
           ||||| ||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db   121 TGGTATCAGGACAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           ||||||||||||||||||||||||||||||||||||||||||||||| || ||
Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACTACTCCACC 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           || |||||||||||| ||| ||||||||||||||||
Db   301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339


RESULT 11
US-09-274-163E-5
;   Sequence 5, Application US/09274163E
;   Patent No. US20020137897A1
;   GENERAL INFORMATION:
;   APPLICANT: STEVENS, Fred J.
;   APPLICANT: WILKINS STEVENS, Priscilla
;   APPLICANT: RAFFEN, Rosemarie
;   APPLICANT: SCHIFFER, Marianne
;   TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
;   FILE REFERENCE: 051583/0224
;   CURRENT APPLICATION NUMBER: US/09/274,163E
;   CURRENT FILING DATE: 1999-03-22
;   PRIOR APPLICATION NUMBER: US 08/373,380
;   PRIOR FILING DATE: 1995-01-17
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
;   LENGTH: 343
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(342)
;   OTHER INFORMATION:
US-09-274-163E-5

Query Match        85.8%;    Score 291;   DB 11;   Length 343;
Best Local Similarity   91.2%;   Pred. No. 5.3e-90;
Matches  309;   Conservative   0;   Mismatches  30;   Indels  0;   Gaps  0;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTCTCTGGGGGAGAGGGCCACC 60
           ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTCTCTGGGGGAGAGGGCCACC 60

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
           ||||||||||||||||||||||||||||||||||||||||   || || ||
Db    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
           ||||| ||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db   121 TGGTATCAGGACAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
           |||||||||||||||||||||||||||||||||||||||||| || ||
Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACTACTCCACC 300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
           || |||||||||||| ||| ||||||||||||||||
Db   301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339
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RESULT 12
US-10-158-646-59
; Sequence 59, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
;   APPLICANT: Lasek, Amy K.W.
;   APPLICANT: Sornasse, Thierry
;   TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;   FILE REFERENCE: PA-0030-1 US
;   CURRENT APPLICATION NUMBER: US/10/158,646
;   CURRENT FILING DATE: 2002-05-29
;   PRIOR APPLICATION NUMBER: 60/295,239
;   PRIOR FILING DATE: 2001-05-31
;   NUMBER OF SEQ ID NOS: 78
;   SOFTWARE: PERL Program
; SEQ ID NO 59
;   LENGTH: 1230
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.15
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1143-1160
;   OTHER INFORMATION: a, t, c, g, or other
US-10-158-646-59

Query Match   85.0%; Score 288; DB 15; Length 1230;
Best Local Similarity 92.4%; Pred. No. 1e-88;
Matches 314; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCT-GGCTGTGTCTCTGGGCGAGAGGGCCAC 59
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   263 GAAATTGTGATGACCCAGTCTCCATCCTCCCTGGGCTGTGTCTCTGGGCGAGAGGGCCAC 322

Qy   60 CATCAACTGCAAGTCCAGCCAGCCAGAGTGTTTATACAGCTCCAACAACAAGAATTACTTAAC 119
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   323 CATCAACTGCAGGGCCAGCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGC 382

Qy   120 TTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCTCACCCG 179
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   383 TTGGTACCAGCAGAAACCAGGACAGCCCTCCTAAGGTGCTCATTTACTGGCATCTCACCCG 442

Qy   180 GGAATCCGGGGTCCCTGACCGATTCAGTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   443 GGAATCCGGGGTCCCCAGACCGATTCCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 502

Qy   240 CATCAGCAGCCTGCAGGCTGAAGATGTGCAGTTTATTACTGTCAGCAATATTATAGTAC 299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 CATCAGCAGCCTCTGCAGTCTGAAGATGTGCAGTTTATTACTGTCAGCAATATTATAGTAC 562

Qy   300 TCCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
             ||| |||||||||||||||||||||||||||||||||||
Db   563 TCCGTACACTTTTGGCCAGGGGACCAAGGTGGAGATCAAA 602

RESULT 13
US-09-187-693-22
; Sequence 22, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;   APPLICANT: Jakobovits, Aya
;   APPLICANT: Yang, Xiao-Dong
;   APPLICANT: Gallo, Michael
;   APPLICANT: Jia, Xiao-Chi
;   TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;   TITLE OF INVENTION: Growth Factor Receptor
;   FILE REFERENCE: Cell 4.20 CIP2
;   CURRENT APPLICATION NUMBER: US/09/187,693
;   CURRENT FILING DATE: 1998-11-05

; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 460
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(460)
;   OTHER INFORMATION: n = A,T,C or G
US-09-187-693-22

Query Match   82.7%; Score 280.2; DB 11; Length 460;
Best Local Similarity   93.3%; Pred. No. 3.2e-86;
Matches 291; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy   27 CTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGT 86
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   9 CTTCNTGGCGCGTGTCTCTCNGGCGCGAGGGCCACCATCAACTGCAAGTCCAGCCAGCGTGT 68

Qy   87 TTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAGAAACCAGGACAGCC 146
             ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   69 TTTATACANCTCCAACAATAAGAAGCTGCTTAGCTTGGTACCAGCAGAAACCAGGACAGCC 128

Qy   147 TCCTAAGCTGCTCATTTACTGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAG 206
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   129 TCCTAAGCTGCTCATTTACTGGCATCTACCCGGGAATCCGGGGTCCCTGCCCGATTCAG 188

Qy   207 TGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCTGAAGATGT 266
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   189 TGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCTGAAGATGT 248

Qy   267 GGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTGCAAACGTTCGGCCAAGGGACCAA 326
             ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   249 GGCAGTTTATTACTGTCAGCAATATTATAGTACTCCACTCCACTTTCGGCGGAGGGACCAT 308

Qy   327 GGTGAAATCAA 338
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Db   309 GGTGAGATCAA 320

RESULT 14
US-09-187-693-24
; Sequence 24, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;   APPLICANT: Jakobovits, Aya
;   APPLICANT: Yang, Xiao-Dong
;   APPLICANT: Gallo, Michael
;   APPLICANT: Jia, Xiao-Chi
;   TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;   TITLE OF INVENTION: Growth Factor Receptor
;   FILE REFERENCE: Cell 4.20 CIP2
;   CURRENT APPLICATION NUMBER: US/09/187,693
;   CURRENT FILING DATE: 1998-11-05
;   PRIOR APPLICATION NUMBER: 09/162,280
;   PRIOR FILING DATE: 1998-09-29
;   PRIOR APPLICATION NUMBER: 08/851,362
;   PRIOR FILING DATE: 1997-05-05
;   NUMBER OF SEQ ID NOS: 75
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 456
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(456)
;   OTHER INFORMATION: n = A,T,C or G

US-09-187-693;24

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Query Match         82.3%;   Score 279; DB 11; Length 456;
Best Local Similarity   93.2%;   Pred. No. 8.3e-86;
Matches 302;   Conservative   0;   Mismatches  21;   Indels   1;   Gaps   1;

Qy   17  AGTCTCCAGACTCCCTGCGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCA  76
         |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  AGTCTCCAGACTCCCTGTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCA  60

Qy   77  GCCAGAGTGTTTATACAGCTCCAACA-CAAGAATTACTTAACTTGGTACCAGCAGAAA  135
         |  ||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||
Db   61  GNCAGAGTATTTTATACAGCTCCAACATCAAAAAACTTCTTAGCTTGGTACCAGCAGAAA  120

Qy  136  CCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCT  195
         |||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db  121  CCAGGACAGCCCTCGAAGTTGCTCATTTACTGGGCATCTATTCGGGAATCCGGGGTCCCT  180

Qy  196  GACCGATTCAGTGGCAGCGGGTCTGGGACAGATTCACTCTCCACCATCAGCAGCCTGCAG  255
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCCACCATCAGCAGCCTGCAG  240

Qy  256  GCTGAAGATGTGGCAGTTTATTACTGTGTCAGCAATATTATAGTACTCCTCGAACGTTCGGC  315
         ||||||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db  241  GCTGAAGATGTGGCAGTTTATTACTGTGTCAGCAGTATTATAGTAGTACTCCGTGACGTTCGGC  300

Qy  316  CAAGGGACCAAGTGGGAAATCAAA  339
         ||||||||||||||||||| ||||
Db  301  CAGGGGACCAAGCTGGAGATCAAA  324
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RESULT 15
US-09-187-693-30:
; Sequence 30, Application US/09187693
; Patent No. US2002017362A1
; GENERAL INFORMATION:
;   APPLICANT: Jakobovits, Aya
;   APPLICANT: Yang, Xiao-Dong
;   APPLICANT: Gallo, Michael
;   APPLICANT: Jia, Xiao-Chi
;   TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;   TITLE OF INVENTION: Growth Factor Receptor
;   FILE REFERENCE: Cell 4.20 CIP2
;   CURRENT APPLICATION NUMBER: US/09/187,693
;   CURRENT FILING DATE: 1998-11-05
;   PRIOR APPLICATION NUMBER: 09/162,280
;   PRIOR FILING DATE: 1998-09-29
;   PRIOR APPLICATION NUMBER: 08/851,362
;   PRIOR FILING DATE: 1997-05-05
;   NUMBER OF SEQ ID NOS: 75
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 30
;   LENGTH: 476
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(476)
;   OTHER INFORMATION: n = A,T,C or G
US-09-187-693-30

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Query Match         81.5%;   Score 276.4; DB 11; Length 476;
Best Local Similarity   92.6%;   Pred. No. 6.6e-85;
Matches 289;   Conservative   0;   Mismatches  23;   Indels   0;   Gaps   0;

Qy   28  TCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTT  87
         |||| ||  ||||   |||||||||||||||||||||||||||||||||||||||||||
Db    1  TCTTTGGTAGCGNGTCTTGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTT  60

Qy   88  TTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAGAAACCAGGACAGCCT  147
         ||||||||||||||||| |  |||||| || ||||||||||||||||||||||||||||
Db   61  TTATACNGCTCCAAGAATCAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCT  120
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Qy  148  CCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGT  207
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGG  180

Qy  208  GGCAGCGGGTCTGGGACAGATTCACTCTCCACCATCAGCAGCCTGCAGGCTGAAGATGTG  267
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GGCAGCGGGTCTGGGACAGATTTCACTCTCCACCATCAGCAGCCTGCAGGCTGAAGATGTG  240

Qy  268  GCAGTTTATTACTGTGTCAGCAATATTATAGTACTCCTCGAACGTTCGGCCAAGGGACCAAG  327
         ||||||||||||||||||||||||| |||||||| |  ||||||||||||| | |||||||||
Db  241  GCAGTTTACTTCTGTGTCACAATATTATAGTACTACTCCGTGACGTTCGGCCAGGGGACCAAG  300

Qy  328  GTGGAAATCAAA  339
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Db  301  GTGGAAATCAAA  312
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Search completed: July 18, 2003, 15:38:39
Job time : 83.9507 secs

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OM nucleic - nucleic search, using sw model

Copyright GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 18, 2003, 09:26:19 ; Search time 17.9759 Seconds
                                            (without alignments)
                                   5783.490 Million cell updates/sec

Title: US-09-627-896B-26
Perfect score: 339
Sequence: 1 gacatccagttgacccagtc.........ggaccaaggtggaaatcaaa 339

Scoring table: IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
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    2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
    3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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    5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	321.4	94.8	342	1	US-08-360-125-4	Sequence 4, Appli
2	321.4	94.8	342	2	US-08-450-578-4	Sequence 4, Appli
3	321.4	94.8	342	2	US-09-017-628-4	Sequence 4, Appli
4	321.4	94.8	342	2	US-09-014-880-4	Sequence 4, Appli
5	321.4	94.8	342	4	US-08-450-363-4	Sequence 4, Appli
6	319	94.1	360	1	US-08-026-320A-3	Sequence 3, Appli
7	314	92.6	1330	3	US-08-463-903-5	Sequence 5, Appli
8	314	92.6	1330	4	US-07-935-695-5	Sequence 5, Appli
9	312.4	92.2	1027	3	US-08-463-903-19	Sequence 19, Appl
10	312.4	92.2	1027	4	US-07-935-695-19	Sequence 19, Appl
11	309.2	91.2	1361	3	US-08-463-903-21	Sequence 21, Appl
12	309.2	91.2	1361	4	US-07-935-695-21	Sequence 21, Appl
13	308.6	91.0	1088	3	US-08-463-903-3	Sequence 3, Appli
14	308.6	91.0	1088	4	US-07-935-695-3	Sequence 3, Appli
15	301.6	89.0	836	3	US-08-463-903-1	Sequence 1, Appli
16	301.6	89.0	836	4	US-07-935-695-1	Sequence 1, Appli
17	292.4	86.3	302	3	US-08-724-752-6	Sequence 6, Appli
18	284	83.8	470	3	US-08-724-752-13	Sequence 13, Appl
19	281.4	83.0	470	4	US-08-828-741B-10	Sequence 10, Appl
20	281.4	83.0	470	4	US-09-160-567-10	Sequence 10, Appl
21	281.4	83.0	1031	3	US-08-828-741B-5	Sequence 5, Appli
22	281.4	83.0	1031	4	US-09-160-567-5	Sequence 5, Appli
23	281.4	83.0	1490	4	US-08-828-741B-3	Sequence 3, Appli
24	281.4	83.0	1490	4	US-09-160-567-3	Sequence 3, Appli
25	268.6	79.2	339	5	PCT-US93-08435-7	Sequence 7, Appli
26	267	78.8	339	5	PCT-US93-08435-5	Sequence 5, Appli
27	254.2	75.0	339	1	US-08-467-420A-20	Sequence 20, Appl
28	254.2	75.0	339	1	US-08-470-110A-20	Sequence 20, Appl
29	254.2	75.0	339	1	US-08-667-769A-20	Sequence 20, Appl
30	254.2	75.0	339	2	US-08-940-371-20	Sequence 20, Appl
31	254.2	75.0	339	5	US-08-637-647-20	Sequence 50, Appl
32	254.2	75.0	5703	5	PCT-US95-17082A-20	Sequence 50, Appl
33	254.2	75.0	5703	1	US-08-467-420A-50	Sequence 50, Appl
34	254.2	75.0	5703	1	US-08-470-110A-50	Sequence 50, Appl
35	254.2	75.0	5703	2	US-08-667-769A-50	Sequence 50, Appl
36	254.2	75.0	5703	3	US-08-940-371-50	Sequence 5, Appl
37	254.2	75.0	5703	3	US-08-637-647-50	Sequence 103, App
38	254.2	75.0	5703	5	PCT-US95-17082A-50	Sequence 3, Appli
39	246.2	72.6	339	4	US-09-301-593-5	Sequence 1, Appli
40	246.2	72.6	339	4	US-09-301-593-103	Sequence 31, Appl
41	246.2	72.6	339	5	PCT-US93-08435-3	Sequence 35, Appl
42	244.6	72.2	339	4	US-09-301-593-1	Sequence 7, Appli
43	244.6	72.2	339	4	US-09-301-593-31	
44	244.6	72.2	8068	4	US-09-301-593-35	
45	243.6	71.9	442	3	US-08-724-752-7	

ALIGNMENTS

RESULT 1
US-08-360-125-4
; Sequence 4, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
;   APPLICANT: Saiko HOSOKAWA
;   APPLICANT: Toshiaki TAGAWA
;   APPLICANT: Yoko HIRAKAWA
;   APPLICANT: No. 5767246ihiko ITO
;   APPLICANT: Kazuhiro NAGAIKE
;   TITLE OF INVENTION: Human Monoclonal Antibody
;   TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
;   TITLE OF INVENTION: Cell Membrane
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Wenderoth, Lind & Ponack
;   STREET: 805 Fifteenth Street, N.W., #700
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/360,125
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/905,534
;   FILING DATE: June 29, 1992
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Warren M. Cheek, Jr.
;   REGISTRATION NUMBER: 33,367
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-371-8850
;   TELEFAX:
;   TELEX:
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 342 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA

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;   HYPOTHETICAL:
;   ANTI-SENSE:
;   FRAGMENT TYPE:
;   ORIGINAL SOURCE:
;     ORGANISM:
;     STRAIN:
;     INDIVIDUAL ISOLATE:
;     DEVELOPMENTAL STAGE:
;     HAPLOTYPE:
;     TISSUE TYPE:
;     CELL TYPE:  Hybridoma producing human
;     CELL TYPE:  antibody GAH
;     CELL LINE:
;     ORGANELLE:
;   IMMEDIATE SOURCE:
;     LIBRARY:
;     CLONE:
;   POSITION IN GENOME:
;     CHROMOSOME/SEGMENT:
;     MAP POSITION:
;     UNITS:
;   FEATURE:
;     NAME/KEY:
;     LOCATION:
;     IDENTIFICATION METHOD:
;     OTHER INFORMATION:
;   PUBLICATION INFORMATION:
;     AUTHORS:
;     TITLE:
;     JOURNAL:
;     VOLUME:
;     ISSUE:
;     PAGES:
;     DATE:
;     DOCUMENT NUMBER:
;     FILING DATE:
;     PUBLICATION DATE:
;     RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-4

Query Match     94.8%;  Score 321.4;  DB 1;  Length 342;
Best Local Similarity   96.8%;  Pred. No. 2.9e-97;
Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db    1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACCAACTCCAACAATAAGAAATACTTAGCT 120

Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTCCTCATTTACTGGGCATCTACCCCGG 180

Qy  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCGCAATATTATAGTACT 300
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Db  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCGCAGTATTATAGTACT 300

Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db  301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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;   PUBLICATION INFORMATION:
;     AUTHORS:
;     TITLE:
;     JOURNAL:
;     VOLUME:
;     ISSUE:
;     PAGES:
;     DATE:
;     DOCUMENT NUMBER:
;     FILING DATE:
;     PUBLICATION DATE:
;     RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-4

Query Match    94.8%;  Score 321.4; DB 2;  Length 342;
Best Local Similarity  96.8%;  Pred. No. 2.9e-97;
Matches  328;  Conservative  0;  Mismatches  11;  Indels  0;  Gaps  0;

Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db     1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT  120
           ||||||||||||||||||||||||||||||||||  ||||||||  ||||  ||||||
Db    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT  120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGGACACAGATTTCACTCTCACC  240
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Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGGACACAGATTTCACTCTCACC  240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
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Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT  300

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Db   301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  339
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RESULT 3
US-09-017-628-4
;   Sequence 4, Application US/09017628
;   Patent No. 5990287
;   GENERAL INFORMATION:
;     APPLICANT: HOSOKAWA, Saiko
;     APPLICANT: TAGAWA, Toshiaki
;     APPLICANT: HIRAKAWA, Yoko
;     APPLICANT: ITO, No. 5990287ihiko
;     APPLICANT: NAGAIKE, Kazuhiro
;     TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
;     TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;     FILE REFERENCE: 177/527361KH
;     CURRENT APPLICATION NUMBER: US/09/017,628
;     CURRENT FILING DATE: 1998-02-02
;     EARLIER APPLICATION NUMBER: 08/360,125
;     EARLIER FILING DATE: 1994-12-20
;     NUMBER OF SEQ ID NOS: 42
;     SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 4
;     LENGTH: 342
;     TYPE: DNA
;     ORGANISM: Unknown
;     FEATURE:
;     OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-4

Query Match    94.8%;  Score 321.4; DB 2;  Length 342;
Best Local Similarity  96.8%;  Pred. No. 2.9e-97;
Matches  328;  Conservative  0;  Mismatches  11;  Indels  0;  Gaps  0;
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Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    61 ATCAACTGCAAGTCAGCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT  120
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Db    61 ATCAACTGCAAGTCAGCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT  120

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  180
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Db   121 TGGTACCAGCAGAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  180

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGGACACAGATTTCACTCTCACC  240
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Db   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGGTCTGGGACACAGATTTCACTCTCACC  240

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT  300

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  339
           ||  ||||||||||||||||||||||||||||||||||
Db   301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA  339
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RESULT 4
US-09-014-880-4
;   Sequence 4, Application US/09014880
;   Patent No. 5990297
;   GENERAL INFORMATION:
;     APPLICANT: Saiko HOSOKAWA et al.
;     TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
;     TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;     NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
;     STREET: 2033 K Street, N.W., #800
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20006
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: Wordperfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/014,880
;     FILING DATE: January 28, 1998
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/450,578
;     FILING DATE: May 25, 1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/360,125
;     FILING DATE: December 20, 1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/905,534
;     FILING DATE: June 29, 1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Warren M. Cheek, Jr.
;     REGISTRATION NUMBER: 33,367
;     REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-721-8200
;     TELEFAX: 202-721-8250
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 342 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
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;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;   CELL TYPE: Hybridoma producing human
;   CELL TYPE: antibody GAH
US-09-014-880-4

Query Match   94.8%; Score 321.4; DB 2; Length 342;
Best Local Similarity 96.8%; Pred. No. 2.9e-97;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
         |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCAACAACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAACAATAAGAAATACTTAGCT 120

Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db  121 TGGTACCAGCAGAAACCAGGACAGCCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 5
US-08-450-363-4
; Sequence 4, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
;   APPLICANT: Saiko HOSOKAWA
;   APPLICANT: Toshiaki TAGAWA
;   APPLICANT: Yoko HIRAKAWA
;   APPLICANT: No. 6436434ihiko ITO
;   APPLICANT: Kazuhiro NAGAIKE
;   TITLE OF INVENTION: Human Monoclonal Antibody
;   TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
;   TITLE OF INVENTION: Cell Membrane
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Wenderoth, Lind & Ponack
;   STREET: 805 Fifteenth Street, N.W., #700
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/450,363
;   FILING DATE: May 25, 1995
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/360,125
;   FILING DATE: December 20, 1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/905,534
;   FILING DATE: June 29, 1992
;   ATTORNEY/AGENT INFORMATION:

;   NAME: Warren M. Cheek, Jr.
;   REGISTRATION NUMBER: 33,367
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-371-8850
;   TELEFAX:
;   TELEX:
INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 342 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL:
;   ANTI-SENSE:
;   FRAGMENT TYPE:
;   ORIGINAL SOURCE:
;   ORGANISM:
;   STRAIN:
;   INDIVIDUAL ISOLATE:
;   DEVELOPMENTAL STAGE:
;   HAPLOTYPE:
;   TISSUE TYPE:
;   CELL TYPE: Hybridoma producing human
;   CELL TYPE: antibody GAH
;   CELL LINE:
;   ORGANELLE:
;   IMMEDIATE SOURCE:
;   LIBRARY:
;   CLONE:
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT:
;   MAP POSITION:
;   UNITS:
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:
;   PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-4

Query Match   94.8%; Score 321.4; DB 4; Length 342;
Best Local Similarity 96.8%; Pred. No. 2.9e-97;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
         |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCAACAACAAGAATTACTTAACT 120
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Db   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAACAATAAGAAATACTTAGCT 120

Qy  121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Qy  181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy  241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Qy  301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db  301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 6
US-08-026-320A-3
; Sequence 3, Application US/08026320A
; Patent No. 5419904
; GENERAL INFORMATION:
; APPLICANT: Irie, Reiko F
; TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
; TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Poms, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States of America
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,320A
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/609803
; FILING DATE: 05-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J
; REGISTRATION NUMBER: 29421
; REFERENCE/DOCKET NUMBER: 94268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310788046
; TELEFAX: 3102771297
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Epstein Barr Virus transformed B
; INDIVIDUAL ISOLATE: cell
; CELL TYPE: B-cell
; CELL LINE: L612
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..360
; OTHER INFORMATION: /function= "Immunoglobulin light
; OTHER INFORMATION: chain"
; OTHER INFORMATION: /product= "HuMab L612 Light Chain Variable Region"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 58..I08
; OTHER INFORMATION: /function= "Complementary
; OTHER INFORMATION: determining region 1 (CDR1)"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 154..174
; OTHER INFORMATION: /function= "Complementary
; OTHER INFORMATION: determining region 2 (CDR2)"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 271..297
; OTHER INFORMATION: /function= "Complementary
; OTHER INFORMATION: determining region 3 (CDR3)"
US-08-026-320A-3

Query Match   94.1%; Score 319; DB 1; Length 360;
Best Local Similarity 98.5%; Pred. No. 1.9e-96;
Matches 322; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy   13 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 72
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Db    1 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 60

Qy   73 TCCAGCCAGAGTGTTTTATACAGCTCCAACACAACAAGAATTACTTAACTTGGTACCAGCAG 132
         |||||||||||||||||||||||||||    ||    ||    ||  |||||||||||||||
Db   61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAG 120

Qy  133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 192
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 180

Qy  193 CCTGACCGATTCAGTGGCGCAGCGGGTCTGGGACAGACAGATTTCACTCTCACCATCAGCAGCCTG 252
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Db  181 CCTGACCGATTCAGTGGCGCAGCGGGTCTGGGACAGACAGATTTCACTCTCACCATCAGCAGCCTG 240

Qy  253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTGAACGTTC 312
         |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db  241 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCCGACGTTC 300

Qy  313 GGGCCAAGGGACCAAGGTGGAAATCAAA 339
         ||||||||||||||||||||||||||||
Db  301 GGGCCAAGGGACCAAGGTGGAAATCAAA 327
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RESULT 7
US-08-463-903-5
; Sequence 5, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 5
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Hum4VL-VH scFv from pSCFV UHH
; LOCATION: 1..1330
US-08-463-903-5

Query Match   92.6%; Score 314; DB 3; Length 1330;
Best Local Similarity 95.6%; Pred. No. 1.6e-94;
Matches 323; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
        ||||||        |||||||||||||||||||||||||||||||||||||||||||||||
Db  359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418
```

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Qy    61  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCCAACAACAAGAATTACTTAACT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCCAACAACAAGAATTACTTAGCT  478

Qy   121  TGGTACCAGCAGAAACCAGGACAGCCTCCTCAAGCTCGTCATTTACTGGGCATCTACCCGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479  TGGTACCAGCAGAAACCAGGACAGCCTCCTCAAGCTCGTCATTTACTGGGCATCTACCCGG  538

Qy   181  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  598

Qy   241  ATCAGCAGCGTGACCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
          ||||    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599  ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT  658

Qy   301  CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA  338
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Db   659  CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA  696
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RESULT 8
US-07-935-695-5
; Sequence 5, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;   APPLICANT: Mezes, Peter S.
;   APPLICANT: Richard, Ruth A.
;   APPLICANT: Affholter, Joseph A.
;   APPLICANT: Kotite, Nicolas J.
;   TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;   FILE REFERENCE: 40224A US
;   CURRENT APPLICATION NUMBER: US/07/935,695
;   CURRENT FILING DATE: 1992-08-21
;   PRIOR APPLICATION NUMBER: US 08/463,903
;   PRIOR FILING DATE: 1995-06-05
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 5
;   LENGTH: 1330
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
; FEATURE:
;   NAME/KEY: Hum4VL-VH scFv from pSCFV UHH
;   LOCATION: 1..1330
; OTHER INFORMATION: :
US-07-935-695-5

Query Match   92.6%; Score 314; DB 4; Length 1330;
Best Local Similarity   95.6%; Pred. No. 1.6e-94;
Matches   323; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy     1  GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  60
          ||||||  |||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   359  GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  418

Qy    61  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCCAACAACAAGAATTACTTAACT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCCAACAACAAGAATTACTTAGCT  478

Qy   121  TGGTACCAGCAGAAACCAGGACAGCCTCCTCAAGCTCGTCATTTACTGGGCATCTACCCGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479  TGGTACCAGCAGAAACCAGGACAGCCTCCTCAAGCTCGTCATTTACTGGGCATCTACCCGG  538

Qy   181  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  598

Qy   241  ATCAGCAGCGTGACCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
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Db   599  ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT  658

Qy   301  CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA  338
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RESULT 9
US-08-463-903-19
; Sequence 19, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
;   APPLICANT: Mezes, Peter S.
;   APPLICANT: Richard, Ruth A.
;   APPLICANT: Affholter, Joseph A.
;   APPLICANT: Kotite, Nicolas J.
;   TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;   FILE REFERENCE: 40224A US
;   CURRENT APPLICATION NUMBER: US/08/463,903
;   CURRENT FILING DATE: 1995-06-05
;   EARLIER APPLICATION NUMBER: US 07/935,695
;   EARLIER FILING DATE: 1992-08-21
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 19
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
; FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
;   LOCATION: 1..1027
US-08-463-903-19

Query Match   92.2%; Score 312.4; DB 3; Length 1027;
Best Local Similarity   95.3%; Pred. No. 4.7e-94;
Matches   322; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db   359  GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  418

Qy    61  ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTCCCAACAACAAGAATTACTTAACT  120
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Qy   121  TGGTACCAGCAGAAACCAGGACAGCCTCCTCAAGCTCGTCATTTACTGGGCATCTACCCGG  180
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Qy   181  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  240
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Db   539  GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  598

Qy   241  ATCAGCAGCCTGACCCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
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Db   599  ATCAGCAGCCTGAAGATGCGGCAGTTTATTACTGTCAGCAATATTATAGTTAT  658

Qy   301  CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA  338
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Db   659  CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA  696
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RESULT 10
US-07-935-695-19
; Sequence 19, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;   APPLICANT: Mezes, Peter S.
;   APPLICANT: Richard, Ruth A.
;   APPLICANT: Affholter, Joseph A.
;   APPLICANT: Kotite, Nicolas J.
;   TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;   FILE REFERENCE: 40224A US
;   CURRENT APPLICATION NUMBER: US/07/935,695
;   CURRENT FILING DATE: 1992-08-21
;   PRIOR APPLICATION NUMBER: US 08/463,903

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;   PRIOR FILING DATE: 1995-06-05
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: MS-Word for Windows, Ver. 7.0
;   SEQ ID NO 19
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
;   LOCATION: 1..1027
;   OTHER INFORMATION: :
US-07-935-695-19

Query Match             92.2%;  Score 312.4;  DB 4;  Length 1027;
Best Local Similarity   95.3%;  Pred. No. 4.7e-94;
Matches  322;  Conservative  0;  Mismatches  16;  Indels  0;  Gaps  0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  418

Qy         61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACACAACAATAAGAACTACTTAACT  120
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Db        419 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT  478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGCATCATCACCCGG  180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  538

Qy        181 GAATCCGGGGTCCCTGACCGGTCTGGGACAGATTCAGTGGCAGCGGGTCTGGGACAGATTCACTCTCACC  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGGTCTGGGACAGTGGCAGCGGGTCTGGGACAGATTCACTCTCACC  598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
              |||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
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Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA  338
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Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA  696

RESULT 11
US-08-463-903-21
;   Sequence 21, Application US/08463903
;   Patent No. 6071515
;   GENERAL INFORMATION:
;   APPLICANT: Mezes, Peter S.
;   APPLICANT: Richard, Ruth A.
;   APPLICANT: Affholter, Joseph A.
;   APPLICANT: Kotite, Nicolas J.
;   TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;   FILE REFERENCE: 40224A US
;   CURRENT APPLICATION NUMBER: US/08/463,903
;   CURRENT FILING DATE: 1995-06-05
;   EARLIER APPLICATION NUMBER: US 07/935,695
;   EARLIER FILING DATE: 1992-08-21
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: MS-Word for Windows, Ver. 7.0
;   SEQ ID NO 21
;   LENGTH: 1361
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pSC49FLAG
;   LOCATION: 1..1361
US-08-463-903-21

Query Match             91.2%;  Score 309.2;  DB 3;  Length 1361;
Best Local Similarity   94.7%;  Pred. No. 6.2e-93;
Matches  320;  Conservative  0;  Mismatches  18;  Indels  0;  Gaps  0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  60
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Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  418

Qy         61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACACAACAATAAGAACTACTTAACT  120
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        419 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT  478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  538

Qy        181 GAATCCGGGGTCCCTGACCGGTCTGGGACAGTGGCAGCGGGTCTGGGACAGATTCACTCTCACC  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGGTCTGGGACAGTGGCAGCGGGTCTGGGACAGATTCACTCTCACC  598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT  658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA  338
              |||||||||||||||||||||||||||||||||||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA  696

RESULT 12
US-07-935-695-21
;   Sequence 21, Application US/0793569
;   Patent No. 6329507
;   GENERAL INFORMATION:
;   APPLICANT: Mezes, Peter S.
;   APPLICANT: Richard, Ruth A.
;   APPLICANT: Affholter, Joseph A.
;   APPLICANT: Kotite, Nicolas J.
;   TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;   FILE REFERENCE: 40224A US
;   CURRENT APPLICATION NUMBER: US/07/935,695
;   CURRENT FILING DATE: 1992-08-21
;   PRIOR APPLICATION NUMBER: US 08/463,903
;   PRIOR FILING DATE: 1995-06-05
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: MS-Word for Windows, Ver. 7.0
;   SEQ ID NO 21
;   LENGTH: 1361
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pSC49FLAG
;   LOCATION: 1..1361
;   OTHER INFORMATION: :
US-07-935-695-21

Query Match             91.2%;  Score 309.2;  DB 4;  Length 1361;
Best Local Similarity   94.7%;  Pred. No. 6.2e-93;
Matches  320;  Conservative  0;  Mismatches  18;  Indels  0;  Gaps  0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  60
              ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGCGAGAGGGCCACC  418

Qy         61 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACACAACAATAAGAACTACTTAACT  120
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        419 ATCAACTGCAAGTCCAGCGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT  478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  538

Qy        181 GAATCCGGGGTCCCTGACCGGTCTGGGACAGTGGCAGCGGGTCTGGGACAGATTCACTCTCACC  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGGTCTGGGACAGTGGCAGCGGGTCTGGGACAGATTCACTCTCACC  598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
              |
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Db   599 ATCAGCAGCCTGCAGCTGAAGATGCGGCAGTTGATTACTGTCAGCAATATTATTAGTTAT 658

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
         ||| ||||||| |||| |||||||||||||||||
Db   659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGTGATCAA 696

RESULT 13
US-08-463-903-3
; Sequence 3, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 3
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
; LOCATION: 1..1088
US-08-463-903-3

Query Match   91.0%; Score 308.6; DB 3; Length 1088;
Best Local Similarity 94.4%; Pred. No. 8.9e-93;
Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy   1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
Db   727 GACACTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 786

Qy   61 ATCAACTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
Db   787 ATCAACTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACAACAATAAGAACTACTTAGCT 846

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
Db   847 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 906

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
Db   907 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 966

Qy   241 ATCAGCAGCCTGCAGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATTAGTACT 300
Db   967 ATCAGCAGCCTGCAGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATTAGTTAT 1026

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
Db 1027 CCTCTCACTTTCGGCGGAGGGACCAAGGTGTGATCAAA 1065

RESULT 14
US-07-935-695-3
; Sequence 3, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US

RESULT 15
US-08-463-903-1
; Sequence 1, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 1
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SCFv1 from pCGS515
; LOCATION: 1..836
US-08-463-903-1

Query Match   89.0%; Score 301.6; DB 3; Length 836;
Best Local Similarity 94.3%; Pred. No. 1.6e-90;
Matches 313; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC   60
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Db    77 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC  136

Qy    61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT  120
          ||||||||||||||||||||||| |  |||||||||||| |||||  ||||| || ||
Db   137 ATCAACTGCAAGTCCAGCTGCAAGGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT  196

Qy   121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  180
          |||||||||||||||||||||||||  |||||||||||| ||  ||||||||| ||||||
Db   197 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG  256

Qy   181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  240
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Db   257 GAATCCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC  316

Qy   241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT  300
          |||||||||||||||||||||||||||||||||||||||||||||| | ||||||||
Db   317 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT  376

Qy   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGA  332
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Search completed: July 18, 2003, 19:59:07
Job time : 18.9759 secs

OM nucleic - nucleic search, using sw model

Copyright GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 18, 2003, 04:46:48 ; Search time 1030.02 Seconds
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Title: US-09-627-896B-29
Perfect score: 368
Sequence: 1 aggtgcagctggtgcagtct.........ccctgctcatcgtctcctca 368

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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    2: gb_htg:*
    3: gb_in:*
    4: gb_om:*
    5: gb_ov:*
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    7: gb_ph:*
    8: gb_pl:*
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   33: em_htg_mus:*
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   35: em_htg_rod:*
   36: em_htg_mam:*
   37: em_htg_vrt:*
   38: em_sy:*
   39: em_htgo_hum:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	311.2	84.6	428	9	AF062105	AF062105 Homo sapi
4	308.6	83.9	525	9	HUMIGHDNN	M65093 Human Ig re
5	307.2	83.5	426	9	HSVHIB8	Z47233 H.sapiens m
6	307.2	83.5	512	9	HSU84173	U84173 Homo sapien
7	307.2	83.5	515	9	HSU79581	U79581 Human clone
8	305.8	83.1	521	9	HSU84180	U84180 Homo sapien
9	305.6	83.0	528	9	HUMIGHDYN	M65104 Human Ig re
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11	303.8	82.6	515	9	HSU84178	U84178 Homo sapien
12	303	82.3	372	9	AB067158	AB067158 Homo sapi
13	302.8	82.3	363	9	U00583	U00583 Human immun
14	300.8	81.7	518	9	HSU84161	U84161 Homo sapien
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20	296.8	80.7	369	9	AB063921	AB063921 Homo sapi
21	296.8	80.7	369	12	AF527046	AF527046 Synthetic
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23	296.4	80.5	510	9	HS203E2	Z47264 H.sapiens m
24	296.4	80.5	510	9	HS203E6	Z47265 H.sapiens m
25	296.4	80.5	510	9	HS203E7	Z47266 H.sapiens m
26	296.4	80.5	510	9	HS203E9	Z47267 H.sapiens m
27	296.4	80.5	525	9	HS203G4	Z47271 H.sapiens m
28	296.2	80.5	381	9	AF062216	AF062216 Homo sapi
29	295.8	80.4	432	9	AF062193	AF062193 Homo sapi
30	294.8	80.1	483	9	HS203M7	Z47273 H.sapiens m
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42	293	79.6	438	9	AF062161	AF062161 Homo sapi
43	292	79.3	501	9	HUMIGHDQN	M65096 Human Ig re
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ALIGNMENTS

RESULT 1
HSVH1I2RM
LOCUS   HSVH1I2RM   368 bp   DNA   linear   PRI 23-FEB-1993
DEFINITION   H.sapiens DNA for anti-DNA antibody heavy chain variable
                region,subgroup V(H)1 (III-2R IgM line).
ACCESSION   X70487 X63851
VERSION   X70487.1 GI:38449
KEYWORDS   anti-DNA antibody; complementarity determining region; Ig heavy
                chain; Ig kappa light chain; Ig variable region; IgM;
                immunoglobulin; systemic lupus erythematosus.
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 368)

Pred. No. is the number of results predicted by chance to have a

AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
           and Diamond,B.
TITLE   Molecular characteristics of antibodies bearing an
           anti-DNA-associated idiotype
JOURNAL   J. Exp. Med. 174 (6), 1639-1652 (1991)
MEDLINE   92078875
PUBMED   1660528
FEATURES   Location/Qualifiers
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           /sub_clone="pBluescript"
           /cell_line="EBV-transformed 3I(+) B cell line,III-2R IgM"
           /tissue_type="spleen"
           /clone_lib="genomic DNA in Charon 40"
     misc_feature <1..>368
           /note="IgM light chain variable region"
     misc_feature 90..104
           /note="complementarity determining region, CDR 1"
     misc_feature 138..197
           /note="complementarity determining region, CDR 2"
BASE COUNT   84 a   92 c   116 g   76 t
ORIGIN

Query Match   100.0%;   Score 368;   DB 9;   Length 368;
Best Local Similarity 100.0%;   Pred. No. 8.9e-102;
Matches 368; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCTATCAGCGTGCGACAGGCCC   120
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Db   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCTATCAGCGTGCGACAGGCCC   120

Qy 121 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCGTATCCTTGGACTAGCAAATTACG   180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCGTATCCTTGGACTAGCAAATTACG   180

Qy 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGCGGACAAATCCACGAGCACAGCCTACA   240
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Db 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGCGGACAAATCCACGAGCACAGCCTACA   240

Qy 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG   300
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Qy 301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGCCAGGGAACCCTGCTCATCG   360
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Db 301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGCCAGGGAACCCTGCTCATCG   360

Qy 361 TCTCCTCA 368
        ||||||||
Db 361 TCTCCTCA 368

RESULT 2
AF021950
LOCUS   AF021950   370 bp   mRNA   linear   PRI 02-APR-1998
DEFINITION Homo sapiens ID:CLL008 IgM heavy chain variable region mRNA,
            partial cds.
ACCESSION   AF021950
VERSION   AF021950.1   GI:3004689
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 370)
AUTHORS   Chiorazzi,N.
TITLE   Differences in Ig variable region gene use and mutation in IgM vs

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IgG CLL suggest selection for distinct surface membrane Ig
           receptors
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 370)
AUTHORS   Chiorazzi,N.
TITLE   Direct Submission
JOURNAL   Submitted (02-SEP-1997) Medicine, North Shore University Hospital,
           350 Community Drive, Manhasset, NY 11030, USA
FEATURES   Location/Qualifiers
     source 1..370
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           /chromosome="14"
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           /product="IgM heavy chain variable region"
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           /translation="QVQLVQSGAEVKKPGSSVKVSCKASGTFSSYAISWVRQAPGQG
           LEWMGGIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVWGG
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BASE COUNT   77 a   92 c   123 g   78 t
ORIGIN

Query Match   85.7%;   Score 315.2;   DB 9;   Length 370;
Best Local Similarity 91.0%;   Pred. No. 1.4e-85;
Matches 335; Conservative   0; Mismatches   33; Indels   0; Gaps   0;

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Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCGTGCGACAGGCCC   120
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Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATGCTATCAGCTGGGTGCGACAGGCCC   121

Qy 121 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATGCGTATCCTATCCTTGGACTAGCAAATTACG   180
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Db 122 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATCCTATCTTTGGTACAGCAAACTACG   181

Qy 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGCGGACAAATCCACGAGCACAGCCTACA   240
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Db 182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGACACGGCCGTCGTG   241

Qy 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG   300
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Db 242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTTTGGG   301

Qy 301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGCCAGGGAACCCTGCTCATCG   360
        ||||||||| ||| ||| | ||||| | ||||||||||||| ||||||||| ||||||
Db 302 GTGGTTCGGGAGGTTATTATTATTATCGTTCGACCCCTGGGCCAGGGAACCCTGGTCACCG   361

Qy 361 TCTCCTCA 368
        ||||||||
Db 362 TCTCCTCA 369

RESULT 3
AF062105
LOCUS   AF062105   428 bp   mRNA   linear   PRI 08-MAY-2001
DEFINITION Homo sapiens clone 21u-19 immunoglobulin heavy chain variable
            region (IGH) mRNA, partial cds.
ACCESSION   AF062105
VERSION   AF062105.1   GI:3170672
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 428)
AUTHORS   Wang,X. and Stollar,B.D.

```
DEFINITION  Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L22,
            subgroup VH-I.
ACCESSION   M65093
VERSION     M65093.1  GI:185322
KEYWORDS    V-region; immunoglobulin heavy chain subgroup VH-I; rearranged DNA.
SOURCE      Homo sapiens tonsil DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Kipps,T.J. and Duffy,S.F.
  TITLE     Relationship of the CD5 B cell to human tonsillar lymphocytes that
            express autoantibody-associated cross-reactive idiotypes
  JOURNAL   J. Clin. Invest. 87 (6), 2087-2096 (1991)
  MEDLINE   91250563
   PUBMED   1710233
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /codon_start=1
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                     /protein_id="AAB00781.1"
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ORIGIN

Query Match             83.9%;  Score 308.6;  DB 9;  Length 525;
Best Local Similarity   91.4%;  Pred. No. 1.5e-83;
Matches 339;   Conservative    0;  Mismatches   29;   Indels    3;  Gaps    1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db  155 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 214

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db  215 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTATCAGCTGGGTGCGACAGGCCC 274

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGACTAGCAAATTACG 180
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Db  275 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTACAGCAAACTACG 334

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db  335 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 394
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TITLE      Immunoglobulin VH gene expression in human aging
JOURNAL    Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE    99459182
 PUBMED    10527689
REFERENCE  2  (bases 1 to 428)
 AUTHORS   Wang,X. and Stollar,B.D.
 TITLE     Direct Submission
 JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
           School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1..428
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                     /db_xref="taxon:9606"
                     /chromosome="14"
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                     /clone="21u-19"
                     /cell_type="peripheral B lymphocyte"
                     /tissue_type="blood"
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     gene            1..>428
                     /gene="IGH"
     CDS             1..>428
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC18141.1"
                     /db_xref="GI:3170673"
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BASE COUNT       89 a    107 c    144 g     88 t
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Best Local Similarity   92.1%;  Pred. No. 2.3e-84;
Matches 339;   Conservative    0;  Mismatches   28;   Indels    1;  Gaps.    1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db   59 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 118

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db  119 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTATCAGCTGGGTGCGACAGGCCC 178

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGACTAGCAAATTACG 180
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Db  179 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTACAGCAAACTACG 238

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACACGAGCACAGCCTACA 240
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Db  239 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACACGCGAGCACAGCCTACA 298

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db  299 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCGCGG 358

Qy  301 ATTATGTTGGGGAGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
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Db  359 TCAGTGGTAGTGGATACAACTGGTTCGA-CCCTGGGGCCAGGGAACCCTGGTCACCG 417

Qy  361 TCTCCCTCA 368
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Db  418 TCTCCCTCA 425

RESULT 4
HUMIGHDNN
LOCUS       HUMIGHDNN                525 bp    DNA        linear    PRI 23-MAY-1996
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Qy   241  TGGAGCTGAGCAGCCTGAGATCTGTGTATTACTGTGCGAGAGATCCCG            300
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Db   395  TGGAGCTGAGCAGCCTGAGATCTGTGTATTACTGTGCGAGAGAGGAT            454

Qy   301  ATTATGTTTGGGGGAGCGGAC--AACTGGTTCGACCCCTGGGCCAGGGACCCTGCTCA   357
          ||||   |||  | |||  |||   |||||||||||||| |||||||||||||||||
Db   455  ATTGTAGTAGTACCAGTGCTCGGTTCGACAACTGGT...                     514

Qy   358  TCGTCTCCTCA                                                 368
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Db   515  CCGTCTCCTCA                                                 525
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RESULT 5
HSVHIB8
LOCUS   HSVHIB8   426 bp   mRNA   linear   PRI 15-FEB-1996
DEFINITION H.sapiens mRNA for immunoglobulin heavy chain V-region (clone
            CDN31B8).
ACCESSION   Z47233
VERSION   Z47233.1 GI:1197314
KEYWORDS   immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE   Homo sapiens
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 113)
  AUTHORS   Demaison,C., David,D., Letourneur,F., Zouali,M., Saragosti,S. and
            Theze,J.
  TITLE   A cDNA/anchor-PCR approach to analyse the human VH gene repertoire
            expressed by peripheral CD19+ B cells reveals a strong bias usage
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 426)
  AUTHORS   Demaison,C.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-DEC-1994) Christophe Demaison, Immunologie, Unite
            d'Immunogenetique Cellulaire-institut Pasteur, 25, rue du Docteur
            Roux, Paris, 75015, FRANCE
REFERENCE   3 (bases 1 to 426)
  AUTHORS   Demaison,C., David,D., Letourneur,F., Theze,J., Saragosti,S. and
            Zouali,M.
  TITLE   Analysis of human VH gene repertoire expression in peripheral CD19+
            B cells
  JOURNAL   Immunogenetics 42 (5), 342-352 (1995)
  MEDLINE   96006568
   PUBMED   7590967
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                     /tissue_type="peripheral blood lymphocyte"
                     /dev_stage="adult"
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ORIGIN

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  Best Local Similarity   89.7%;
  Matches 330;   Conservative   0; Mismatches   38; Indels   0; Gaps   0;

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Qy     1  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGTCCTCGGTAAAGGTCT   60
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Qy    61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCC   120
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Db   119  CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCC   178

Qy   121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCTATCCTTTGGTGACTAGCAAATTACG  180
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Db   179  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCTATCCTTTGGTACAGCAAACTACG  238
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Qy   181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA  240
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Db   239  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA  298

Qy   241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGTGGGGCCC  358

Qy   301  ATTATGTTTGGGGGAGCGACAAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG  360
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Db   359  CCAATGACTACGGTGACTACGGGGGGCGGCGGACTACTGGGGCCAGGGAACCCTGGTCACCG  418

Qy   361  TCTCCTCA                                                      368
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Db   419  TCTCCTCA                                                      426
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RESULT 6
HSU84173
LOCUS   HSU84173   512 bp   DNA   linear   PRI 27-AUG-1997
DEFINITION Homo sapiens isolate HOW IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84173
VERSION   U84173.1 GI:2344939
KEYWORDS   .
SOURCE   Homo sapiens
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 512)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE   Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
   PUBMED   8977195
REFERENCE   2 (bases 1 to 512)
  AUTHORS   Johnson,T.A.
  TITLE   Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES   Location/Qualifiers
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                     /note="CLL: chronic lymphocytic leukemia"
     gene   1..512
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                     /db_xref="GI:2344940"
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                     SSLRSEDTAVYYCARDRSGSYYVKNWFDPWGQGTLVTVSS"
     sig_peptide   join(1..46,133..143)
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     mat_peptide   144..512
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BASE COUNT   113 a   128 c   159 g   112 t
ORIGIN

Query Match   83.5%; Score 307.2; DB 9; Length 512;

Left column

Best Local Similarity 89.7%; Pred. No. 3.9e-83;
Matches 330; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Db  145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCGGTGAAGGTCT   204

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
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Db  205 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTATCAGCTGGGTGCGACAGGCCC 264

Qy  121 CTGGACAAGGGCTTGAGTGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG      180
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Db  265 CTGGACAAGGGCTTGAGTGGATGGGATCATCCCTATCTTTGGAACAGCACAACTACG     324

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACAGAGCACAGCCTACA  240
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Db  325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAGAATCACGAGCACAGCCTACA   384

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
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Db  385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATATTACTGTGCGAGAGAGGGT   444

Qy  301 ATTATGTTTGGGGGAGCCAACTGGTTCGACCCCTGGGGCCAGGGAACCCTCGTCTCATCG  360
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Db  445 ATGATAGTAGTGGTTCGAAAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG  504

Qy  361 TCTCCCTCA 368
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Db  505 TCTCCCTCA 512
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RESULT 7

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HSU79581
LOCUS       HSU79581      515 bp    DNA      linear   PRI 01-FEB-1997
DEFINITION  Human clone OR immunoglobulin heavy chain gene, partial cds.
ACCESSION   U79581
VERSION     U79581.1  GI:1813665
KEYWORDS    .
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 515)
AUTHORS     Bahler,D.W., Miklos,J.A. and Swerdlow,S.H.
TITLE       Ongoing Ig Gene Hypermutation by Salivary Gland Mucosa-Associated
            Lymphoid Tissue-Type Lymphomas
JOURNAL     Blood (1997) In press
REFERENCE   2 (bases 1 to 515)
AUTHORS     Bahler,D.W., Miklos,J.A. and Swerdlow,S.H.
TITLE       Direct Submission
JOURNAL     Submitted (26-NOV-1996) Pathology, Montefiore University Hospital,
            200 Lothrop Street, Pittsburgh, PA 15213-2582, USA
FEATURES             Location/Qualifiers
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                     SSLRSEDTAVYYCAREGYDSSGSPKPFDYWGQGTLVTVSSG"
BASE COUNT    112 a    130 c    160 g    113 t
ORIGIN
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Query Match 83.5%; Score 307.2; DB 9; Length 515;
Best Local Similarity 89.7%; Pred. No. 3.9e-83;

Right column

Matches 330; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```
Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db  145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCGGTGAAGGTCT   204

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
        |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Db  205 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTATCAGCTGGGTGCGACAGGCCC 264

Qy  121 CTGGACAAGGGCTTGAGTGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG      180
        |||||||||||||||||||| |||||| ||||| ||||  ||  |||| ||| ||||
Db  265 CTGGACAAGGGCTTGAGTGGATGGGATCATCCCTATCTTTGGAACAGCACAACCACG     324

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACAGAGCACAGCCTACA  240
        |||||||||||||||||||||||||||||||||||||  ||| |||||||||||||||||
Db  325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAGAATCACGAGCACAGCCTACA   384

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
        |||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATATTACTGTGCGAGAGAGGGT   444

Qy  301 ATTATGTTTGGGGGAGCCAACTGGTTCCCCGAACCCCTGGGGCCAGGGAACCCTCGTCTCATCG 360
        ||   ||  ||  ||||  |  |||||||||||||||||||||||||||||||| ||| ||||
Db  445 ATGATAGTAGTGGTTCCCGAAACCCTTGACTACTGGGGCCAGGGAACCCTGGTCACCG      504

Qy  361 TCTCCCTCA 368
        |||||||||
Db  505 TCTCCCTCA 512
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RESULT 8

```
HSU84180
LOCUS       HSU84180      521 bp    DNA      linear   PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate LID IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84180
VERSION     U84180.1  GI:2344953
KEYWORDS    .
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 521)
AUTHORS     Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
TITLE       Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
JOURNAL     J. Immunol. 158 (1), 235-246 (1997)
MEDLINE     97131694
PUBMED      8977195
REFERENCE   2 (bases 1 to 521)
AUTHORS     Johnson,T.A.
TITLE       Direct Submission
JOURNAL     Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
     source          1..521
                     /organism="Homo sapiens"
                     /isolate="patient LID"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
     gene            1..521
                     /gene="VH1-69"
     CDS             join(1..46,133..>521)
                     /gene="VH1-69"
                     /codon_start=1
                     /note="CLL: chronic lymphocytic leukemia"
                     /note="Allele: variant 4"
                     /product="IgM heavy chain VH1 region precursor"
                     /protein_id="AAC51707.1"
                     /db_xref="GI:2344954"
                     /translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
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sig_peptide      GGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMEL
                 SSLRSEDTAVYYCASNPVTIFGVVIKTNWFDPWGQGTLVTVSS"
                 join(1..46,133..143)
                 /gene="VH1-69"
mat_peptide      144..521
                 /gene="VH1-69"
                 /product="IgM heavy chain VH1 region"
                 /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
BASE COUNT       115 a     128 c     157 g     121 t
ORIGIN

Query Match      83.1%;   Score 305.8;  DB 9;   Length 521;
Best Local Similarity   90.5%;   Pred. No. 1.1e-82;
Matches   341;   Conservative   0;   Mismatches  27;  Indels   9;  Gaps    1;

Qy     1  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   145  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT   204

Qy    61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC   120
          |||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||
Db   205  CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATCAGCTGGGTGCGACAGGCCC    264

Qy   121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG   180
          |||||||||||||||||||||||||||||||||||||||||  ||||||||  |||||
Db   265  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTATCAGCAAACTACG    324

Qy   181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325  CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA   384

Qy   241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGCAATCCTG   444

Qy   301  ATTATGTTTGGGG--------GAGGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCC   351
          ||||| ||| |||        |||| |||
Db   445  TTACGATTTTTGGAGTGGTTATTAAAACAAACTGGTTCGACCCCTGGGGCCAGGGAACCC   504

Qy   352  TGCTCATCGTCTCCTCA   368
          ||||| ||||||||||
Db   505  TGGTCACTGTCTCCTCA   521
```

```
RESULT 9
HUMIGHDYN
LOCUS        HUMIGHDYN              528 bp      DNA         linear     PRI 09-MAY-1996
DEFINITION   Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L42,
             subgroup VH-I.
ACCESSION    M65104
VERSION      M65104.1    GI:185344
KEYWORDS     V-region; immunoglobulin heavy chain subgroup VH-I; rearranged DNA.
SOURCE       Homo sapiens tonsil DNA.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 528)
AUTHORS      Kipps,T.J. and Duffy,S.F.
TITLE        Relationship of the CD5 B cell to human tonsillar lymphocytes that
             express autoantibody-associated cross-reactive idiotypes
JOURNAL      J. Clin. Invest. 87 (6), 2087-2096 (1991)
MEDLINE      91250563
PUBMED       1710233
FEATURES             Location/Qualifiers
     source          1..528
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="14q32.33"
                     /cell_type="B lymphocytes"
                     /tissue_type="tonsil"
     gene            11..528
                     /gene="IGH@"
     CDS             join(11..56,143..528)
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sig_peptide              /partial
                         /gene="IGH@"
                         /codon_start=1
                         /product="Ig heavy chain"
                         /protein_id="AAA99225.1"
                         /db_xref="GI:185345"
                         /db_xref="GDB:G00-118-731"
                         /translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                         GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
                         SSLRSEDTAVYYCARGGMGYCSGGSCYWFDPWGQGTLVTVSS"
                         join(11..56,143..153)
                         /gene="IGH@"
                         /note="G00-118-731"
exon             <11..56
                         /gene="IGH@"
                         /product="Ig heavy chain"
                         /note="G00-118-731"
intron           57..142
                         /gene="IGH@"
                         /note="G00-118-731"
exon             143..528
                         /gene="IGH@"
                         /product="Ig heavy chain"
                         /note="G00-118-731"
BASE COUNT       108 a    131 c    170 g    119 t
ORIGIN

Query Match      83.0%;   Score 305.6;  DB 9;   Length 528;
Best Local Similarity   90.6%;   Pred. No. 1.2e-82;
Matches   339;   Conservative   0;   Mismatches  29;  Indels   6;  Gaps    1;

Qy     1  AGGTGCAGCTGGTGCAGTCTGGGGCTCAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT    60
          |||||||||||||||||||||||||| |||||||||||||||||||||||||| |||||||
Db   155  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT   214

Qy    61  CCTGCAAGGCTTCTGGAGGCACCTCAGTAGTTATATACTAGCTGGGTGCGACAGGCCC   120
          ||||||||||||||||||||||||| ||||||| ||| ||||| ||||||||||||||||
Db   215  CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTATCAGCTGGGTGCGACAGGCCC   274

Qy   121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG   180
          ||||||||||||||||||||||||||||||||| ||||||| |||||||  |||| |||
Db   275  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTATCTTGGTACAGCAAACTACG   334

Qy   181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   335  CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA   394

Qy   241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG------   294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   395  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGAACCCTGGGGA   454

Qy   295  ATCCCGATTATGTTTGGGGAGGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC   354
          |||                       ||||||||||||||||||||||||||||||||||
Db   455  TGGGATATTGTAGTGGTGGTAGCTGCTACTGGTTCGACCCCTGGGGCCAGGGAACCCTGG   514

Qy   355  TCATCGTCTCCTCA   368
          |||||||||||||
Db   515  TCACCGTCTCCTCA   528
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```
RESULT 10
AF062189
LOCUS        AF062189              387 bp      mRNA        linear     PRI 08-MAY-2001
DEFINITION   Homo sapiens clone 48u-22 immunoglobulin heavy chain variable
             region (IGH) mRNA, partial cds.
ACCESSION    AF062189
VERSION      AF062189.1   GI:3170840
KEYWORDS     .
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 387)
```

```
AUTHORS     Wang,X. and Stollar,B.D.
TITLE       Immunoglobulin VH gene expression in human aging
JOURNAL     Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE     99459182
PUBMED      10527689
REFERENCE   2  (bases 1 to 387)
AUTHORS     Wang,X. and Stollar,B.D.
TITLE       Direct Submission
JOURNAL     Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1..387
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.33"
                     /clone="48u-22"
                     /cell_type="peripheral B lymphocyte"
                     /tissue_type="blood"
                     /note="from elderly repertoire 48u"
     gene            <1..>387
                     /gene="IGH"
     CDS             <1..>387
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC18225.1"
                     /db_xref="GI:3170841"
                     /translation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQG
                     LEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARQADC
                     SGGSCYDIFPNWFDPWGQGTLVTVSSG"
     V_region        1..>387
                     /gene="IGH"
BASE COUNT     84 a    100 c    124 g     79 t
ORIGIN
Query Match          82.8%;   Score 304.6; DB 9;  Length 387;
Best Local Similarity 89.8%;   Pred. No. 2.4e-82;
Matches 344;   Conservative   0;  Mismatches  24;  Indels  15;  Gaps   1;

Qy     1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||
Db     2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy    61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||| || || ||| ||||||||||||||||||||||
Db    62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||| |||||||||||||||||||||||||||||||||||| |||| ||||||| ||||
Db   122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACACAGCCACAGCCTACA 241

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||||||||||| ||| || |||||| |||||||||
Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACAAGCCG 301

Qy   301 ATTATGTTTGGGGGAGGGAC------------AACTGGTTCGACCCCTGGGGCCAGG 345
                                ||||||||||||||
Db   302 ATTGTAGTGGTGTGCTACGATATTTTTCCGAACTGGTTCGACCCCTGGGGCCAGG 361

Qy   346 GAACCCTGGTCATCGTCTCCTCA 368
          ||||| ||||||||||||||||||
Db   362 GAACCCTGGTCACCGTCTCCTCA 384

RESULT 11
HSU84178   HSU84178
LOCUS      HSU84178    515 bp    DNA    linear    PRI 27-AUG-1997
DEFINITION Homo sapiens isolate LAN IgM heavy chain VH1 region precursor
```

```
ACCESSION   U84178
VERSION     U84178.1  GI:2344949
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
  PUBMED    8977195
REFERENCE   2  (bases 1 to 515)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
     source          1..515
                     /organism="Homo sapiens"
                     /isolate="patient LAN"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /note="CLL: chronic lymphocytic leukemia"
     gene            1..515
                     /gene="VH1-69"
                     join(1..46,133..>515)
     CDS             /gene="VH1-69"
                     /note="Allele: variants 1,5"
                     /codon_start=1
                     /product="IgM heavy chain VH1 region precursor"
                     /protein_id="AAC51705.1"
                     /db_xref="GI:2344950"
                     /translation="MDWTWRFLFVVAAATDVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                     GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
                     SSLRSEDTAVYYCASCGSGSYWPLCNWFDPWGQGTLVTVSS"
     sig_peptide     join(1..46,133..143)
                     /gene="VH1-69"
     mat_peptide     144..515
                     /gene="VH1-69"
                     /product="IgM heavy chain VH1 region"
                     /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
BASE COUNT    105 a    130 c    163 g    117 t
ORIGIN
Query Match          82.6%;   Score 303.8; DB 9;  Length 515;
Best Local Similarity 90.6%;   Pred. No. 4.4e-82;
Matches 336;   Conservative   0;  Mismatches  32;  Indels   3;  Gaps   1;

Qy     1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||
Db   145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy    61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||| || || ||| ||||||||||||||||||||||
Db   205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 264

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||| |||||||||||||||||||||||||||||||||||| |||| ||||||| ||||
Db   265 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 324

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 384

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGA---GAGATC 297
          |||||||||||||||||||||||||||||||||||||||||||||||||||   | |
Db   385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGTGCGAGTT 444
```

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Qy    298  CCGATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
           | |  | |||   |||         |||||||| |||||||||||||||||||||||||||
Db    445  CGGGGAGTTATTGGCCTTTGTGCAACTGGTTCCACCCCTGGGGCCAGGGAACCCTGGTCA 504

Qy    358  TCGTCTCCTCA 368
           |||||||||||
Db    505  CCGTCTCCTCA 515

RESULT 12
AB067158
LOCUS       AB067158              372 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
            partial cds, clone:ya0037h.
ACCESSION   AB067158
VERSION     AB067158.1  GI:21670372
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:ya0037h.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 372)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University,
            Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1..372
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="ya0037h"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..372
                     /gene="IGH"
     CDS             <1..>372
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain VHDJ region"
                     /protein_id="BAC02196.1"
                     /db_xref="GI:21670373"
                     /translation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRHAPGQG
                     LEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARCHTY
                     YDFWSGYYFDYWGQGTLVTVSS"
BASE COUNT    84 a    89 c    115 g    84 t
ORIGIN

Query Match       82.3%;  Score 303; DB 9; Length 372;
Best Local Similarity   91.0%;  Pred. No. 7.5e-82;
Matches 334;   Conservative  0;  Mismatches  30;   Indels  3;  Gaps  1;

Qy     1  AGGTGCAGCTGCTGTGCAGTCTGCAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||| || |||||||||||||||||||||||||||||||||||||||||| |||
Db     2  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy    61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCAGCTGGGTGCGACAGGCCC 120
          |||||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||
Db    62  CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACATGCCC 121

Qy   121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGGGAAGAAATTACG 180
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```
Db    122  CTGGACAAGGGCTTGAGTGGATGGGAGGGATCACCTATCCTATCCTTGGTATAGCACAACTACG 181
                  | || |||           |||||||||||||||||||||||||||
Qy    181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGCAAATCCACGAGCACAGCCTACA 240
           || || || |||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    182  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGCAAATCCACGAGCACAGCCTACA 241

Qy    241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA--GATC 297
           ||||||||||||||| |||||||||||||||||||||||||||||||| ||||     ||
Db    242  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGATGCCATA 301

Qy    298  CCGATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
           |  | |  |||   | |||       |||| |||||||||||||||||||||||||||||
Db    302  CGTATTACGATTTTGGAGTGGTTATTATTTTGACTACTGGGGCCAGGGAACCCTGGTCA 361

Qy    358  TCGTCTCC 364
           |||||||||
Db    362  CCGTCTCTC 368
```

```
RESULT 13
U00583
LOCUS       U00583                   363 bp    mRNA    linear   PRI 25-MAY-1994
DEFINITION  Human immunoglobulin heavy chain variable region (clone Tmu60)
            mRNA, partial cds.
ACCESSION   U00583
VERSION     U00583.1  GI:392755
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Huang,C. and Stollar,B.D.
  TITLE     A majority of Ig H chain cDNA of normal human adult blood
            lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
  JOURNAL   J.Immunol. 151 (10), 5290-5300 (1993)
   MEDLINE  94044753
   PUBMED   8228225
REFERENCE   2  (bases 1 to 363)
  AUTHORS   Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-1993) Stollar B.D., Tufts University,
            Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1..363
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Tmu60"
                     /sex="male"
                     /cell_type="B-lymphocyte"
                     /tissue_type="peripheral blood"
                     /clone_lib="Tmu"
                     /dev_stage="adult"
     CDS             <1..>363
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAA18279.1"
                     /db_xref="GI:392756"
                     /translation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQG
                     LEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGDIL
                     TGLNWFDPWGQGTLVTVSS"
BASE COUNT    80 a    94 c    114 g    75 t
ORIGIN

Query Match       82.3%;  Score 302.8; DB 9; Length 363;
Best Local Similarity   91.0%;  Pred. No. 8.6e-82;
Matches 335;   Conservative  0;  Mismatches  27;   Indels  6;  Gaps  1;

Qy     1  AGGTGCAGCTGCTGTGCAGTCTGCGGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db     2  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61
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Qy    1  CTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGTGCGACAGGCCC  120
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Db   62  CTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCGCTATCAGCTGGGTGCGACAGGCCC  121

Qy  121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCTTCAGCACTAGCAAATTACG  180
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Db  122  CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG  181

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA  240
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Qy  241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACAGGCCGTGTATTACTGTGCGAGAGATCCCG  300
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Db  242  TGGAGCTGAGCAGCCTGAGATCTGAGGACACAGGCCGTGTGTATTACTGTGCGAGA-----G  295

Qy  301  ATTATGTTTGGGGGAGCGAC-------GGTTCGCACCCTGGGGCCCAGGGAACCCTCATCG  360
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Db  296  GCGATATTTGACTGGCCTTAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG  355

Qy  361  TCTCCTCA  368
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Db  356  TCTCCTCA  363


RESULT 14
HSU84161
LOCUS       HSU84161                 518 bp      DNA      linear      PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate BRA IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84161
VERSION     U84161.1  GI:2344915
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
  PUBMED    8977195
REFERENCE   2  (bases 1 to 518)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="14"
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     gene            1..518
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Query Match            81.7%;   Score 300.8;  DB 9;  Length 518;
Best Local Similarity  89.8%;   Pred. No. 3.6e-81;
Matches  336;  Conservative  0;  Mismatches  32;  Indels  6;  Gaps  1;

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Db  145  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  204

Qy   61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCATCAGCTGGTGCGACAGGCCC  120
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Db  205  CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTATCGGGTGCGACAGGCCC  264

Qy  121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCATCCTATCCTTGGACTAGCAAATTACG  180
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Db  265  CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG  324

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
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Db  325  CACAGAAGTTCCAGGGCAGCAGTCACGATTACCGCGGACACACGGCCGTGTGTATTACTGTGCGAGAGATGGTT  444

Qy  241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  385  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTGTATTACTGTGCGAGAGATGGTT  444

Qy  301  ATTATGTTTGGGGGAGCGAC------AACTGGTTCGACCCCTGGGGCCCAGGGAACCCTGC  354
         ||||||||||||||||||||      ||||||||||||||||||||||||||||
Db  445  GTAGTGGTGTAGCTGCTACTTTTGGGGCGTCGGTTTCGACCCCTGGGGCCAGGGAACCCTGG  504

Qy  355  TCATCGTCTCCTCA  368
         || |||||||||||
Db  505  TCACCGTCTCCTCA  518


RESULT 15
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LOCUS       HSU84164                 518 bp      DNA      linear      PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate CRA IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84164
VERSION     U84164.1  GI:2344921
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
  PUBMED    8977195
REFERENCE   2  (bases 1 to 518)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
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                     /isolate="patient CRA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
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                     /note="CLL: chronic lymphocytic leukemia"
     gene            1..518
                     /gene="VH1-69"
     CDS             join(1..46,133. .>518)
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     sig_peptide   join(1..46,133..143)
                    /gene="VH1-69"
     mat_peptide   144..518
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                    /product="IgM heavy chain VH1 region"
                    /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"

BASE COUNT      107 a    127 c    165 g    119 t
ORIGIN

Query Match       81.7%;   Score 300.8;   DB 9;   Length 518;
Best Local Similarity   89.8%;   Pred. No. 3.6e-81;
Matches 336;   Conservative   0;   Mismatches   32;   Indels   6;   Gaps   1;

Qy    1  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||||
Db  145  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGTGAAGGTCT  204

Qy   61  CCTCCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
         |||||||||||||||||||||||||||| ||| || |||||| |||||||||||||||||
Db  205  CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAACTGGGTGCGACAGGCCC  264

Qy  121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
         ||||||||||||||||||||||||||| || |||| || ||| ||||  ||| ||||||
Db  265  CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG  324

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCCACAGCCTACA  240
         |||||||||||||||||||||||||||||||||||||||  ||||||  |||||||||||
Db  325  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAACACAGCCTACA  384

Qy  241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  385  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATGGTT  444

Qy  301  ATTATGTTTGGGGGAGCGAC------AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC  354
         ||||| | |  ||| ||| |      ||| |||||||||||||||||| ||| ||||| |
Db  445  GTAGTGGTGGTAGCTGCTACTTTGGGGCTGGTTCGACCCCTGGGGCCAGGGAACCCTGG  504

Qy  355  TCATCGTCTCCTCA  368
         ||||||||||||||
Db  505  TCACCGTCTCCTCA  518

Search completed: July 18, 2003, 13:47:37
Job time : 1032.02 secs
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      July 18, 2003, 04:16:54 ; Search time 637.709 Seconds
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Title:         US-09-627-896B-29
Perfect score: 368
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Scoring table: IDENTITY.NUC
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Searched:      16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:        32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match  0%
                 Maximum Match  100%
                 Listing first 45 summaries

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         13:   gb_est4:*
         14:   gb_est5:*
         15:   em_estfun:*
         16:   em_estom:*
         17:   gb_gss:*
         18:   em_gss_hum:*
         19:   em_gss_inv:*
         20:   em_gss_pln:*
         21:   em_gss_vrt:*
         22:   em_gss_fun:*
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         26:   em_gss_rod:*
         27:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	Length	ID	Description
1	297.4	80.8	477	12	BF975791	BF975791 602246355
2	297.4	80.8	909	12	BG397239	BG397239 602439015
3	297.4	80.8	1012	12	BF974633	BF974633 602243363
4	287.8	78.2	959	14	BQ706226	BQ706226 AGENCOURT
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 11    279     75.8   970   14   BQ706539  BQ706539  AGENCOURT
 12   278.8   75.8   417   10   AW408371  AW408371  UI-HF-BK0
 13   277.2   75.3   884   14   BQ708380  BQ708380  AGENCOURT
 14   277.2   75.3   937   12   BQ711877  BQ711877  AGENCOURT
 15   276.6   75.2   418   10   AW401468  AW401468  UI-HF-BK0
 16   276.6   75.2   920   14   BQ708488  BQ708488  AGENCOURT
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 18   275.2   74.8   937   12   BG685980  BG685980  60263854
 19    275     74.7   896   14   BQ711903  BQ711903  AGENCOURT
 20   273.6   74.3   516   10   AW402422  AW402422  UI-HF-BK0
 21   273.2   74.2   485   10   AW403940  AW403940  UI-HF-BK0
 22   272.2   74.0   477   10   AW408484  AW408484  UI-HF-BK0
 23   271.6   73.8   863   14   BQ708543  BQ708543  AGENCOURT
 24   271.6   73.8   939   14   BQ708868  BQ708868  AGENCOURT
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 28   270.8   73.6   934   14   BQ710011  BQ710011  AGENCOURT
 29   270.8   73.6   948   14   BQ707622  BQ707622  AGENCOURT
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 36   270.2   73.5   885   14   BQ710560  BQ710560  AGENCOURT
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 41   269.2   73.2   930   14   BQ709430  BQ709430  AGENCOURT
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ALIGNMENTS

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            mRNA sequence.
ACCESSION   BF975791
VERSION     BF975791.1  GI:12342993
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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            High quality sequence stop: 473.
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                    Site_2: EcoRI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                    for average insert size 1.8kb. Library constructed by Ling
                    Hong in the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies).
                    Note: this is a NIH_MGC Library."
BASE COUNT     102 a     127 c     150 g      98 t
ORIGIN

Query Match     80.8%;     Score 297.4;  DB 12;  Length 477;
Best Local Similarity  89.5%;   Pred. No. 1.1e-73;
Matches  332;   Conservative   0;   Mismatches  36;   Indels   3;   Gaps   1;

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Db    85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy    61 CCTGCAAGGCTTCTGAGGCCACCTTCAGTAGTATACTATCAGCTGGGTGCGACAGGCCC  120
           |||||||||||||||||||||||||||||||||  ||| ||||||||||||||||||||
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Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCTTGGACTAGCAAATTACG  180
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Qy   181 CACGAGAAGTTCCAGGGCAGAGTCACGATTACCCGGACAAATCCACGAGACCAGCCTACA 240
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Qy   241 TGGAGCTGAGCAGCCGTGATCTGAGGACACGGCACCGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Qy   301 ATTATGTTGGGGAGGGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA 357
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Qy   358 TCGTCTCCTCA 368
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RESULT 2
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DEFINITION     602439015F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565546 5',
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ACCESSION      BG397239
VERSION        BG397239.1  GI:13290687
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 909)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
               cDNA Library Preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
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               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
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                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT     195 a     261 c     271 g     180 t      2 others
ORIGIN

Query Match     80.8%;     Score 297.4;  DB 12;  Length 909;
Best Local Similarity  89.5%;   Pred. No. 1.8e-73;
Matches  332;   Conservative   0;   Mismatches  36;   Indels   3;   Gaps   1;

Qy     1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
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Db    85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy    61 CCTGCAAGGCTTCTGGAGGCCACCTTCAGTAGTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db   145 CCTGCAAGGCTTCTGGAGGCCACCTTCAGCAGCTATCAGCTGGGTGCGACAGGCCC 204

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db   205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGCAGAATCAGCCTACA 240
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Db   265 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGGCAGCACGACAGCCTACA 324

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db   325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384

Qy   301 ATTATGTTGGGGAGGGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCTCA 357
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Db   385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCA 444

Qy   358 TCGTCTCCTCA 368
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Db   445 CCGTCTCCTCA 455


RESULT 3
BF974633
LOCUS          BF974633          1012 bp   mRNA      linear   EST 22-JAN-2001
DEFINITION     602243363F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4334774 5',
               mRNA sequence.
ACCESSION      BF974633
VERSION        BF974633.1  GI:12341848
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 1012)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
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JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1204 row: m column: 15
           High quality sequence stop: 716.
FEATURES            Location/Qualifiers
     source         1..1012
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                    /db_xref="taxon:9606"
                    /clone="IMAGE:4434774"
                    /clone_lib="NIH_MGC_48"
                    /tissue type="primary B-cells from tonsils (cell line)"
                    /lab_host="DH10B (phage-resistant)"
                    /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                    Site_2: EcoRI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                    for average insert size 1.8kb. Library constructed by Ling
                    Hong in the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies).
                    Note: this is a NIH_MGC Library."
BASE COUNT     236 a    299 c    300 g    176 t    1 others
ORIGIN

Query Match      80.8%;   Score 297.4;  DB 12;  Length 1012;
Best Local Similarity  89.5%;   Pred. No. 1.9e-73;
Matches  332;  Conservative   0;  Mismatches   36;  Indels   3;  Gaps  1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
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Db     85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCATCAGCTGGGTGCGACAGGCC 120
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Db    145 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTGGGTGCGACAGGCC 204

Qy    121 CTGGACACAAGGGCTTGAGTGGATGGAAGGAGATCATGCCTATCCTTGACAAATTACG 180
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Db    205 CTGGACACAAGGGCTTGAGTGGATGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||||||||||||||||||| | ||||||| |||||||||
Db    265 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAACCGCACGAGCACAGCCTACA 324

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db    325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384

Qy    301 ATTATGTTTGGGGAGGGAC---AACTGTTCGACCCCTGGGGGCCAGGGAACCCTGCTCA 357
          ||||| || | ||| ||||     |||||||| | |||||||||||||||||||||||||
Db    385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCA 444

Qy    358 TCGTCTCCTCA 368
          |||||||||||
Db    445 CCGTCTCCTCA 455

RESULT 4
BQ706226
LOCUS      BQ706226          959 bp    mRNA          linear   EST 16-JUL-2002
DEFINITION AGENCOURT 8474971 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301349
           5', mRNA sequence.
ACCESSION  BQ706226
VERSION    BQ706226.1  GI:21845125
KEYWORDS   EST.
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SOURCE     human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 959)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Mark Watson
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2517 row: b column: 06
           High quality sequence stop: 647.
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:9606"
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                    /lab_host="DH10B (phage-resistant)"
                    /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
BASE COUNT     205 a    298 c    281 g    170 t    5 others
ORIGIN

Query Match      78.2%;   Score 287.8;  DB 14;  Length 959;
Best Local Similarity  87.9%;   Pred. No. 9.5e-71;
Matches  326;  Conservative   0;  Mismatches   42;  Indels   3;  Gaps  1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
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Db    107 AGGTGCCACCTGGTGCAGTCTGGGGCTGAGGTGAGTGAAGAAGCCTGGGTCCTCAGTGAAGGTCT 166

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db    167 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCCATGGTATCAGCTGGGTGCGACAGGCCC 226

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db    227 CTGGACAAGGGCTTGAGTGGATGGGATGGGATCATCCCTATCTTTGCTACAGCAAAGTACG 286

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 240
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Db    287 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACGAATCCACGAGCACAGCCTACA 346

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db    347 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTATTGTGCGAGAGTGCCCC 406

Qy    301 ATTATGTTTGG---GGGAGGGACACAACTGGTTCGACCCCTGGCGGGCCAGGGAGATCCCG 357
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Db    407 GTATGGGTCGGGGAGGTATCGGGCGTCGTTGACCCCTGGTCGTTCGACCCCCGGGAGTGCCCC 466

Qy    358 TCGTCTCCTCA 368
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RESULT 5
BG754936
LOCUS      BG754936          903 bp    mRNA          linear   EST 15-MAY-2001
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DEFINITION   602711631F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852039 5',
             mRNA sequence.
ACCESSION    BG754936
VERSION      BG754936.1  GI:14065589
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 903)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1695 row: n column: 08
             High quality sequence stop: 813.
FEATURES             Location/Qualifiers
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                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC_Library."
BASE COUNT     200 a    260 c    270 g    172 t   1 others
ORIGIN
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Query Match                   Score 286.4;  DB 12;  Length 903;
Best Local Similarity  77.8%;      Pred. No. 2.3e-70;
Matches 332;  Conservative  0;  Mismatches 36;  Indels 4;  Gaps 2;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db   85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 144

Qy   61 CCTGCAAGGCTTCTGGGGCCACCTTCAGTAGTTATACTATCAGCTGGACTAGCAAATTAC 119
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Db  145 CCTGCAAGGCTTCTGGGGCCACCTTCAGCAGCTATCAGCTGGACTAGCAACTAC 204

Qy  120 CCTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTAC 179
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Db  205 CCTGGACAAGGGCTTGAGTGGATGGGAGGGGATCATCCCTATCTTTGGTACAGCAAACTAC 264

Qy  180 GCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTAC 239
          ||||||||||||||||||||||||||||||||||  ||||| ||||||||||||||||
Db  265 GCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTAC 324

Qy  240 ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCC 299
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Db  325 ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGA 384

Qy  300 GATTATGTTTGGGGAGCGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTC 356
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Db  385 TRATTGTAGTAGTACCAGCTGCCTGTACTTTGACTACTTTGACTACTTTGGGGGCCAGGGAACCCTGGTC 444

Qy  357 ACCGTCTCCTCA 368
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RESULT 6
LOCUS        BG758459
DEFINITION   602712658F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852934 5',
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ACCESSION    BG758459
VERSION      BG758459.1  GI:14069112
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 878)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1698 row: c column: 15
             High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1..878
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC_Library."  1 others
BASE COUNT   196 a    258 c    246 g    177 t   1 others
ORIGIN
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Query Match                   Score 285.4;  DB 12;  Length 878;
Best Local Similarity  77.6%;      Pred. No. 4.3e-70;
Matches 331;  Conservative  0;  Mismatches 36;  Indels 4;  Gaps 2;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db   85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCAGCTGGACTGGGTCGACAGGCCC 120
          ||||||||||||    |||||||||    ||| ||||||||||||||  |||  ||||
Db  145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGACTGGGTGCGACAGGCCC 204

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCTATCCTTGGACTAGCAAATTACG 180
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Db  205 CTGGACAAGGGCTTGAGTGGATGGGAGGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db  265 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACACGAGCACAGCCTACA 324

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db 325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384
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Qy 301 ATTATGTTTGGGGGAGGGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
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Db 385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCA-GGAACCCTGGTCA 443

Qy 358 TCGTCTCCTCA 368
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Db 444 CCGTCTCCTCA 454

RESULT 7
BQ706171
LOCUS   BQ706171   903 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8354485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281064
            5', mRNA sequence.
ACCESSION   BQ706171
VERSION   BQ706171.1 GI:21845070
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 903)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2473 row: e column: 01
            High quality sequence stop: 576.
FEATURES   Location/Qualifiers
     source   1..903
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   202 a   272 c   246 g   181 t   2 others
ORIGIN

Query Match   77.4%; Score 284.8; DB 14; Length 903;
Best Local Similarity   87.8%; Pred. No. 6.5e-70;
Matches 323; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
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Db 102 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 161
Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db 162 CCTGCAAGGCTTCTGGAGGCACCTTCAGTGGCTATGCTATCAGCTGGGTGCGACAGGCCC 221
Qy 121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db 222 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGTTACGGCAAAACTACG 281
Qy 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCCGGACAAATCCACGAGCACAGCCTACA 240
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Db 282 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCCGGACGATTACCCGGACGACGAATCCACGAGCACAGCAGCCTACA 341

Qy 301 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Qy 342 TGGAGCTGAACAGCCTGAGATCTGAGGACACGACCGTGTATTACTGTGCGAGAGTGGGGA 401
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Qy 301 ATTATGTTTGGGGGAGGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
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Qy 361 TCTCCTCA 368
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Db 459 TCTCCTCA 466

RESULT 8
BQ881378
LOCUS   BQ881378   1035 bp   mRNA   linear   EST 16-AUG-2002
DEFINITION AGENCOURT_8642770 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295574
            5', mRNA sequence.
ACCESSION   BQ881378
VERSION   BQ881378.1 GI:22273386
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
REFERENCE   1 (bases 1 to 1035)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2502 row: a column: 15
            High quality sequence start: 71
            High quality sequence stop: 599.
FEATURES   Location/Qualifiers
     source   1..1035
                     /organism="Homo sapiens"
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                     /clone="IMAGE:6295574"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   219 a   340 c   276 g   196 t   4 others
ORIGIN

Query Match   76.9%; Score 283; DB 14; Length 1035;
Best Local Similarity   87.1%; Pred. No. 2.3e-69;
Matches 323; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164 AGGTCCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTCT 223
Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
         ||||||||||||||||| ||||||||||||
Db 224 CCTGCAAGGCTTCTGGAGGCACCTTCAGCGGGTATCAGCAGCCATGGTATCAGCGTGGGTGCGACAGGCCC 283

Column 1 (RESULT 11)

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Query Match             76.5%;    Score 281.6;   DB 14;   Length 991;
Best Local Similarity   86.6%;    Pred. No. 5.5e-69;
Matches   324;  Conservative  0;  Mismatches 44;  Indels 6;  Gaps 1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAGGAAGCCTGGGTCCTCCGTAAAGGTCT 60
          |||||||||||||||||||||| ||||  |||| |||||||||||||||| ||||||||||
Db   94 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAGGAAGCCTGGGTCCTCGGTGAAGGTCT 153

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCATCAGTCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||||| |  ||  |||  |||||||||||||||||||
Db  154 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATGCTATCAGCTCTGGGTGCGACAGGCCC 213

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||||||  ||| |||| ||| |  |||||  |||||
Db  214 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTACAGCAAACTACG 273

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||||||||||||||||| | |||||||||||||||||||||
Db  274 CACAGAAGTTCCAGGGCAGAGTCACGATTATCCGGGACGAATCCACGAGCACAGCCTACA 333

Qy  241 TGGAGCTGACGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||||||||||||||||||||||||||||| |   |||  |||
Db  334 TGGAGCTGACGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACATTACT 393

Qy  301 ATTAT------GTTTGGGGGAGCGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
          |||||      ||| ||||||||| ||| |  |||||| |||| |||||| ||||| ||||
Db  394 ATGGTTGGGGGAGTTATAGAGAATATTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGG 453

Qy  355 TCATCGTCTCCTCA 368
          |||| |||||||||
Db  454 TCACTGTCTCCTCA 467
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RESULT 11
BQ706539
LOCUS        BQ706539    970 bp    mRNA    linear    EST 16-JUL-2002
DEFINITION   AGENCOURT_8487914 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300622
             5', mRNA sequence.
ACCESSION    BQ706539
VERSION      BQ706539.1   GI:21845438
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 970)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2515  row: c  column: 23
             High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1..970
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6300622"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
```

Column 2 (RESULT 12)

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                     Supercript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

Query Match             75.8%;    Score 279;   DB 14;   Length 970;
Best Local Similarity   86.9%;    Pred. No. 3e-68;
Matches   319;  Conservative  0;  Mismatches 45;  Indels 3;  Gaps 1;

BASE COUNT      204 a      312 c      273 g      178 t
ORIGIN

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAGGAAGCCTGGGTCCTCCGTAAAGGTCT 60
          |||| |||||||||||||||||| ||||  ||||||||||||||||||||| |||||||
Db   91 AGGTCCAGCTGGTGCAGTCTGGGGACTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 150

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCATCAGTCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||| |  ||  ||  ||||||||||||||||||||||
Db  151 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTATCATCAGTCTGGGTGCGACAGGCCC 210

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||||||| |||||||| ||||| ||||  ||||||
Db  211 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTACGTACAGCAAATTACG 270

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 240
          |||||||  |||| |||||||||||||||||||||||  ||||||||||||||||||||
Db  271 CACAGAAATTCCTGGGCAGAGTCACGATTACCGGGACGAATCCACGAGCACAGCCTACA 330

Qy  241 TGGAGCTGACGACCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  331 TGGAGCTGACGACCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 390

Qy  301 ATTATGTTTGGGGGAGCGGACAACTGGTTCGCTCTGGGGCCCAGGGAACCCTGCTCATCG 360
          |||||||| ||||||  ||||| |  |  |||||  ||||||| ||||||||  |  |||
Db  391 ---AAGTGGGGTTCTCTCGGCCGCCGTTGACTACTGGGGCCAGGGAACCCTGATCATCATTG 447

Qy  361 TCTCCTC 367
          |||||||
Db  448 TCTCCTC 454
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RESULT 12
AW408371
LOCUS        AW408371    417 bp    mRNA    linear    EST 16-FEB-2000
DEFINITION   UI-HF-BK0-abk-c-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
             IMAGE:3056620 5', mRNA sequence.
ACCESSION    AW408371
VERSION      AW408371.1   GI:6927428
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 417)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..417
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3056620"
                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
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/cell_line="MGC85"
/lab_host=DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT   91 a   106 c   130 g   90 t
ORIGIN

Query Match   75.8%; Score 278.8; DB 10; Length 417;
Best Local Similarity   88.5%; Pred. No. 2.2e-68;
Matches 317; Conservative   0; Mismatches 32; Indels   9; Gaps   1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   60 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 119

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db 120 CCTGCAAGGCTTCTGGAGGCACCTTCACCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 179

Qy 121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||
Db 180 CTGGACAAGGGCTTGAGTGGATGGGATCATTCCTATCCTTTGGTACAGCAAAACTACG 239

Qy 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 CACAGAAGTTCCAGGGCAGAGTCACCATTACCGCGGACGAATCCACGAGCACAGCCTACA 299

Qy 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db 300 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGAAC 359

Qy 301 ATTATG-------TTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAAC 349
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Db 360 TTTTAGATATTTTGACTCGTTACAAACCTCAACTGGTTCGACCCCTGGGGCCAGGGAAC 417

RESULT 13
BQ708380
LOCUS   BQ708380   884 bp   mRNA   linear EST 16-JUL-2002
DEFINITION   AGENCOURT_7983360 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215351
              5', mRNA sequence.
ACCESSION   BQ708380
VERSION   BQ708380.1   GI:21847279
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 884)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Dr. Mark Watson
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2384 row: b column: 24
              High quality sequence stop: 631.
FEATURES   Location/Qualifiers
     source   1..884
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215351"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT   185 a   291 c   246 g   162 t
ORIGIN

Query Match   75.3%; Score 277.2; DB 14; Length 884;
Best Local Similarity   86.7%; Pred. No. 9.1e-68;
Matches 319; Conservative   0; Mismatches 43; Indels   6; Gaps   1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   85 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCCAGTGACGGTCT 144

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACAATGCTATCAGTTGGGTGCGACAGGCCC 204

Qy 121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db 205 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATCCCCATCTTTGGTTCAGCAAACTACG 264

Qy 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 265 CTCAGAGGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 324

Qy 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db 325 TGGAGTTGAGCGGCGGCTGACATCTGAGGACACGGCCGTGTATTACTGTGCGGCA 378

Qy 301 ATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 379 GTGGAAGCCCGGAACAGCACAACCAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 438

Qy 361 TCTCCTCA 368
          ||||||||
Db 439 TCTCCTCA 446

RESULT 14
BQ711877
LOCUS   BQ711877   937 bp   mRNA   linear EST 16-JUL-2002
DEFINITION   AGENCOURT_7975529 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215114
              5', mRNA sequence.
ACCESSION   BQ711877
VERSION   BQ711877.1   GI:21850776
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 937)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Dr. Mark Watson
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2383 row: i column: 03
              High quality sequence stop: 516.
FEATURES   Location/Qualifiers
     source   1..937

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              /organism="Homo sapiens"
              /db_xref="taxon.9606"
              /clone="IMAGE:6215114"
              /clone_lib="NIH MGC 113"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dT priming. Directionally cloned
              into EcoRI/XhoI sites using the following 5' adaptor:
              GGCACGAG(G). Library constructed by Ling Hong in the
              laboratory of Gerald M. Rubin (University of California,
              Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
              Superscript II RT (Life Technologies). Note: this is a
              NIH MGC Library."
BASE COUNT    222 a   279 c   266 g   170 t
ORIGIN

Query Match    75.3%;   Score 277.2;  DB 14;  Length 937;
Best Local Similarity  86.7%;  Pred. No. 9.4e-68;
Matches 319;  Conservative  0;  Mismatches 43;  Indels 6;  Gaps  1;

Qy    1 AGGTGCAGCTGGTGAGTCTGGGGCTGAGGTGAGGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||| ||||||||| ||||||||||||||||||||||||||||||||||| |||| ||||
Db   85 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAGGAAGAAGCCTGGGTCCTCAGTGACGGTCT 144

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||||||| || |||| | |||||||||||||||||
Db  145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCACAATGCTATCAGTTGGGTGCGACAGGCCC 204

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGTGGACTAGCAGTAGGACTAGCAGTAGG... 180
Db  205 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGTGGACTAGCAGTAGGACTAGCAGTAGG... 264

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
Db  265 CTCAGAGGTTCCAGGGCAGAGTCACGATTACCGCGGCAGAATCCACGAGCACAGCCTACA 324

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACAGGCCGTGTATTACTGTGCGGAGAGATCCCG 300
Db  325 TGGAGTTGAGCGGCCTGACATCTGAGGACACGGCCGTGTATTACTGTGCGCGA-----C 378

Qy  301 ATTATGTTTGGGGAGGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCATCG 360
Db  379 GTGGAAGCCCGGAACAGCACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 438

Qy  361 TCTCCTCA 368
          ||||||||
Db  439 TCTCCTCA 446
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RESULT 15
AW401468

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LOCUS       AW401468                 418 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aad-f-06-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3053339 5', mRNA sequence.
ACCESSION   AW401468
VERSION     AW401468.1  GI:6920051
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 418)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source          1..418
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT     95 a   117 c   122 g   84 t
ORIGIN

Query Match    75.2%;   Score 276.6;  DB 10;  Length 418;
Best Local Similarity  86.0%;  Pred. No. 9.3e-68;
Matches 319;  Conservative  0;  Mismatches 49;  Indels 3;  Gaps  1;

Qy    1 AGGTGCAGCTGGTGAGTCTGGGGCTGAGGTGAGGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||| ||||||||| ||||||||||||||||||||||||||||||||||| ||||
Db   15 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAGGAAGAAGCCTGGGATCCTCGGTGAAGGTCT 74

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACATCAGCTGGGTGGTGGCACAGGCCC 120
Db   75 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATGCTGGGTGGTGGCACAGGCCC 134

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
Db  135 CTGGACAAGGGCTTGAGTGGATGGGATCATCCCTATCTTTGATATAACAAACTACG 194

Qy  181 CACAGAAGTTCCAGGGCAGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
Db  -195 CACAGAAGTTCCAGGGCAGCAGAGTCACGATTACCGCGGACAAATCGACGAGCACAGCCTACA 254

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACAGGCCGTGTATTACTGTGCGGAGATCCCG 300
Db  255 TGGAGCTGAGCAGCCTGAGATCTGAGGACACACGGCCGTGTATTACTGTGCGGAGACTTCGTT 314

Qy  301 ATTATGTTTGGG---GGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
Db  315 ACAGTAACCGCGACTACTTCTACATGGACGTCTGGGCAAAGGGGACCACCGTCA 374

Qy  358 TCGTCTCCTCA 368
Db  375 CCGTCTCCTCA 385
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Job time : 639.709 secs

OM nucleic - nucleic search, using sw model

Copyright   GenCore version 5.1.6
(c) 1993 - 2003   Compugen Ltd.

Run on: July 18, 2003, 04:14:58 ; Search time 95.4001 Seconds
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Title: US-09-627-896B-29
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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 6: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1985.DAT:*
 7: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1986.DAT:*
 8: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1987.DAT:*
 9: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-embl/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB Length	ID	Description
1	293.2	79.7	2287	13	AAQ25443	Sequence encoding
2	293.2	79.7	2287	18	AAT60739	IgG1 gene. Homo s
3	289.6	78.7	378	22	AAF29080	Human HIV-1 monocl
4	286.4	77.8	747	21	AAC67868	Recombinant human
5	284.8	77.4	354	21	AAA48411	Human LH13 monoclo
6	282.8	76.8	1517	22	AAF29714	G71-1 immunoconjug
7	280.8	76.3	812	13	AAQ22419	Human heavy chain
8	280.8	76.3	812	14	AAQ44185	Human heavy chain
9	280.8	76.3	812	17	AAT37243	DNA fragment vH49.
10	280.8	76.3	812	18	AAV12538	Human VHI family g
11	280.8	76.3	812	18	AAT70522	Human immunoglobul
12	280.8	76.3	812	18	AAT73471	Human VH1 gene VH4
13	280.8	76.3	812	20	AAZ21897	Nucleotide sequenc
14	280.8	75.7	812	20	AAX06042	Sequence of human
15	278.6	75.7	495	16	AAQ89328	HV1263 VH gene. H
16	277.6	75.4	375	21	AAC98082	Human colon cancer
17	275.8	74.9	375	22	AAS03455	DNA encoding anti-
18	275.2	74.8	488	21	AAZ42325	Human 5' EST isola
19	274.8	74.7	354	15	AAX79685	Human cancer cell
20	274	74.5	1599	24	ABK64550	Human benign prost
21	274	74.5	1599	24	ABL62673	Colon adenocarcino
22	274	74.5	1599	24	ABL65479	Lung cancer relate
23	274	74.5	1599	24	ABL66294	Lung cancer relate
24	273.8	74.4	294	16	AAQ89327	DP10 VH gene. Hom
25	273.4	74.3	360	22	AAS03466	DNA encoding anti-
26	273.2	74.2	295	21	AAS03456	DNA encoding anti-
27	273.2	74.2	357	22	AAT72131	CEA-specific antib
28	272.8	74.1	369	18	AAQ35099	Antibody D heavy c
29	272.4	74.1	1617	24	ABA05279	Human Ig-M heavy c
30	272.2	74.0	1884	22	AAS22828	Human cDNA encodin
31	272	73.9	3229	22	AAS22829	Human cDNA encodin
32	272	73.9	363	22	AAS03498	Human cDNA encodin
33	269.2	73.2	363	22	AAS22828	Human cDNA encodin
34	268.8	73.0	3229	22	AAS22829	Human cDNA encodin
35	268.8	73.0	3229	21	AAC00054	Human secreted pro
36	266.6	72.4	492	21	AAX05452	Human secreted pro
37	266.4	72.4	786	20	AAS03473	CEA6 antibody sing
38	266	72.3	363	22	AAH26788	DNA encoding anti-
39	265.4	72.1	354	24	AAK98400	Anti-human CD154 a
40	265.4	72.1	396	24	AAK98405	Humanised murine a
41	264.6	71.9	782	20	AAV72234	Anti-FAPalpha anti
42	264.2	71.8	366	22	AAS03450	Anti-GPIIb/I
43	263.4	71.6	378	21	AAZ43867	DNA encoding anti-
44	260	70.7	342	21	AAC00055	Human FVIII antibo
45			425	21		Human secreted pro

ALIGNMENTS

RESULT 1
AAQ25443
```
ID   AAQ25443 standard; DNA; 2287 BP.
XX
AC   AAQ25443;
XX
DT   02-JAN-1992 (first entry)
XX
DE   Sequence encoding antibody molecule IgG1.
XX
KW   Antibody; immunoglobulin G1; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..453
FT                   /*tag= a
FT   exon            619..972
FT                   /*tag= b
FT   exon            1361..1405
FT                   /*tag= c
FT   exon            1524..1853
FT                   /*tag= d
FT   exon            1950..2273
FT                   /*tag= e
XX
PN   WO9209293-A.
XX
PD   11-JUN-1992.
XX
PF   18-NOV-1991;  91WO-US08605.
XX
```

Left column (RESULT 2)

```
PR   23-NOV-1990;  .90US-0618314.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B, Walz G;
XX
DR   WPI; 1992-216789/26.
DR   P-PSDB; AAR24442.
XX
PT   Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PT   - used in treating chronic inflammation, rheumatoid arthritis,
PT   psoriasis, etc.
XX
PS   Disclosure; Fig 1; 46pp; English.
XX
CC   The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC   inventors designed a molecule including several such sites for
CC   attachment of sialyl-Lex side chains (see AAR24442, FT). The
CC   additional N-linked glycosylation sites are introduced at locations
CC   which impair complement fixing and Fc receptor binding ability. They
CC   are preferably located in the CH2 region of the Ig molecule.
CC   Antibodies bearing multiple sialyl-Lex determinants are useful for
CC   disrupting undesirable interactions between cells or proteins.
CC   Disrupting this interaction has therapeutic applications, for
CC   example, in minimising inflammation following tissue injury.
XX
SQ   Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;

Query Match          79.7%;   Score 293.2;   DB 13;   Length 2287;
Best Local Similarity 88.2%;   Pred. No. 5.6e-75;
Matches 335;   Conservative  0;   Mismatches 33;   Indels 12;   Gaps 1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||| |||||||||||||||||||||||||| ||||||||||
Db   74 AGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||||| |||| ||||||||||||||| |||||||||
Db  134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTCATGCTATCCTATCAGGCCC 193

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||| |||||| |||||| ||| |||| ||||| |||||
Db  194 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy  301 ---------ATTATGTTTGGGGGAGCCAGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                   |||||||||||||||||||||  ||| |||||||||||||||||||||||
Db  374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGCTACTCGGGCCAGGGAA 433

Qy  349 CCCTGCTCATCGTCTCCTCA 368
          |||||  |||||||||  ||
Db  434 CCCTGGTCACCGTCTCTTCA 453
```

```
RESULT 2
AAT60739
ID   AAT60739 standard; DNA; 2287 BP.
XX
AC   AAT60739;
XX
DT   22-APR-1997 (first entry)
XX
DE   IgG1 gene.
XX
KW   IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin;
KW   sialyl-Lewis X; antiinflammatory; inflammation;
```

Right column

```
KW   extravasation-dependent adverse reaction; organ damage; clotting;
KW   adult respiratory distress syndrome; glomerular nephritis;
KW   ischaemic myocardial injury; immune reaction; septic shock;
KW   septicaemia; therapy; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9700079-A1.
XX
PD   03-JAN-1997.
XX
PF   11-JUN-1996;   96WO-US10043.
XX
PR   14-JUN-1995;   95US-0000213.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Pouyani T, Seed B;
XX
DR   WPI; 1997-077356/07.
DR   P-PSDB; AAW10550.
XX
PT   P-selectin and opt. E-selectin binding organic mol. - having
PT   sialyl-Le(x) and sulphated determinant, useful for protecting
PT   against inflammatory or immune reactions
XX
PS   Disclosure; Page 40-41; 81pp; English.
XX
CC   The gene (AAT60739) encoding IgG1 (AAW10550) can be subjected to site-
CC   directed mutagenesis in order to introduce one or more N-linked
CC   glycan addition sites into the IgG1 molecule (see also AAW10551).
CC   Eukaryotic host cells co-transfected with a vector carrying the
CC   the mutated IgG1 gene and with a vector that expresses an alpha-
CC   (1,3)fucosyltransferase capable of attaching sialyl-Le(x) groups at
CC   the glycosylation sites of the antibody molecule can be used in the
CC   prodn. of sialyl-Le(x)-modified antibody. Such an antibody has
CC   therapeutic applns., e.g. in minimising inflammation and
CC   decreasing extravasation-dependent organ damage and/or clotting.
XX
SQ   Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;

Query Match          79.7%;   Score 293.2;   DB 18;   Length 2287;
Best Local Similarity 88.2%;   Pred. No. 5.6e-75;
Matches 335;   Conservative  0;   Mismatches 33;   Indels 12;   Gaps 1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||| |||||||||||||||||||||||||| ||||||||||
Db   74 AGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||||| |||| |||||||||||||||||||||||||
Db  134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTCATGCTATCCTATCAGGCCC 193

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||| |||||| |||||| ||| |||| ||||| |||||
Db  194 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy  301 ---------ATTATGTTTGGGGGAGCCAGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                   |||||||||||||||||||||  ||| |||||||||||||||||||||||
Db  374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGCTACTCGGGCCAGGGAA 433

Qy  349 CCCTGCTCATCGTCTCCTCA 368
          |||||  |||||||||  ||
Db  434 CCCTGGTCACCGTCTCTTCA 453
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Qy    355 TCATCGTCTCCTCA 368
          ||||| |||||||
Db    365 TCACCGTCTCCTCA 378
```

RESULT 3
AAF29080
ID   AAF29080 standard; DNA; 378 BP.
XX
AC   AAF29080;
XX
DT   03-APR-2001 (first entry)
XX
DE   Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 36.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200100678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US17327.
XX
PR   30-JUN-1999; 99US-0141701.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA, Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   P-PSDB; AAB62779.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal -
XX
PS   Claim 4; Page 47; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ   Sequence 378 BP; 81 A; 93 C; 122 G; 82 T; 0 other;

Query Match   78.7%; Score 289.6; DB 22; Length 378;
Best Local Similarity 88.0%; Pred. No. 3.9e-74;
   Matches 329; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   5 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 64

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCATCATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Db   65 CCTGCAAGGCCTCTGGAGGCACCTTCATCAGCTGGGTGCGACAGGCCC 124

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCGTCATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||| ||||| |||| |||||||| |||||||||
Db   125 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTATAGCAAACTACG 184

Qy   181 CACAGAGAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 CACAGAGAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 244

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG------ 294
          ||||||||||||||||||| |||||||||||||| |||||||||||||||||||
Db   245 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTGGGAA 304

Qy   295 ATCCCGATTATGTTTGGGGGAGCGACAAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
          |||||||| ||||||||| ||||||| ||||| |||||||||||||||||||||||||
Db   305 GTATGACGCGATTTTGGAGTGGTGCTCCACGTCTTCTTGACTACTGGGGCCAGGGAACCCTGG 364
```

```
Qy    355
```

RESULT 4
AAC67868
ID   AAC67868 standard; DNA; 747 BP.
XX
AC   AAC67868;
XX
DT   16-FEB-2001 (first entry)
XX
DE   Recombinant human antibody scFv TN11 nucleotide sequence.
XX
KW   Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
KW   cTN-C; ds.
XX
OS   Homo sapiens.
XX
PN   WO20006369-A1.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-EP03550.
XX
PR   20-APR-1999; 99IT-FI00094.
XX
PA   (PHIL-) PHILOGEN SRL.
XX
PI   Zardi L;
XX
DR   WPI; 2000-687225/67.
DR   P-PSDB; AAB36083.
XX
PT   Ligands used for diagnosis and treatment of human neoplasias, are
PT   capable of identifying the tenascin-C isoform containing domain C of
PT   tenascin-C -
XX
PS   Claim 8; Page 5-6; 31pp; English.
XX
CC   The present sequence encodes a recombinant human antibody scFv. Antibody
CC   TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
CC   recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
CC   only capable of recognising TN-C isoforms containing domain C (cTN-C).
CC   TN11 is useful for detecting the presence of TN-C isoforms in vitro or
CC   in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C.
CC   It is useful for the preparation of formulations for the treatment of
CC   human neoplasias.
XX
SQ   Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;

Query Match   77.8%; Score 286.4; DB 21; Length 747;
Best Local Similarity 86.1%; Pred. No. 3.9e-73;
   Matches 317; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||||| ||| |||| |||||||||||||||||||||
Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCCATGAGCTGGGTGCGGCAGGCCC 121

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||||||||| |||||||||| ||||||||| ||||
Db   122 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy   181 CACAGAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 CACAGAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241
```

```
Query Match          77.4%;    Score 284.8;   DB 21;   Length 354;
Best Local Similarity 88.6%;    Pred. No. 9.5e-73;
Matches 326;   Conservative   0;   Mismatches 27;   Indels 15;   Gaps  1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGTCCTCGGTAAAGGTCT  60
          ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db      2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGTCCTCGGTGAAGGTCT  61

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTACTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     62 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 121

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    122 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGGGACAAATCCAGCAGCACCAGCCTACA 240
          |||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db    182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGGGACGAATCACCAGCAGCCTACA 241

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| -----
Db    242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGA------ 296

Qy    301 ATTATGTTTGGGGAGGGGAGGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
            |||         |||||||   |||  ||  || |||||  |||||||||||||
Db    297 -------------AGATAGCAGTGGCTGGTGGTATCACTACTGGGGCCAGGGAACCCTGGTCACCG 346

Qy    361 TCTCCCTCA 368
          |||||||||
Db    347 TCTCCCTCA 354
```

```
Db    242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCCGTGTATTACTGTGCGAGGATCGAGAC 301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 ATTATGTTTGGGGAGGGGAGCCTGACCAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                               ||||
Db    302 GTATTACGATTTTTGGAGGAGGTGCTTTCGATATCTGGGGCCCGAGGCACCATGGTCACCG 361

Qy    361 TCTCCCTCA 368
          |||| |||
Db    362 TCTCCCTCA 369
```

```
RESULT 5
AAA48411
ID   AAA48411 standard; cDNA; 354 BP.
XX
AC   AAA48411;
XX
DT   20-SEP-2000  (first entry)
XX
DE   Human LH13 monoclonal antibody heavy chain variable region cDNA.
XX
KW   Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;
KW   cytostatic; cytotoxic; heavy chain variable region; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..354
FT                  /*tag= a
FT                  /partial
FT                  /product= "LH13 antibody heavy chain variable region"
XX
PN   WO200032635-A2.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;  99WO-US28485.
XX
PR   02-DEC-1998;  98US-0203768.
XX
PA   (IXSY-) IXSYS INC.
XX
PI   Watkins JD, Huse WD;
XX
DR   WPI; 2000-412293/35.
DR   P-PSDB; AAY99558.
XX
PT   New tumor-specific human monoclonal antibody, useful for the treatment
PT   and diagnosis of cancer, comprises at least one complementarity
PT   determining region -
XX
PS   Claim 16; Page 82; 84pp; English.
XX
CC   The present sequence encodes the heavy chain variable region of a human
CC   tumour-specific monoclonal antibody. Neoplastic cells selectively express
CC   antigens which are not present on normal cells. Thus monoclonal
CC   antibodies can be produced that are specifically directed against
CC   tumour-specific antigens. The antibodies can be conjugated to cytotoxic
CC   or cytostatic agents and used to selectively target cancer cells for the
CC   elimination of tumours. They can also be linked to diagnostic moieties
CC   that allow the imaging of neoplastic cells. Nucleic acids encoding human
CC   tumour-specific monoclonal antibodies can be used to express the
CC   antibodies and can be recombinantly engineered to produced modified
CC   antibodies with higher affinity or higher selectivity for tumour cells.
CC   Tumour-specific antibodies were produced by hybridomas that were
CC   generated by in vitro immunisation of human spleen cell cultures with
CC   breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
CC   was then isolated from the hybridoma by RT-PCR. The present sequence
CC   encodes a human monoclonal antibody heavy chain variable region which was
CC   produced by LH13 hybridoma cell line.
XX
SQ   Sequence 354 BP; 80 A; 90 C; 115 G; 69 T; 0 other;
```

```
RESULT 6
AAF29714
ID   AAF29714 standard; DNA; 1517 BP.
XX
AC   AAF29714;
XX
DT   05-APR-2001  (first entry)
XX
DE   G71-1 immunoconjugate coding sequence.
XX
KW   Mouse; scFv; immunoconjugate; IgG1 effector domain; cancer;
KW   atherosclerosis; tissue factor; macular degeneration;
KW   rheumatoid arthritis; ds.
XX
OS   Synthetic.
XX
PN   WO20010243 9-A1.
XX
PD   11-JAN-2001.
XX
PF   14-JUN-2000;  2000WO-US16481.
XX
PR   01-JUL-1999;  99US-0142161.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Garen A;
XX
DR   WPI; 2001-123105/13.
XX
PT   Immunoconjugate protein for treatment of neovascularization, comprises
PT   protein comprising Fc region of human immunoglobulin (Ig)GI conjugated
PT   to the targeting domain which comprises factor VII mutant -
XX
PS   Example 2; Page 65-66; 69pp; English.
XX
CC   The present invention provides a composition comprising a homodimeric
CC   immunoconjugate protein made up of two chains, each containing an IgG1 Fc
CC   effector domain and a targeting domain. The targeting domain may be
```

```
CC   either the human IgG1 Fc region or a mutant form of human factor VII. The
CC   immunoconjugate is targeted at the transmembrane receptor tissue factor.
CC   This enables the composition to be used in the treatment of diseases
CC   associated with neovascularisation, including cancer, atherosclerosis,
CC   rheumatoid arthritis and macular degeneration.
XX
SQ   Sequence 1517 BP; 338 A; 444 C; 441 G; 294 T; 0 other;

Query Match             76.8%;  Score 282.8;  DB 22;  Length 1517;
Best Local Similarity   88.0%;  Pred. No. 5.2e-72;
Matches  324;  Conservative   0;  Mismatches  32;  Indels  12;  Gaps   1;

Qy    1  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         |||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||
Db   65  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  124

Qy   61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
         |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  125  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTCATCAGCTGGGTGCGACAGGCCC  184

Qy  121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
         ||||||||||||||||||||||||||| |||||| ||||||    |||    ||||||||
Db  185  CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCCCTATCAGCTGTACAGCAAACTACG  244

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGACCAGCCTACA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  245  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGACCACGCCTACA  304

Qy  241  TGGAGCTGAGCAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  305  TGGAGCTGAGCAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA-------  357

Qy  301  ATTATGTTTGGGGAGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG  360
              ||||  |||||||||  ||  ||   |||| |||||||||||||||    |||||
Db  358  -----GGAGGAGGAGATATGATGCTTTTGATATCTCGGGCCAAGGACACTGGTCACCG  412

Qy  361  TCTCCTCA  368
         ||||| ||
Db  413  TCTCTTCA  420
```

```
RESULT 7
AAQ22419
ID   AAQ22419 standard; DNA; 812 BP.
XX
AC   AAQ22419;
XX
DT   17-AUG-1992 (first entry)
XX
DE   Human heavy chain V region gene VH49.8.
XX
KW   Heavy chain; variable region; VH1 family; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   exon           1..286
FT                  /*tag= a
FT   intron         287..373
FT                  /*tag= b
FT   exon           373..812
FT                  /*tag= c
FT   CDS            241..689
FT                  /*tag= d
FT   misc_recomb    678..686
FT                  /*tag= e
FT                  /note= "recombination signal"
FT   misc_recomb    709..718
FT                  /*tag= f
FT                  /note= "recombination signal"
XX
PN   WO9203918-A.
XX
```

```
PD   19-MAR-1992.
XX
PF   28-AUG-1991;  91WO-US06185.
XX
PR   31-AUG-1990;  90US-0575962.
PR   29-AUG-1990;  90US-0574748.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N, Kay R;
XX
DR   WPI; 1992-113962/14.
DR   P-PSDB; AAR22358.
XX
PT   Immunoglobulin trans:genes - for prodn. of heterologous
PT   non-rearranged and/or rearranged Ig chains
PS   Example 14; Page 87; 172pp; English.
XX
CC   The human placental genomic DNA library cloned into the phage
CC   vector lambda FIX II was screened with the human VH1 family
CC   specific oligonucleotide (see AAQ22418).  Phage clone lambda
CC   49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
CC   segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
CC   An 800 bp region of this insert was sequenced.  VH49.8 was found
CC   to have an open reading frame and intact splicing and recombination
CC   signals, thus indicating that the gene is functional.
CC   See also AAQ22419-49, AAQ22417-30.
XX
SQ   Sequence 812 BP; 204 A; 189 C; 222 G; 197 T; 0 other;

Query Match             76.3%;  Score 280.8;  DB 13;  Length 812;
Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
Matches  288;  Conservative   0;  Mismatches  12;  Indels   0;  Gaps   0;

Qy    1  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         |||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  385  AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  444

Qy   61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  445  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTCATCAGCTGGGTGCGACAGGCCC  504

Qy  121  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
         |||||||||||||||||||||||||| ||||||| ||||||    |||   |||||||||
Db  505  CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCCTATCAGCTGTACAGCAAACTACG  564

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGACAGCCTACA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  565  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGACCACGCCTACA  624

Qy  241  TGGAGCTGAGCAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625  TGGAGCTGAGCAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACAGCAG  684
```

```
RESULT 8
AAQ44185
ID   AAQ44185 standard; DNA; 812 BP.
XX
AC   AAQ44185;
XX
DT   10-NOV-1993 (first entry)
XX
DE   Human heavy chain V region gene VH49.8.
XX
KW   Immunoglobulin; IgG; heavy chain; minilocus transgene;
KW   isotype switching; H chain variable region; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   exon           1..286
```

```
RESULT 9
AAT37243
ID   AAT37243 standard; DNA; 812 BP.
XX
AC   AAT37243;
XX
DT   21-APR-1997  (first entry)
XX
DE   DNA fragment vh49.8, containing variable heavy chain gene.
XX
KW   Variable; heavy chain; gene segment; human; DNA fragment; vh49.8;
KW   unrearranged; minilocus; transgene; transgenic; mouse;
KW   production; heterologous; antibody; gamma; immunoglobulin; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   exon           241..286
FT                  /*tag= a
FT   exon           373..677
FT                  /*tag= b
XX
PN   US5545806-A.
XX
PD   13-AUG-1996.
XX
PF   29-AUG-1990;     90US-0574748.
XX
PR   16-DEC-1992;     92US-0990860.
PR   29-AUG-1990;     90US-0574748.
PR   31-AUG-1990;     90US-0575962.
PR   17-DEC-1991;     91US-0810279.
PR   18-MAR-1992;     92US-0853408.
PR   23-JUN-1992;     92US-0904068.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1996-383736/38.
DR   P-PSDB; AAW03950.
XX
PT   Prodn. of heterologous human immunoglobulin(s) - by immunising
PT   transgenic mice
XX
PS   Example 12; Columns 61-62; 94pp; English.
XX
CC   The present sequence is the variable heavy chain gene segment
CC   containing human DNA fragment, vh49.8, which was injected into half
CC   day mouse embryo pronuclei, to generate an unrearranged heavy chain
CC   minilocus transgene. The resulting transgenic mice can be used for
CC   the production of heterologous (i.e. human) antibodies against
CC   specific antigens, this comprises immunising a mouse with a
CC   preselected antigen and collecting antigen binding heterologous
CC   human gamma immunoglobulins.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

Query Match             76.3%;  Score 280.8;  DB 17;  Length 812;
Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
Matches  288;  Conservative  0;  Mismatches  12;  Indels  0;  Gaps  0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||| ||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTATCAGCTGGGTGCGACAGGCCC 504

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||||||| ||||||||||| | ||||| |||||||
Db    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 180
```

```
FT                   /*tag= a
FT     intron        /number= 1
FT                   287..372
FT                   /*tag= b
FT     exon          /number= 1
FT                   373..812
FT                   /*tag= c
FT                   /number= 2
FT     CDS           241..689
FT                   /*tag= d
FT                   /note= "CDS is interrupted by intron #1; the
FT                   last three codons of the CDS are not
FT                   translated in the amino acid sequence
FT                   AAR38623"
XX
PN     WO9312227-A.
XX
PD     24-JUN-1993.
XX
PF     17-DEC-1992;     92WO-US10983.
XX
PR     17-DEC-1991;     91US-0810279.
PR     18-MAR-1992;     92US-0853408.
PR     23-JUN-1992;     92US-0904068.
XX
PA     (GENP-) GENPHARM INT INC.
XX
PI     Kay RM, Lonberg N;
XX
DR     WPI; 1993-214169/26.
DR     P-PSDB; AAR38623.
XX
PT     Transgenic non-human animals contg. immunoglobulin heavy chain
PT     trans gene - used to produce useful antibodies by isotype
PT     switching
XX
PS     Example 12; Page 96; 196pp; English.
XX
CC     A human placental genomic DNA library cloned into the phage vector
CC     lambda FIX II was screened with the human VHI family specific
CC     oligonucleotide AAQ44184. Phage clone lambda 49.8 was isolated and a
CC     6.1kb XbaI fragment containing the variable segment VH49.8 was
CC     subcloned into pNNO3 to generate plasmid pVH49.8. An 800bp
CC     region of this insert was sequenced (AAQ44185) and VH49.8 found to
CC     have an open reading frame and intact splicing and recombination
CC     signals, indicating that the gene is functional.
XX
SQ     Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

Query Match             76.3%;  Score 280.8;  DB 14;  Length 812;
Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
Matches  288;  Conservative  0;  Mismatches  12;  Indels  0;  Gaps  0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||| ||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATCAGCTATCAGCTGGGTGCGACAGGCCC 504

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||||||| ||||||||||| | ||||| |||||||
Db    505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGCGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGCGACAAATCCACGAGCACAGCCTACA 624

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||| || |
Db    625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
```

Left column

```
Db  505  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCTATCCTTGGTATAGCAAACTACG  564

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA  624

Qy  241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  684
```

```
RESULT 10
AAV12538
ID   AAV12538 standard; DNA; 812 BP.
XX
AC   AAV12538;
XX
DT   26-MAY-1998  (first entry)
XX
DE   Human VHI family gene VH49.8.
XX
KW   Transgenic mouse; human; immunoglobulin; heavy chain segment; J region;
KW   joining region; constant region; VH family; variable gene; gamma isotype;
KW   diversity gene; isotype switching sequence; mu isotype; Ig production;
KW   monoclonal antibody; MAb production; antigen; heavy chain isotype;
KW   antigenic stimulation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             241..678
FT                   /*tag= a
FT                   /note= "contains an intron, no stop codon given"
FT   exon            241..286
FT                   /*tag= b
FT                   /number= 1
FT   intron          287..372
FT                   /*tag= c
FT                   /number= 1
FT   exon            373..678
FT                   /*tag= d
FT                   /number= 2
XX
PN   US5625126-A.
XX
PD   29-APR-1997.
XX
PF   07-DEC-1994;    94US-0352322.
XX
PR   07-DEC-1994;    94US-0352322.
PR   29-AUG-1990;    90US-0574748.
PR   31-AUG-1990;    90US-0575962.
PR   17-DEC-1991;    91US-0810279.
PR   05-FEB-1992;    92US-0834539.
PR   18-MAR-1992;    92US-0853408.
PR   23-JUN-1992;    92US-0904068.
PR   16-DEC-1992;    92US-0990860.
PR   26-APR-1993;    93US-0053131.
PR   22-JUL-1993;    93US-0096762.
PR   18-NOV-1993;    93US-0155301.
PR   03-DEC-1993;    93US-0161739.
PR   10-DEC-1993;    93US-0165699.
PR   09-MAR-1994;    94US-0209741.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1997-258277/23.
DR   P-PSDB; AAW41113.
XX
PT   Human antibody producing transgenic mouse - containing transgene
PT   comprising human V, D and J genes and sequences to provide isotype
```

Right column

```
PT   switching in lymphocytes
XX
PS   Example 12; Column 73-74; 153pp; English.
XX
CC   This sequence represents the human VHI family gene VH49.8. This DNA
CC   sequence can be used in a plasmid, which is used to develop the
CC   transgenic mouse of the invention. The transgenic mouse of the invention
CC   contains in its genome a transgene comprising in operable linkage human
CC   variable (V), diversity (D) and junction (J) genes, a human mu constant
CC   region gene (muCH), at least 2 different non-mu human CH genes and
CC   associated isotype switching sequences, where human mu and gamma switch
CC   sequences are located in closer proximity to each other than in the
CC   naturally occurring human immunoglobulin (Ig) locus, and where in
CC   lymphocytes of the mouse the transgene undergoes productive VDJ
CC   rearrangement and mu to gamma isotype switching by recombination between
CC   the human mu and gamma sequences, so that the mouse produces a serum
CC   containing Ig of at least 3 human heavy chain isotypes in response to
CC   antigenic stimulation. The transgenic mice can be used to produce human
CC   Ig and monoclonal antibodies (MAb), which are specifically reactive with
CC   human antigens. The MAb can be used in therapeutic or diagnostic
CC   applications. The transgenic mice can produce human MAb of multiple
CC   isotypes by undergoing isotype switching.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
```

```
Query Match             76.3%;    Score 280.8;   DB 18;   Length 812;
Best Local Similarity   96.0%;    Pred. No. 1.7e-71;
Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    1  AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         ||||   |||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db  385  AGGTTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  444

Qy   61  CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
         |||||||||||||||||||||||||||||||  ||||  |||||||||||||||||||||
Db  445  CCTGCAAGGCTTCTGGAGGCACCTTCAGCTGTTATCAGTGGGTGCGACAGGCCC        504

Qy  121  CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
         ||||||||||||||||||||||||  ||||||| ||||||||||   |||||||  ||||
Db  505  CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCTATCCTTGGTATAGCAAACTACG  564

Qy  181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA  624

Qy  241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  684
```

```
RESULT 11
AAT70522
ID   AAT70522 standard; DNA; 812 BP.
XX
AC   AAT70522;
XX
DT   09-MAR-1998  (first entry)
XX
DE   Human immunoglobulin VH1 family VH49-8 gene.
XX
KW   Immunoglobulin heavy chain; variable region; V region; VH1 family;
KW   transgene; monoclonal antibody; heterologous antibody; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             241..677
FT                   /*tag= a
FT                   /product= VH49.8
FT                   /note="heavy chain V region gene"
FT   intron          287..372
FT                   /*tag= b
```

```
FT   misc_feature      680..684
FT                     /*tag= c
FT                     /note= "mentioned in specification"
FT   misc_feature      710..718
FT                     /*tag= d
FT                     /note= "Mentioned in specification"
XX
PN   US5633425-A.
XX
PD   27-MAY-1997.
XX
PF   05-FEB-1992;   92US-0834539.
XX
PR   29-AUG-1990;   90US-0574448.
PR   31-AUG-1990;   90US-0575962.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1997-297410/27.
DR   N-PSDB; AAW18840; AAW18841.
XX
PT   Transgenic mouse for heterologous antibody production - containing
PT   DNA encoding human immunoglobulin components
XX
PS   Example 14; Column 54; 90pp; English.
XX
CC   This sequence encodes the VH49.8 gene from the human heavy chain
CC   V region and a member of the VH1 family. This gene was sequenced from the
CC   plasmid pVH49.8 which is used in a novel method of developing transgenic
CC   non-human animals capable of producing heterologous antibodies encoded by
CC   human immunoglobulin genes. Such transgenically produced monoclonal
CC   antibodies should alleviate the intrinsic immunogenicity of non-human
CC   immunoglobulins allowing the development of new in vivo applications.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

Query Match       76.3%;   Score 280.8;   DB 18;   Length 812;
Best Local Similarity   96.0%;   Pred. No. 1.7e-71;
Matches  288;   Conservative   0;  Mismatches  12;  Indels  0;  Gaps  0;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||| |||||||||||||| |||| ||||| ||||||||||||||||||
Db  445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||||| |||||||||||| |||||||||| ||||
Db  505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACCAGCACCAGCCTACA 240
          |||| ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||| |||||||||| |||||||||||| |||||||||| |||
Db  625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684

RESULT 12
AAT73471
ID   AAT73471 standard; DNA; 812 BP.
XX
AC   AAT73471;
XX
DT   23-JAN-1998 (first entry)
XX
DE   Human VH1 gene VH49.8.
XX
```

```
KW   Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW   transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW   transplant rejection; immunoglobulin; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   exon             241..286
FT                    /*tag= a
FT                    /number= 1
FT   intron           287..372
FT                    /*tag= b
FT                    /anticodon= 1
FT                    /note= "DNA sequence in the specification is unclear,
FT                            so this is the best estimate of the sequence"
FT   exon             373..812
FT                    /*tag= c
FT                    /number= 2
FT                    /note= "The protein shown in the specification ends at
FT                            position 677, not at the stop codon ending at
FT                            position 689"
XX
PN   WO9713852-A1.
XX
PD   17-APR-1997.
XX
PF   10-OCT-1996;   96WO-US16433.
XX
PR   10-OCT-1995;   95US-0544404.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1997-235888/21.
DR   P-PSDB; AAW24777.
XX
PT   Novel anti-CD4 antibody produced by transgenic mice - used in the
PT   treatment of auto-immune disease etc.
XX
PS   Example 12; Page 138; 396pp; English.
XX
CC   A novel composition has been developed which comprises an immunoglobulin
CC   (Ig) having an affinity constant (Ka) of at least 2 multiply
CC   1000000000 M-1 for binding to a predetermined human antigen. The
CC   present sequence represents the human VH1 gene VH49.8 isolated from
CC   a human placental genomic library lambda. Anti-CD4 antibodies
CC   may be used in therapeutic and diagnostic applications, especially
CC   for the treatment of human diseases. These antibodies reduce
CC   activity of CD4 cells and reduce undesirable autoimmune reactions,
CC   inflammatory response and transplant rejection. Transgenic animals are
CC   capable of producing heterologous antibodies of multiple isotypes by
CC   undergoing isotype switching. These animals produce a first Ig type that
CC   is necessary for antigen-stimulated B-cell maturation and can switch to
CC   encode and produce one or more subsequent heterologous isotypes.
XX
SQ   Sequence 812 BP; 203 A; 194 C; 223 G; 192 T; 0 other;

Query Match       76.3%;   Score 280.8;   DB 18;   Length 812;
Best Local Similarity   96.0%;   Pred. No. 1.7e-71;
Matches  288;   Conservative   0;  Mismatches  12;  Indels  0;  Gaps  0;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db  385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||| |||||||||||||| |||| ||||| ||||||||||||||||||
Db  445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Qy   181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db   565  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy   241  TGGAGCTGAGCAGCCTGAGATCTGATGAGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db   625  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
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RESULT 13
AAZ21897
ID   AAZ21897 standard; DNA; 812 BP.
XX
AC   AAZ21897;
XX
DT   24-NOV-1999 (first entry)
XX
DE   Nucleotide sequence of human heavy chain V region gene VH49.8.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
KW   transgenic mouse; human heavy chain transgene; digoxin;
KW   human light chain transgene; immortalized cell; immunoglobulin;
KW   Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999; 99WO-US05535.
XX
PR   13-MAR-1998; 98US-0042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N, Fishwild DM, Ball WJ;
XX
DR   WPI; 1999-551219/46.
DR   P-PSDB; AAY40381.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies
XX
PS   Example 12; Page 168; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable
CC   amount of an immunoglobulin that specifically binds digoxin or
CC   Shinga-like toxin. B cells from transgenic animals can be used to
CC   generate hybridomas expressing monoclonal high affinity human sequence
CC   antibodies. Antibodies produced from the transgenic animals of the
CC   invention can be used to treat human diseases, e.g. autoimmune
CC   diseases, cancer, infectious disease, transplant rejection, blood
CC   disorders such as coagulation disorders and other diseases. The
CC   present sequence represents human heavy chain V region gene VH49.8,
CC   which is used in the course of the invention.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 196 T; 1 other;

Query Match   76.3%; Score 280.8; DB 20; Length 812;
Best Local Similarity 96.0%; Pred. No. 1.7e-71;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCT 60
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Db   385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGTCCTCGGTGAAGGTCT 444
```

```
Qy    61  CCTGCAAGGCTTCTTGGAGGCACCTTCAGTAGTTACTATCAGTCATCATCGTCGACAGGCCC 120
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Db   445  CCTGCAAGGCTTCTTGGAGGCACCTTCAGTAGTTATATACTATTCAGTCATGGGTGCGACAGGCCC 504

Qy   121  CTGGACAAGGGCTTGAGTGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||| |||||||||| |||||||||| |||||||||||||
Db   505  CTGGACAAGGGCTTGAGTGATGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy   181  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db   565  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy   241  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATTACTGTGCGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||| | |
Db   625  TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
```

RESULT 14
AAX06042
ID   AAX06042 standard; DNA; 812 BP.
XX
AC   AAX06042;
XX
DT   10-MAY-1999 (first entry)
XX
DE   Sequence of human VH1 family gene VH 49.8.
XX
KW   Human; Immunoglobulin transgene; Ig; VH gene; D gene; JH gene; mu gene;
KW   switch sequence; gamma gene; IgM; IgG; ss.
XX
OS   Homo sapiens.
XX
PN   US5874299-A.
XX
PD   23-FEB-1999.
XX
PF   14-FEB-1997; 97US-0800353.
XX
PR   05-FEB-1992; 92US-0834539.
PR   29-AUG-1990; 90US-0574748.
PR   31-AUG-1990; 90US-0575962.
PR   28-AUG-1991; 91WO-US06185.
PR   14-FEB-1997; 97US-0800353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM, Lonberg N;
XX
DR   WPI; 1999-179989/15.
DR   P-PSDB; AAW94854, AAW94855.
XX
PT   Human immunoglobulin transgene - with mu and gamma isotype switching
PT   segments
XX
PS   Example 14; Column 53-54; 88pp; English.
XX
CC   The invention relates to a heavy chain (human) immunoglobulin (Ig)
CC   transgene. The transgene comprises: (i) human VH gene segments; (ii)
CC   human D gene segments; (iii) human JH gene segments; and either (iv) a
CC   mu constant region comprising a mu switch sequence upstream from a mu
CC   coding segment; (v) a gamma constant region comprising a gamma switch
CC   sequence upstream from a human gamma coding segment; where (vi) the mu
CC   and gamma constant regions are closer than in wild type human Ig heavy
CC   chain loci; or (vii) a heavy chain enhancer; (vii) a mu constant region
CC   comprising a mu switch sequence upstream from a mu coding segment; (ix) a
CC   gamma constant region comprising a gamma switch sequence upstream from a
CC   human gamma coding segment; and (x) at least one discontinuity of at
CC   least 2 kb between the mu and gamma gene segments as compared to a human
CC   germ-line heavy chain locus; or (xi) a human mu CH gene and at least two
CC   non-mu human CH genes and their associated isotype switching sequences;
CC   where (xii) the human mu and human gamma switch sequences are closer than
CC   in wild type human Ig heavy chain loci. The transgenes allow non-human
```

CC animals to produce heterologous (human) Ig's with varying specificities.
CC The presence of mu and gamma switch segments allows isotype switching of
CC the human heavy chain mini-locus from IgM (for maturation) to IgG.
XX
SQ Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

Query Match   76.3%;   Score 280.8; DB 20; DB 20; Length 812;
Best Local Similarity   96.0%;   Pred. No. 1.7e-71;
Matches 288; Conservative   0; Mismatches 12; Indels   0; Gaps   0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
            ||| ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            |||||||||||||||||||||| || ||||||||||||| | |||||||||||||||||||
Db   445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db   505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db   565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684

RESULT 15
AAQ89328
ID AAQ89328 standard; DNA; 294 BP.
XX
AC AAQ89328;
XX
DT 26-SEP-1995 (first entry)
XX
DE HV1263 VH gene.
XX
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; heavy chain; H chain;
KW variable region; VH; autoimmunity; ss.
XX
OS Homo sapiens.
XX
PN WO9508336-A.
XX
PD 30-MAR-1995.
XX
PF 22-SEP-1994; 94WO-US10756.
XX
PR 22-SEP-1993; 93US-0124469.
XX
PA (NICH-) NICHOLS INST DIAGNOSTICS.
XX
PI Mclachlan SM, Rapoport B;
XX
DR WPI; 1995-139383/18.
DR P-PSDB; AAR72069.
XX
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
XX
PS Disclosure; Page 68; 94pp; English.
XX
CC L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
CC showed homology to the closest germline genes, DP10 (AAQ89327) and
CC HV1263 (AAQ89328). The DNA (AAQ89329) and corresp. amino acid
CC (AAR72070) sequences of the VH region of a representative clone,

---

CC OF7H1.2, are provided.
XX
SQ Sequence 294 BP; 69 A; 74 C; 94 G; 57 T; 0 other;

Query Match   75.7%;   Score 278.6; DB 16; Length 294;
Best Local Similarity   96.9%;   Pred. No. 5.6e-71;
Matches 284; Conservative   0; Mismatches   9; Indels   0; Gaps   0;

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Db   2 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            |||||||||||||||||||||| || ||||||| | |||||||||||||||||||||||||
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Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   122 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 181

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 293
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 294

Search completed: July 18, 2003, 06:44:06
Job time : 96.4001 secs

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              GenCore version 5.1.6
      Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    July 18, 2003, 06:19:39 ; Search time 88.9613 Seconds
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Title:           US-09-627-896B-29
Perfect score:   368
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Searched:        1439767 seqs, 103150376 residues
Total number of hits satisfying chosen parameters:    2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	277.6	75.4	495	10	US-09-925-299-92	Sequence 92, Appl
2	277.6	75.4	495	12	US-09-925-299-92	Sequence 92, Appl
3	276.8	75.2	723	15	US-10-151-882-9	Sequence 9, Appl
4	276	75.0	375	15	US-10-091-300-19	Sequence 19, Appl
5	274	74.5	1599	11	US-09-954-456-789	Sequence 789, App
6	274	74.5	1599	11	US-09-954-456-1604	Sequence 1604, Ap
7	272.2	74.0	1884	15	US-10-047-542-61	Sequence 61, Appl
8	272.2	74.0	2213	15	US-10-047-542-46	Sequence 46, Appl
9	268	72.8	735	15	US-10-151-882-3	Sequence 3, Appl
10	267.6	72.7	720	15	US-10-151-882-10	Sequence 10, Appl
11	265.4	72.1	396	10	US-09-811-737-12	Sequence 12, Appl
12	265.4	72.1	782	10	US-09-811-737-22	Sequence 22, Appl
13	263.6	71.6	717	15	US-10-151-882-11	Sequence 11, Appl
14	263.6	71.6	744	15	US-10-151-882-7	Sequence 7, Appli
15	262.8	71.4	744	15	US-10-151-882-5	Sequence 5, Appli
16	251	68.2	396	10	US-09-811-737-13	Sequence 13, Appl
17	251	68.2	782	10	US-09-811-737-21	Sequence 21, Appl
18	250.4	68.0	699	15	US-10-006-593-54	Sequence 54, Appl
19	249.2	67.7	726	15	US-10-151-882-4	Sequence 4, Appli
20	248.4	67.5	372	8	US-08-844-215-24	Sequence 24, Appl
21	248.2	67.4	378	8	US-08-844-215-27	Sequence 27, Appl
22	247.8	67.3	762	15	US-10-151-882-12	Sequence 12, Appl
23	247.6	67.3	750	15	US-10-151-882-8	Sequence 8, Appli
24	246	66.8	376	11	US-09-828-708-122	Sequence 122, App
25	244.2	66.4	369	10	US-09-905-243-8	Sequence 8, Appli
26	242.8	66.0	415	10	US-10-160-232-35	Sequence 35, Appl
27	242	65.8	1449	11	US-09-747-669-1	Sequence 2, Appli
28 c	242	65.8	1449	11	US-09-747-669-2	Sequence 1, Appli
29	242	65.8	1449	15	US-10-290-703-1	Sequence 1, Appli
30 c	240.4	65.3	1563	15	US-10-290-703-2	Sequence 2, Appli
31	240.4	65.3	510	11	US-09-822-830A-505	Sequence 505, App
32	237.8	64.6	747	15	US-10-106-698-2502	Sequence 2502, Ap
33	237.6	64.5	409	15	US-10-151-882-6	Sequence 6, Appli
34	237.2	64.5	317	10	US-10-160-232-42	Sequence 42, Appl
35	236	64.1	463	12	US-09-864-761-31160	Sequence 31160, A
36	236	64.1	463	15	US-09-925-299-277	Sequence 277, App
37	236	64.1	409	15	US-09-925-299-277	Sequence 277, App
38	232.4	63.2	1616	15	US-10-160-232-78	Sequence 78, Appl
39	232	63.0	395	11	US-09-859-053-27	Sequence 27, Appl
40	230	62.5	690	10	US-09-753-436-85	Sequence 85, Appl
41	229.8	62.4	789	12	US-09-791-153A-52	Sequence 52, Appl
42	229.8	62.4	947	15	US-09-791-153A-54	Sequence 54, Appl
43	229.6	62.4	418	15	US-10-060-585-10	Sequence 10, Appl
44	228	62.0		15	US-10-158-646-53	Sequence 53, Appl
45	226.4	61.5		10	US-09-760-723-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-09-925-299-92
; Sequence 92, Application US/09992299
; Patent No. US2002005527A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 92
;  LENGTH: 495
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (402)
;  OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-92

Query Match       75.4%;  Score 277.6;  DB 10;  Length 495;
Best Local Similarity   85.7%;  Pred. No. 3.3e-84;
Matches 318;  Conservative   3;  Mismatches 43;  Indels   7;  Gaps   1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db    125 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCCGGTGAAGGTCT 184

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Qy    121 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db   305 CACAGAGAGTTCCAGGGCCAGAGTCACGATTACCGCGACGAATCCAGGACGCAGCAGCCTACA 364

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db   365 TGGAGCTGAGCAGCCTGAGATCTGAGGACATCGAGGACACNTATTACTGTGCGARAAGKCCCT 424

Qy   301 ATTATGTTT------GGGGGAGCGACAACTGGTTCGACCCCCTGGGGCCAGGGAACCCTG 353

Db   425 MAGCGGGTTATCATCCCAACTACCACGGTATGGACGTCTGGGGCCAAGGGACCACG 484

Qy   354 CTCATCGTCTC 364

Db   485 GTCACCGTCTC 495

RESULT 2
US-09-925-299-92
; Sequence 92, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA102
;   CURRENT APPLICATION NUMBER: US/09/925,299
;   CURRENT FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: PCT/US00/05883
;   PRIOR FILING DATE: 2000-03-08
;   PRIOR APPLICATION NUMBER: 60/124,270
;   PRIOR FILING DATE: 1999-03-12
;   NUMBER OF SEQ ID NOS: 1556
;   SOFTWARE: PatentIn Ver. 2.0
;
;   SEQ ID NO 92
;   LENGTH: 495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (402)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-92

Query Match   75.4%; Score 277.6; DB 12; Length 495;
Best Local Similarity   85.7%; Pred. No. 3.3e-84;
Matches 318; Conservative   3; Mismatches 43; Indels   7; Gaps   1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

Db   125 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 184

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCAGCTGTCTCGGGTGCGACAGGCCC 120

Db   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCATCAGCTGTCATGCGTGCGACAGGCCC 185

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCGTATCCTATGCCTATCTTACG 180

Db   245 CTGGACAAGGGCTTGAGTGGATGGGATGGGATGGGATCATCCCTATCTTTGGTACAGCAAACTACG 304

Qy   181 CACAGAGAGTTCCAGGGCCAGAGTCACGATTACCGCGACACGGCCCGTGTATTACTGTGCGAGAGATCCCG 240

Db   305 CACAGAGAGTTCCAGGGCCAGAGTCACGATTACCGCGACGAATCCAGGACGCAGCAGCCTACA 364

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db   365 TGGAGCTGAGCAGCCTGAGATCTGAGGACATCGAGGACACGCCATNTATTACTGTGCGARAAGKCCCT 424

Qy   301 ATTATGTTT------GGGGGAGCGACAACTGGTTCGACCCCCTGGGGCGCCAGGGACCAGCCCC 353

Db   425 MAGCGGGTTATCATCCCAACTACTACCACGGTATGGACGTCTGGGGCCAAGGGACCACG 484

Qy   354 CTCATCGTCTC 364

Db   485 GTCACCGTCTC 495

RESULT 3
US-10-151-882-9
; Sequence 9, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;   FILE REFERENCE: PF554
;   CURRENT APPLICATION NUMBER: US/10/151,882
;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
;
;   SEQ ID NO 9
;   LENGTH: 723;
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A010D09 scFv
US-10-151-882-9

Query Match   75.2%; Score 276.8; DB 15; Length 723;
Best Local Similarity   87.2%; Pred. No. 6.8e-84;
Matches 321; Conservative   0; Mismatches 32; Indels 15; Gaps   1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

Db   2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTTGGGTCCTCGGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATCAGCTGGTGGCGACAGGCCC 120

Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCATCAGCTGGTGGCGACAGGCCC 121

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCGTATCCTATCCTTCCTTGGACTAGCAAATTACG 180

Db   122 CTGGACAAGGGCTTGAGTGGATGGGATGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy   181 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACAAATCCAGGACGCACAGCACCAGCCTACA 240

Db   182 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACGACACCAGGACGCACCAGCCTACA 241

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACTGAGGACATCGAGAGATCCG 298

Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGGACATCTGAGGACACGTGTATTACTGTGCCAAGAGATC-- 298

Qy   301 ATTATGTTTGGGGGGAGCCGACAACTGGTTCGACCCCCTGGGGCCAGGGAACCCTGCTCATCG 360

Db   299 ------------TGGAGCAGGCTCGGTATGGACGTCTGGGGCCAAGGGACCACCGGTCACCG 346

Qy   361 TCTCCTCA 368

Db   347 TCTCCTCA 354

RESULT 4
US-10-091-300-19
; Sequence 19, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
;   APPLICANT: Rockwell, Patricia
;   APPLICANT: Goldstein, Neil I.
;   TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
                          Endothelial Growth Factor Receptor Antagonist
;   FILE REFERENCE: 11245/46211
;   CURRENT APPLICATION NUMBER: US/10/091,300
;   CURRENT FILING DATE: 2002-03-04

Left column:

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; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 19
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-19

Query Match      75.0%;   Score 276;   DB 15;   Length 375;
Best Local Similarity   86.2%;   Pred. No. 1.1e-83;
Matches 319;   Conservative 0;   Mismatches 45;   Indels 6;   Gaps 1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||||| |||||||||||||||||||||||||||||||||||||||| |||||||||
Db    2 AGGTCCCAGCTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATACTAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||| |||| ||| ||||||||||||||||||||
Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATCAGCTGGGTGCGACAGGCCC 121

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||||||||| |||| ||||
Db  122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy  181 CACAGAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||| |||| |||| |||||||||
Db  182 CACAGAGTTCCAGGGCAGAGTCACTTTACCGCGGACAAATCCACAGTACAGCCTATA 241

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA------G 294
          |||||||||||||| ||||| ||||||||||||||||
Db  242 TGGAGTTGAGCAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGGATACG 301

Qy  295 ATCCCGATTATGTTTGGGGAGGCGACAACTGTTCGACCCTGGGCAGGAACCCTGC 354
          || ||| || |||| |
Db  302 ATTACTATGATAGTAGTAGTGGCTGTGGCGTTCCCCCTTTGACTACTGGGGCCAGGGAACCCTGG 361

Qy  355 TCATCGTCTC 364
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Db  362 TCACCGTCTC 371


RESULT 5
US-09-954-456-789
; Sequence 789, Application US/09954456
; Patent No. US2002011505TA1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
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Right column:

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 789
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-789

Query Match      74.5%;   Score 274;   DB 11;   Length 1599;
Best Local Similarity   85.0%;   Pred. No. 7.5e-83;
Matches 323;   Conservative 0;   Mismatches 45;   Indels 12;   Gaps 1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||| ||| ||||||||||||||||||||||||| ||||||||||||||||||| ||||
Db   93 AGATGCAGGTGTGCAGTCTGGGGCTGAGGTGAAGTAAAGAAGCCTGGGTCCTGGGTGACGGTCT 152

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATACTAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||| ||||| ||| |||||||||||||||||||
Db  153 CCTGCAAGGCATCTGGAGGCACCTTCAGCAACATGGCTATCATCAGCTGGGTGCGACAGGCCC 212

Qy  121 CTTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||||||| ||| ||| |||
Db  213 CTGGACAAGGGCTTGAGTGGATGGGATCATCCCTCTTTTGGTACACCAACCTACT 272

Qy  181 CACAGAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||| |||| |||| |||||||||
Db  273 CACAGAACTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACAGCACAGCCCACA 332

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATC--- 297
          |||||||| ||||||||||||||||| |||| |||| |||| |||| |||||||||
Db  333 TGGAGCTGATCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGACAGATCGCT 392

Qy  298 --------CCGATTATGTTTGGGGAGGCGACAACTGTTCGACCCTGGGGCCAGGGAA 348
                  ||||||||||| |||||||||||||||||||||||||
Db  393 ACAGGCAGGCAAATTTTGACCGGCCGGGGTTGGCTGGTTCGACCCCTGGGGCCAGGGCA 452

Qy  349 CCCTGCTCATCGTCTCCTCA 368
          |||| ||| ||||||
Db  453 CCCTGGTCACCGTCTCCTCA 472


RESULT 6
US-09-954-456-1604
; Sequence 1604, Application US/09954456
; Patent No. US2002011505TA1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 1604
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1604

Query Match             74.5%;  Score 274;  DB 11;  Length 1599;
Best Local Similarity   85.0%;  Pred. No. 7.5e-83;
Matches 323;  Conservative  0;  Mismatches 45;  Indels 12;  Gaps 1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
            || ||||| ||||| ||||| |||||||||||||||||||||||||||||| |||||||
Db     93 AGATGCAGGTGGTGCAGTCTGGGGCTGAGGTAAAGAAGCCTGGGTCCTCGGTGACGGTCT 152

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            |||||||||  ||| ||||||||||||||||| ||| ||||||||||||||||||||||
Db    153 CCTGCAAGGCATCCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC 212

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
            ||||||||||| ||||||||||||| | |||  ||  |  |  |  ||  |||||||||
Db    213 CTGGACAAGGGGCTTGAGTGGATGGGAGGGATCATCCCTATCCCTCTTTTGGTACACCAACCTACT 272

Qy    181 CACAGAAGTTCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
            |||||| |||| ||||||||||| |  ||||||||||||||||||||||||||||||||
Db    273 CACAGAACTTCAGGGCAGAGTCACGATTACCGCGGACAAATCCACAGCACAGCCCACA 332

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCCGTGTATTACTGTGCGAGATC--- 297
            |||||||||||||||| ||||| ||||||||||||||  |||| |||||||||| |
Db    333 TGGAGCTGATCAGCTGAGGATCTGAGGACACGGCCGTGTATTACTGTGCGACAGATCGCT 392

Qy    298 ----------CCGATTATGTTTGGGGACGGCGACAACTGGTTCGACCCCCTGGGGCAGGGAA 348
                    |||   |: ||||||| |||| |||||||||||||||||||||||||||
Db    393 ACAGGCAGCAAATTTGACCGGCGCCCGGGGTTGCCTGGTTCGACCCCCTGGGGGGCCAGGCA 452

Qy    349 CCCTGCTCATCGTCTCCTCA 368
            ||||| |||||||||||||
Db    453 CCCTGGTCACCGTCTCCTCA 472
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RESULT 7
US-10-047-542-61
; Sequence 61, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION:  AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-047-542-61

Query Match             74.0%;  Score 272.2;  DB 15;  Length 1884;
Best Local Similarity   95.6%;  Pred. No. 3.2e-82;
Matches 280;  Conservative  0;  Mismatches 13;  Indels 0;  Gaps 0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCT 26
            ||||||||||||||||||||||||||
Db     59 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT ...

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            ||||||||||| |||||||||||||| | |||  ...
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                Db    119 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCAGTATGCTATCAGCTGGGTGCGACAGGCCC 178

                Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                           |||||||||| ||||||||||||| | |||  || |  | || |  |||||||||
                Db    179 CTGGACAAGGGCTTGAGTGGATGGGATGGGATCATCCCTATCCTTGGTACAGCAAACTACG 238

                Qy    181 CACAGAAGTTCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                           |||||| |||| ||||||||||| |  ||||||||||||||||||||||||||||||||
                Db    239 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACAGCACAGCCTACA 298

                Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCCGTGTATTACTGTGCGAGA 293
                           |||||||||||||||| ||||| |||||||||||||| ||||||||||||||
                Db    299 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAAA 351
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RESULT 8
US-10-047-542-46
; Sequence 46, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION:  AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 2213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-047-542-46

Query Match             74.0%;  Score 272.2;  DB 15;  Length 2213;
Best Local Similarity   95.6%;  Pred. No. 3.4e-82;
Matches 280;  Conservative  0;  Mismatches 13;  Indels 0;  Gaps 0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    131 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 190

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            ||||||||||| |||||||||||||| | |||  || |  | |||||||||||||||||
Db    191 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCAGTATGCTATCAGCTGGGTGCGACAGGCC 250

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
            ||||||||||| ||||||||||||| | |||  || |  | |  ||  |||||||||
Db    251 CTGGACAAGGGCTTGAGTGGATGGGATGGGATCATCCCTATCCTTGGTACAGCAAACTACG 310

Qy    181 CACAGAAGTTCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
            |||||| |||| ||||||||||| |  ||||||||||||||||||||||||||||||||
Db    311 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAATCCACAGCACAGCCTACA 370

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCCGTGTATTACTGTGCGAGA 293
            |||||||||||||||| ||||| |||||||||||||| ||||||||||||||
Db    371 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAAA 423
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RESULT 9
US-10-151-882-3
; Sequence 3, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
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;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
;
;   SEQ ID NO 3
;   LENGTH: 735
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A004G02 scFv
US-10-151-882-3

  Query Match        72.8%;  Score 268;  DB 15;  Length 735;
  Best Local Similarity  94.9%;  Pred. No. 6.6e-81;
  Matches 277;  Conservative 0;  Mismatches 15;  Indels 0;  Gaps 0;

Qy       1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAGGTCT 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy      61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
           |||||||||||||||||||||||||||  |||||||||  ||||||||||||||||||||
Db      62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATGCTATCCAGTGGGTGCGACAGGCCC 121

Qy     121 CTGGACAAGGGCTTGAGTGGATGGGAGGAAGGATCATGCCTATCCTATCCTTGGACTAGCTAGCAAATTACG 180
           |||||||||||||||| ||||||| |||| |||||||||||||||  || ||||||||||||||||||||||
Db     122 CTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCTATCCTATCCTTGGTACAGCAAACTACG 181

Qy     181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCACGAGCACAGCCTACA 240
           |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db     182 CACAGAAGTTCAGGGCAGAGTCACGATTACCGCGGACAATCACGAGCACAGCCTATA 241

Qy     241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCAG 292
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCAG 293
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RESULT 10
US-10-151-882-10
; Sequence 10, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;   FILE REFERENCE: PF554
;   CURRENT APPLICATION NUMBER: US/10/151,882
;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
;
;   SEQ ID NO 10
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A027B01 scFv
US-10-151-882-10

  Query Match        72.7%;  Score 267.6;  DB 15;  Length 720;
  Best Local Similarity  85.9%;  Pred. No. 9e-81;
  Matches 316;  Conservative 0;  Mismatches 34;  Indels 18;  Gaps 1;

Qy       1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAGGTCT 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 AGGTGCAGCTGTTGCAGTCTGCGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy      61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
           ||||||||||||| ||||||||||||||||||||| | |||||||| ||||||||||||||
Db      62 CCTGCAAGGACTTCTGGAGGCACCTTCAGTAGTTATACTATCAGTGTATCATGTGGGTGCGACAGGCCC 121

Qy     121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db     122 CTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCTATCCTATCCTATGTTTGGTACAGCAGCAAACTACG 181

Qy     181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCACGAGCACAGCCTACA 240
           |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db     182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGGACAAATCACGAGCACAGCCTACA 241

Qy     241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCAGGATCCCG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db     242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGA-------- 292

Qy     301 ATTATGTTTGGGGAGGACGACAACTGGTTCGACCCTGGGGCCAGGGAACCCTGCTCATCG 360
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Db     293 --------GGGGGATATCGGCTGGTATGGACGTCTCGGGCCCAGGGAACCCTGGTCACCG 343

Qy     361 TCTCCTCA 368
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Db     344 TCTCCTCA 351
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RESULT 11
US-09-811-737-12
; Sequence 12, Application US/09811737
; Patent No. US2002009180A1
; GENERAL INFORMATION:
;   APPLICANT: Boehringer Ingelheim Pharma KG
;   TITLE OF INVENTION: Human FAP-alpha-specific antibodies
;   FILE REFERENCE: 1-1129
;   CURRENT APPLICATION NUMBER: US/09/811,737
;   CURRENT FILING DATE: 2001-03-19
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: PatentIn Ver. 2.1
;
;   SEQ ID NO 12
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Humanised Antibody
US-09-811-737-12

  Query Match        72.1%;  Score 265.4;  DB 10;  Length 396;
  Best Local Similarity  84.1%;  Pred. No. 4.3e-80;
  Matches 312;  Conservative 0;  Mismatches 56;  Indels 3;  Gaps 1;

Qy       1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAGGTCT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db       2 AGGTACAGCTGCAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy      61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
           |||||||||||||||||||||||||| ||||||||  |||||| |||||||||||||||||
Db      62 CCTGCAAGGCTTCTGGAGGCACCTTCGAGGCACCATATCAAACTATCAACTGGGTGCGACAGGCCC 121

Qy     121 CTGGACAAGGGCTTGAGTGGATGGGAGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
           ||||||||||||||||||||||| ||| |||||||||||||  || |||||||||||||||||
Db     122 CTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCTATCCTATGTTTGGTACAGCAGCAAACTACG 181

Qy     181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCACGAGCACAGCCTACA 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 CACAGAAGTTCCAGGAGTCACAATTACCGCGGACAAATCACGAGCACAGCCTACA 241

Qy     241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGC---GAGATC 297
           ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||
Db     242 TGGAGATGAGCAGCCTGAGATCTGAGGACACGGCCATGTATGACTACTGGGGTCAAGGAACCCTGGTCA 301

Qy     298 CCGATTATGTTTGGGGAGGACGACAACTGGTTCGACCCTGGGGCCAGGGAACCCTGCTCA 357
                                                                  |||||| |||
Db     302 TCGGCTACGGTTACGACGAGGGCCATCGTGACTACTGGGGTCAAGGAACCCTTGTCA 361

Qy     358 TCGTCTCCTCA 368
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Db     362 CCGTCTCCTCA 372
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RESULT 12
US-09-811-737-22
; Sequence 22, Application US/09811737
; Patent No.US2002009180A1
; GENERAL INFORMATION:
;   APPLICANT: Boehringer Ingelheim Pharma KG
;   TITLE OF INVENTION: Human FAP-alpha-specific antibodies
;   FILE REFERENCE: 1-1129
;   CURRENT APPLICATION NUMBER: US/09/811,737
;   CURRENT FILING DATE: 2001-03-19
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Humanised Antibody
US-09-811-737-22

Query Match    72.1%;  Score 265.4;  DB 10;  Length 782;
Best Local Similarity    84.1%;  Pred. No. 5.2e-80;
Matches  312;  Conservative   0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
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Db      2 AGGTACAGCTGCGCAGTCAGGGGCTGGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  61

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
          ||||||||| ||||||||||||||||||  ||| |||||||| |||||||||||||||||
Db     62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATACTATCAACTGGGTGCGACAGGCCC  121

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGGGCTATTACTCCGGACTAGCAAATTACG  180
          ||||||||||||||||||||||||  || |||| |||| |||||  ||||||||||||||
Db    122 CTGGACACAGGGCTTGAGTGGATGGGAGGGATCATCCGGGCTATTACGTTGGTACAGCAAACTACG  181

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGACAAATCCACGAGCACAGCCTACA  240
          ||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db    182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGCAAATCCACGAGCACAGCCCACA  241

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGATC---GAGAGATC  297
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||   |||||||||
Db    242 TGGAGATGAGCAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCAAGGAACCCTGTCA  301

Qy    298 CCGATTATGTTTGGGGAGGCGACAACCTGTTCCACCCCTGGGGCCAGGGAACCCTGCTCA  357
          ||   ||| |||  ||||||||||  ||||  || |||||||||||||||||||||||
Db    302 TCGCGTACGGTTACGACGAGGGGCCATGCTATATGACTATGGACTACTGGGGTCAAGGAACCCCTGTCA  361

Qy    358 TCGTTCTCCTCA  368
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Db    362 CCGTCTCCTCA  372

RESULT 13
US-10-151-882-11
; Sequence 11, Application US/10151882
; Publication No.US20030059862A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;   FILE REFERENCE: PF554
;   CURRENT APPLICATION NUMBER: US/10/151,882
;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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(second column)

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;   FEATURE:
;   OTHER INFORMATION: DNA encoding A027H08 scFv
US-10-151-882-11

Query Match    71.6%;  Score 263.6;  DB 15;  Length 717;
Best Local Similarity    93.5%;  Pred. No. 2.1e-79;
Matches  275;  Conservative   0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
          ||||| |||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      2 AGGTACAGCTGCGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  61

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
          ||||||||||||||||||||||||||||  ||| |||||||| ||||||||||||||||
Db     62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATCAGCTATCAGCTGGGTGCGACAGACCC  121

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGGGCTATCCTTGGACTAGCAAATTACG  180
          |||||||||||||||||||||||||  || |||||||||| |||| |||||||||||||
Db    122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTCAGCAAACTACG  181

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGACAAATCCACGAGCACAGCCTACA  240
          ||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||
Db    182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGCAAATCCACGAGCACAGCCCACA  241

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG  294
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGAG  295

RESULT 14
US-10-151-882-7
; Sequence 7, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;   FILE REFERENCE: PF554
;   CURRENT APPLICATION NUMBER: US/10/151,882
;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A053H04 scFv
US-10-151-882-7

Query Match    71.6%;  Score 263.6;  DB 15;  Length 744;
Best Local Similarity    93.5%;  Pred. No. 2.1e-79;
Matches  275;  Conservative   0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
          ||||| |||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      2 AAGTGCAGCTGCGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  61

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
          |||||||||||||||||||||||||||||  ||| |||||||| |||||||||||||||
Db     62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC  121

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGGGCTATCCTTGGACTAGCAAATTACG  180
          |||||||||||||||||||||||||  || ||||||| |||| |||| ||||||||||||
Db    122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCTCTCTTGACACACCTAACTACG  181

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGACAAATCCACGAGCACAGCCTACA  240
          ||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||
Db    182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGCAAATCCACGAGCACAGCCCACA  241

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG  294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGACACGGCCGTCTATTACTGTGCGAGAG 295

RESULT 15
US-10-151-882-5
; Sequence 5, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;   FILE REFERENCE: PF554
;   CURRENT APPLICATION NUMBER: US/10/151,882
;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A034G03 scFv
US-10-151-882-5

Query Match   71.4%; Score 262.8; DB 15; Length 744;
Best Local Similarity   85.2%; Pred. No. 3.9e-79;
Matches 310; Conservative   0; Mismatches   42; Indels 12; Gaps   1;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          |||| |||||| ||||||||| ||||||||||||||||| |||||||||||| ||||||||
Db   2 AGGTACAGCTGCGAGCAGTCAGGGGCTCAGGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCCC 120
          |||||||||||| |||||||||||||||||| ||||||| |||||||||||||||||||||
Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCCC 121

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          |||||||||||||||||||||||| ||||||||| || ||| |||| | | ||||
Db   122 CTGGACAAGGGCTTGAGTGGATGGGAGGGGATCATCCCTCTCTTTGACACCACCTAACTACG 181

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||||
Db   182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||| ||||
Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGACACGGCCGTCTATTACTGTGCGAGAGGAAATA 301

Qy   301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGCCAGGGAACCCTGCTCATCG 360
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Db   302 CT--------GGCCCGAGACCCTTCGACCCCTGGGGCCAAGGGCACCCCTGGTCACCG 349

Qy   361 TCTC 364
          ||||
Db   350 TCTC 353

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            GenCore version 5.1.6
       Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    July 18, 2003, 09:26:19 ; Search time 19.5137 Seconds
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Title:           US-09-627-896B-29
Perfect score:   368
Sequence:        1 aggtgcagctggtgcagtct........cctgctcatcgctcctcca 368

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters:     882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	293.2	79.7	2287	1	US-08-480-036-1	Sequence 1, Appli
2	293.2	79.7	2287	1	US-08-461-968A-1	Sequence 1, Appli
3	293.2	79.7	2287	2	US-08-462-571-1	Sequence 1, Appli
4	293.2	79.7	2287	5	PCT-US96-10043-8	Sequence 8, Appli
5	282.4	76.7	369	2	US-08-652-816A-46	Sequence 46, Appl
6	280.8	76.3	369	2	US-08-652-816A-44	Sequence 44, Appl
7	280.8	76.3	812	1	US-07-834-533A-53	Sequence 53, Appl
8	280.8	76.3	812	2	US-08-800-353-53	Sequence 53, Appl
9	280.8	76.3	812	4	US-09-042-353-231	Sequence 231, App
10	280.8	76.3	812	5	US-08-758-417A-79	Sequence 79, Appl
11	280.8	76.3	812	5	PCT-US92-06185-53	Sequence 53, Appl
12	280.8	76.3	813	1	US-08-053-131-61	Sequence 61, Appl
13	280.8	76.3	813	1	US-08-645-641-61	Sequence 61, Appl
14	280.8	76.3	813	1	US-07-853-408B-61	Sequence 61, Appl
15	280.8	76.3	813	1	US-08-096-762-61	Sequence 61, Appl
16	280.8	76.3	813	1	US-08-308-865-61	Sequence 61, Appl
17	280.8	76.3	813	5	PCT-US92-10983-61	Sequence 61, Appl
18	279.2	75.9	369	2	US-08-652-816A-45	Sequence 45, Appl
19	277.6	75.4	369	2	US-08-652-816A-47	Sequence 47, Appl
20	272.8	74.1	369	2	US-08-652-816A-25	Sequence 25, Appl
21	272.4	74.0	1617	2	US-08-378-939-9	Sequence 9, Appli
22	250.4	68.0	4691	4	US-08-591-632-43	Sequence 43, Appl
23	250.4	68.0	4691	4	US-08-611-451-43	Sequence 43, Appl
24	250.4	68.0	6166	4	US-08-591-632-51	Sequence 51, Appl
25	250.4	68.0	6166	4	US-09-611-451-51	Sequence 51, Appl
26	250.2	68.0	441	4	US-08-217-918-3	Sequence 3, Appli
27	248	67.4	687	1	US-08-300-386A-1	Sequence 1, Appli
28	248	67.4	687	3	US-08-931-645-1	Sequence 1, Appli
29	248	67.4	687	5	PCT-US94-01258-1	Sequence 1, Appli
30	248	67.4	687	5	PCT-US95-11235-1	Sequence 1, Appli
31	243.6	66.2	363	1	US-08-264-093-1	Sequence 8, Appli
32	236.4	64.2	564	3	US-08-545-809A-8	Sequence 18, Appl
33	236	64.1	539	3	US-08-545-809A-18	Sequence 46, App
34	234.4	63.7	799	3	US-08-545-809A-46	Sequence 146, App
35	233.2	63.4	246	4	US-09-042-353-146	Sequence 410, App
36	233.2	63.4	246	4	US-08-758-417A-410	Sequence 26, Appl
37	232.8	63.3	936	3	US-09-049-672A-26	Sequence 2, Appli
38	231.2	62.8	512	5	US-08-545-809A-2	Sequence 85, Appl
39	230	62.5	395	1	US-08-482-882-85	Sequence 85, Appl
40	230	62.5	395	1	US-08-483-388-85	Sequence 85, Appl
41	230	62.5	395	2	US-08-487-113D-85	Sequence 85, Appl
42	230	62.5	395	2	US-08-473-503-85	Sequence 85, Appl
43	230	62.5	395	2	US-08-483-932-85	Sequence 85, Appl
44	230	62.5	395	2	US-08-720-420A-85	Sequence 85, Appl
45	230	62.5	395	3	US-08-714-017-85	Sequence 85, Appl

ALIGNMENTS

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RESULT 1
US-08-480-036-1
; Sequence 1, Application US/0480036
; Patent No. 5723583
; GENERAL INFORMATION:
;  APPLICANT: Seed, Brian et al.
;  TITLE OF INVENTION: INHIBITION OF CELL ADHESION
;  TITLE OF INVENTION: PROTEIN-CARBOHYDRATE
;  TITLE OF INVENTION: INTERACTIONS
;  NUMBER OF SEQUENCES: 4
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: U.S.A.
;   ZIP: 02110-2804
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   COMPUTER: IBM PS/2 Model 50Z or 55SX
;   OPERATING SYSTEM: IBM P.C. DOS (Version 5.00)
;   SOFTWARE: WordPerfect (Version 5.1)
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/480,036
;   FILING DATE:
;   CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/618,314C
;   FILING DATE: No. 5723583ember 23, 1990
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Clark, Paul T.
;   REGISTRATION NUMBER: 30,162
;   REFERENCE/DOCKET NUMBER: 00786/067001
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 542-5070
;   TELEFAX: (617) 542-8906
;   TELEX: 200154
;  INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 2287
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
US-08-480-036-1

  Query Match             79.7%;   Score 293.2;  DB 1;  Length 2287;
  Best Local Similarity   88.2%;   Pred. No. 7.4e-83;
  Matches  335;  Conservative   0;  Mismatches  33;  Indels  12;  Gaps  1;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Best Local Similarity 88.2%; Pred. No. 7.4e-83;
Matches 335; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

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Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
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Db   74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  133

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
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Db  134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATATACATCAGCTGGGTGCCACAGGCCC  193

Qy  121 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCTTGGACTAGCAAATTACG  180
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Db  194 CTGGACAAGGGCTTGAGTGGATGGAGGATCATCCCTATCTTTGGTACAGCAAACTACG  253

Qy  181 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA  240
        |||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db  254 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACAATCCACGAGCACAGCCTACA  313

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG  373

Qy  301 -----------ATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA  348
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Db  374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA  433

Qy  349 CCCTGCTCATCGTCTCCTCA  368
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Db  434 CCCTGGTCACCGTCTCTTCA  453
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RESULT 3
US-08-462-571-1
; Sequence 1, Application US/08462571
; Patent No. 5858983
; GENERAL INFORMATION:
;   APPLICANT: Seed, Brian et al.
;   TITLE OF INVENTION: INHIBITION OF CELL ADHESION
;   TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: U.S.A.
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   COMPUTER: IBM PS/2 Model 50Z or 55SX
;   OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
;   SOFTWARE: WordPerfect (Version 5.0)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/462,571
;   FILING DATE: 05 June 1995
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/618,314
;   FILING DATE: 23 No. 5858983ember 1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lech, Karen F.
;   REGISTRATION NUMBER: 35,238
;   REFERENCE/DOCKET NUMBER: 00786/067002
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 542-5070
;   TELEFAX: (617) 542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2287
;   TYPE: nucleic acid
;   STRANDEDNESS: single

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Db   74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  133

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
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Db  134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATATACATCAGCTGGGTGCCACAGGCCC  193

Qy  121 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATCTTGGACTAGCAAATTACG  180
        ||||||||||||||||||||||||| |||||||  |||||||  ||| ||||| |||||
Db  194 CTGGACAAGGGCTTGAGTGGATGGAGGATCATCCCTATCTTTGGTACAGCAAACTACG  253

Qy  181 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA  240
        |||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db  254 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACAATCCACGAGCACAGCCTACA  313

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG  373

Qy  301 -----------ATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA  348
                   ||  |||| |||||||
Db  374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA  433

Qy  349 CCCTGCTCATCGTCTCCTCA  368
        |||||  |||||||| ||||
Db  434 CCCTGGTCACCGTCTCTTCA  453
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RESULT 2
US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
; GENERAL INFORMATION:
;   APPLICANT: Seed et al., Brian
;   TITLE OF INVENTION: INHIBITION OF CELL ADHESION
;   TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 0210-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/461,968A
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/618,314
;   FILING DATE: 23-NOV-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lech, Karen F.
;   REGISTRATION NUMBER: 35,238
;   REFERENCE/DOCKET NUMBER: 00786/067003
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2287
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-461-968A-1

Query Match 79.7%; Score 293.2; DB 1; Length 2287;

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;    TOPOLOGY: linear
US-08-462-571-1
;
Query Match          79.7%;   Score 293.2;   DB 2;   Length 2287;
Best Local Similarity  88.2%;   Pred. No. 7.4e-83;
Matches 335;   Conservative   0;   Mismatches 33;   Indels 12;   Gaps   1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTATATCATCAGCTGGTGCCGACAGGCCC 120
          |||||||||||||||||||||||||| |||||| |||||||||||||||||||||||||
Db  134 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTATCAGCTGTATCAGCTGGTGCCGACAGGCCC 193

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGTACAGCAAATTACG 180
          ||||||||||||||||||||||||||||| ||||| ||||||||||||| ||||||||||
Db  194 CTGGACAAGGGCTTGAGTGGATGGGGATCATCCCTATCATCTTTGGTACAGCAAACTACG 253

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||
Db  254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy  301 --------ATTATGTTTGGGGAGCGCAAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                  ||||||| ||||||||||||||| ||| |||||| ||||||||||||||||
Db  374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCCGGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy  349 CCCTGCTCATCGTCTCCTCA 368
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Db  434 CCCTGGTCACCGTCTCTTCA 453

RESULT 4
PCT-US96-10043-8
; Sequence 8, Application PC/TUS9610043
; GENERAL INFORMATION:
;   APPLICANT: The General Hospital Corporation
;   TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
;   TITLE OF INVENTION: AND METHODS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02210-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30.
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US96/10043
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/000,213
;     FILING DATE: 14-JUN-1995
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Lech, Karen F.
;     REGISTRATION NUMBER:
;     REFERENCE/DOCKET NUMBER: 00786/284001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617/542-5070
;     TELEFAX: 617/542-8906
;     TELEX: 200154
; INFORMATION FOR SEQ ID NO:   8:
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;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 2287 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;    MOLECULE TYPE: DNA (genomic)
PCT-US96-10043-8

Query Match          79.7%;   Score 293.2;   DB 5;   Length 2287;
Best Local Similarity  88.2%;   Pred. No. 7.4e-83;
Matches 335;   Conservative   0;   Mismatches 33;   Indels 12;   Gaps   1;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGTGGTGCCGACAGGCCC 120
          ||||||||||||||||||||||||||| ||||| |||| ||||||||||||||||||||||
Db  134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATCAGCTATCAGCTGGTGCCGACAGGCCC 193

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||| ||||| ||| ||||||||||||||||||||
Db  194 CTGGACAAGGGCTTGAGTGGATGGGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy  301 --------ATTATGTTTGGGGAGCCGCAAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                  |||||||| |||||||||||| ||||| ||||||| ||||||||||||||||
Db  374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCCGGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy  349 CCCTGCTCATCGTCTCCTCA 368
          |||||| ||| |||||||||
Db  434 CCCTGGTCACCGTCTCTTCA 453

RESULT 5
US-08-652-816A-46
; Sequence 46, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
;   APPLICANT: Osbourn, JK
;   APPLICANT: Allen, DJ
;   APPLICANT: McCafferty, JG
;   TITLE OF INVENTION: Specific binding members, materials and
;   TITLE OF INVENTION: methods.
;   NUMBER OF SEQUENCES: 53
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;     STREET: 6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: United States of America
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/652,816A
;     FILING DATE: 23-MAY-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9125579.4
;     FILING DATE: 02-DEC-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9125579.8
;     FILING DATE: 02-DEC-1991
;   PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-816A-46

Query Match   76.7%;   Score 282.4; DB 2;   Length 369;
Best Local Similarity 86.0%;   Pred. No. 9.4e-80;
Matches   313; Conservative   0; Mismatches   51; Indels   0; Gaps   0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2 AGGTTCAGCTGGTTCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTCTCCTATCAACTCTTGGGTGCGACAGGCCC 121

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          | |||||||||||||||||||| ||||| ||||||| || |||||||||||||||| ||||
Db   122 CCGGACAAGGGCTTGAGTGGATGGGAAGTATCATCCCTTGGTACAGCAAACTACG 181

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||| | |||||||||||||||| | | |||||||||||||
Db   182 CTCAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAATCCACGAGCACAGCCTACA 241

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACATAATC 301

Qy   301 ATTATGTTTGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
          ||||| | | | ||||| |||||||||||||||||||||||||||||||||||||||||
Db   302 ATAATTATGAGCTTTACTACTACTACATGGACGTCTGGGGCCAAGGGACCACGGTCACCG 361

Qy   361 TCTC 364
          ||||
Db   362 TCTC 365

RESULT 6
US-08-652-816A-44
; Sequence 44, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and

; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-816A-44

Query Match   76.3%;   Score 280.8; DB 2;   Length 369;
Best Local Similarity 85.7%;   Pred. No. 3e-79;
Matches   312; Conservative   0; Mismatches   52; Indels   0; Gaps   0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2 AGGTTCAGCTGGTTCAGTCTGGGGCTGAGGTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTCTCCTATCAACTGGGTGCGACAGGCCC 121

Qy   121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
          | |||||||||||||||||||| ||||| | |||||| | ||||||||||||||| ||||
Db   122 CCGGACAAGGGCTTGAGTGGATGGGAAGTATCATCATCCCTCCTTTGGTACAGCAAACTACG 181

Qy   181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA 240
          |||||||||||||||||||||| | |||||||||||| | | | |||||||||||||||
Db   182 CTCAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Db   445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGTGCGACAGGCCC 504

Qy   121 CTTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTATAGCTGGACTAGCAAATTACG 180
          ||||||||||||||||||||||||||||||||||| |||||||| |||||||||||
Db   505 CTTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy   181 CACAGAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCAGCACAGCCTACA 240
          ||||||||||||||||| |||||||||| |||| |||||| ||||||||
Db   565 CACAGAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 624

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGCGGAGAGATCCCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGCGGAGAGACACAG 684

RESULT 8
US-08-800-353-53
; Sequence 53, Application US/08800353
; Patent No. 5874299
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils
;   APPLICANT: Kay, Robert M.
;   TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
;   TITLE OF INVENTION: Producing Heterologous Antibodies
;   NUMBER OF SEQUENCES: 77
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: William M. Smith
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/800,353
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/834,539
;   FILING DATE: 1992-02-05
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William M.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 14643-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 812 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: Exon
;   LOCATION: 241..335
;   OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
;   FEATURE:
;   NAME/KEY: Exon
;   LOCATION: 372..677
;   OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
US-08-800-353-53

Query Match   76.3%; Score 280.8; DB 2; Length 812;
Best Local Similarity   96.0%; Pred. No. 4e-79;
Matches 288; Conservative   0; Mismatches   12; Indels   0; Gaps   0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

Qy   241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGCGGAGAGATCCCG 300
          ||||||||||||||||||||||||| |||||||||||||||||||||||||-|-
Db   242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCCGTGTATTACTGTGCGGGATGTTCTC 301

Qy   301 ATTATGTTGGGGGAGCGACAACTGGTTCGACCCTGGGCCAGGGAACCCTGCTCATCG 360
          |||||| ||| |||| ||||||||||||||||||||||||||||| |||||||
Db   302 ATAATTATGAGCTTTACTACTACTACATGGACGTCTGGGGCCAAGGGACAATGGTCACCG 361

Qy   361 TCTC 364
          ||||
Db   362 TCTC 365

RESULT 7
US-07-834-539A-53
; Sequence 53, Application US/07834539A
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils
;   APPLICANT: Kay, Robert M.
;   TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
;   TITLE OF INVENTION: Producing Heterologous Antibodies
;   NUMBER OF SEQUENCES: 77
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: William M. Smith
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/834,539A
;   FILING DATE: 1992-02-05
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William M.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 14643-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 812 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: Exon
;   LOCATION: 241..335
;   OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
;   FEATURE:
;   NAME/KEY: Exon
;   LOCATION: 372..677
;   OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
US-07-834-539A-53

Query Match   76.3%; Score 280.8; DB 1; Length 812;
Best Local Similarity   96.0%; Pred. No. 4e-79;
Matches 288; Conservative   0; Mismatches   12; Indels   0; Gaps   0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTCAAGGTCT 444

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATACTATCATCAGCTGGTGCGACAGGCCC 120
           |||||||||||||||||||||||||||| || |||||| ||||||||||||||||||

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Db  385 AGGTCCAGCCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444
            |||||  ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||
Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            ||||||||||||||||||||||||||||  ||  || ||||||||||||||||||||||||
Db  445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGACTAGCAAATTACG 180
            ||||||||||||||||||||||||||||||||||  ||||||  ||| || ||||| ||||
Db  505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCCTGGTATAGCAAACTACG 564
Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624
Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db  625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
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RESULT 9
US-09-042-353-231
; Sequence 231, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils
;   APPLICANT: Kay, Robert M.
;   TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
;   TITLE OF INVENTION: Producing Heterologous Antibodies
;   NUMBER OF SEQUENCES: 421
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/042,353
;   FILING DATE: 13-MAR-1998
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/810,279
;   FILING DATE: 17-DEC-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/853,408
;   FILING DATE: 18-MAR-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/904,068
;   FILING DATE: 23-JUN-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/990,860
;   FILING DATE: 16-DEC-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/053,131
;   FILING DATE: 26-APR-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/096,762
;   FILING DATE: 22-JUL-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/155,301
;   FILING DATE: 18-NOV-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/161,739
;   FILING DATE: 03-DEC-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/165,699
;   FILING DATE: 10-DEC-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/209,741
;   FILING DATE: 09-MAR-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/352,322
;   FILING DATE: 07-DEC-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/544,404
;   FILING DATE: 10-OCT-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/728,463
;   FILING DATE: 10-OCT-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US96/16433
;   FILING DATE: 10-OCT-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/758,417
;   FILING DATE: 02-DEC-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US97/21803
;   FILING DATE: 01-DEC-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 014643-009040US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 231:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 812 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: join(241..286, 373..677)
;   OTHER INFORMATION: /product= "human V-HI family
;   OTHER INFORMATION: gene V-H49.8"
US-09-042-353-231

Query Match   76.3%; Score 280.8; DB 4; Length 812;
Best Local Similarity 96.0%; Pred. No. 4e-79;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  60
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Db  385 AGGTCCAGCCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444
Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
            ||||||||||||||||||||||||||||  ||  || ||||||||||||||||||||||||
Db  445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGACTAGCAAATTACG 180
            ||||||||||||||||||||||||||||||||||  ||||||  ||| || ||||| ||||
Db  505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCCTGGTATAGCAAACTACG 564
Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624
Qy  241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db  625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
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RESULT 10
US-08-758-417A-79
; Sequence 79, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils

Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                    Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/758,417A
    FILING DATE: 02-Dec-1996
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/728,463
    FILING DATE: 10-OCT-1996
    APPLICATION NUMBER: US 08/544,404
    FILING DATE: 10-OCT-1995
    APPLICATION NUMBER: US 08/352,322
    FILING DATE: 07-DEC-1994
    APPLICATION NUMBER: US 08/209,741
    FILING DATE: 09-MAR-1994
    APPLICATION NUMBER: US 08/165,699
    FILING DATE: 10-DEC-1993
    APPLICATION NUMBER: US 08/161,739
    FILING DATE: 03-DEC-1993
    APPLICATION NUMBER: US 08/155,301
    FILING DATE: 18-NOV-1993
    APPLICATION NUMBER: US 08/096,762
    FILING DATE: 22-JUL-1993
    APPLICATION NUMBER: US 08/053,131
    FILING DATE: 26-APR-1993
    APPLICATION NUMBER: US 07/990,860
    FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
    NAME: Serafini, Andrew T.
    REGISTRATION NUMBER: 41,303
    REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 79:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 812 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
    NAME/KEY: CDS
    LOCATION: join(241..286, 373..677)
    OTHER INFORMATION: /note= "human V-HI family gene V-H49.8"
    SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-08-758-417A-79

Query Match   76.3%; Score 280.8; DB 4; Length 812;
Best Local Similarity   96.0%; Pred. No. 4e-79; Indels 0; Gaps 0;
Matches 288; Conservative   0; Mismatches 12; Indels 0; Gaps 0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db 385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
         |||||||||||||||||||||||||||||| ||||||||||||||
Db 445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTGTCATCAGCTGGGTGCGACAGGCCC 504

Qy 121 CTGGACAAGGGGCTTGAGTGGATGGGAAGGATCATGCATGCCTATCCTTGGACTAGCAAATTACG 180
         ||||||||||||||||||||||||||||||||||| ||||||||||| ||||| || ||
Db 505 CTGGACAAGGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy 181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGGGACAAATCCACGAGCACAGCCTACA 624

Qy 241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGACGGCCGTGTATTACTGTGCGGAGAGATCCCG 300
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| || |
Db 625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGAGACACAG 684

RESULT 11
PCT-US92-06185-53
; Sequence 53, Application PC/TUS9206185
; GENERAL INFORMATION:
;   APPLICANT: Lonberg, Nils
;   APPLICANT: Kay, Robert M.
;   TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
;   TITLE OF INVENTION: Producing Heterologous Antibodies
;   NUMBER OF SEQUENCES: 75
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: William M. Smith
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/06185
;   FILING DATE: 19910828
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William M.
;   REGISTRATION NUMBER: 87654
;   REFERENCE/DOCKET NUMBER: 14643-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 812 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: Exon
;   LOCATION: 241..335
;   OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
;   FEATURE:
;   NAME/KEY: Exon
;   LOCATION: 372..677
;   OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
PCT-US92-06185-53

Query Match   76.3%; Score 280.8; DB 5; Length 812;
Best Local Similarity   96.0%; Pred. No. 4e-79;
Matches 288; Conservative   0; Mismatches 12; Indels 0; Gaps 0;

Qy   1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db 385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
         |||||||||||||||||||||||||||||| ||||||||||||||

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Best Local Similarity   96.0%;  Pred. No. 4e-79;
Matches   288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
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Db    386 AGGTCCAGCTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  445

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATATATCAGCTGGGTGCGACAGGCCC  120
          |||||||||||||||||||||||||||| ||  |||| | ||||||||||||||||||||
Db    446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTATCAGCTGGGTGCGACAGGCCC  505

Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
          ||||||||||||||||||||||||||| ||||||| ||||| ||||| | |||||| |||
Db    506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCCTTGGTATAGCAAACTACG  565

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA  625

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    626 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  685
```

RESULT 13
US-08-645-641-61
; Sequence 61, Application US/0864541
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..285
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..678

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Db    445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTATGCTATCAGCTGGGTGCGACAGGCCC  504
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Qy    121 CTGGACAAGGGCTTGAGTGGATGGGAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
          |||||||||||||||||||||||||| ||||||| ||||| ||||| | |||||| |||
Db    505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCCTGGTATAGCAAACTACG  564

Qy    181 CACAGAAGTTCCAGGGCCGCGACAGATTACCGCGACAAATCCACGAGCACAGCCTACA  240
          ||||||||||||||||||     ||||||||||||||||||||||||||||||||||||
Db    565 CACAGAAGTTCCAGGGCCAGAGTCACGATTACCGCGACAAATCCACGAGCACAGCCTACA  624

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  684
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RESULT 12
US-08-053-131-61
; Sequence 61, Application US/08053131
; Patent No. 5561016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5561016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..285
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..678
US-08-053-131-61

Query Match   76.3%; Score 280.8; DB 1; Length 813;

US-08-645-641-61

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Query Match            76.3%;  Score 280.8;  DB 1;  Length 813;
Best Local Similarity  96.0%;  Pred. No. 4e-79;
Matches 288;  Conservative  0;  Mismatches 12;  Indels  0;  Gaps  0;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  445

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
        ||||||||||||||||||||||||||||| || || ||||||||||||||||||||||||
Db  446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTGGGTGCGACAGGCCC          505

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
        ||||||||||||||||||||||||||||||| |||||||||||| |||||||||| ||||
Db  506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG  565

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA  625

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGTATTACTGTGCGAGAGATCCCG                300
        |||||||||||||||||||||||| |||||||||||||||||||
Db  626 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  685
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RESULT 14
US-07-853-408B-61
; Sequence 61, Application US/07853408B
; Patent No. 5789650
GENERAL INFORMATION:
-; APPLICANT: Lonberg, Nils
-; APPLICANT: Kay, Robert M.
-; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
-; TITLE OF INVENTION: Producing Heterologous Antibodies
-; NUMBER OF SEQUENCES: 150
-; CORRESPONDENCE ADDRESS:
-;   ADDRESSEE: William M. Smith
-;   STREET: One Market Plaza, Steuart Tower, Suite 2000
-;   CITY: San Francisco
-;   STATE: California
-;   COUNTRY: USA
-;   ZIP: 94105
-; COMPUTER READABLE FORM:
-;   MEDIUM TYPE: Floppy disk
-;   COMPUTER: IBM PC compatible
-;   OPERATING SYSTEM: PC-DOS/MS-DOS
-;   SOFTWARE: PatentIn Release #1.0, Version #1.25
-; CURRENT APPLICATION DATA:
-;   APPLICATION NUMBER: US/07/853,408B
-;   FILING DATE: 19920318
-;   CLASSIFICATION: 800
-; ATTORNEY/AGENT INFORMATION:
-;   NAME: Smith, William M.
-;   REGISTRATION NUMBER: 30,223
-;   REFERENCE/DOCKET NUMBER: 14643-9
-; TELECOMMUNICATION INFORMATION:
-;   TELEPHONE: 415-326-2400
-;   TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 61:
-; SEQUENCE CHARACTERISTICS:
-;   LENGTH: 813 base pairs
-;   TYPE: NUCLEIC ACID
-;   STRANDEDNESS: single
-;   TOPOLOGY: linear
-; MOLECULE TYPE: DNA (genomic)
-; FEATURE:
-;   NAME/KEY: CDS
-;   LOCATION: 241..285
-; FEATURE:
-;   NAME/KEY: CDS
-;   LOCATION: 373..678

US-07-853-408B-61

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Query Match            76.3%;  Score 280.8;  DB 1;  Length 813;
Best Local Similarity  96.0%;  Pred. No. 4e-79;
Matches 288;  Conservative  0;  Mismatches 12;  Indels  0;  Gaps  0;

Qy    1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT   60
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  445

Qy   61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
        ||||||||||||||||||||||||||||| || || ||||||||||||||||||||||||
Db  446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCTATCAGCTGGGTGCGACAGGCCC          505

Qy  121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
        ||||||||||||||||||||||||||||||| |||||||||||| |||||||||| ||||
Db  506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG  565

Qy  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCCGCGACAAATCCACGAGCACAGCCTACA  625

Qy  241 TGGAGCTGAGCAGCCTGAGATCTGTATTACTGTGCGAGAGATCCCG                300
        |||||||||||||||||||||||| |||||||||||||||||||
Db  626 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  685
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RESULT 15
US-08-096-762-61
; Sequence 61, Application US/08096762
; Patent No. 5814318
GENERAL INFORMATION:
-; APPLICANT: Lonberg, Nils
-; APPLICANT: Kay, Robert M.
-; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
-; TITLE OF INVENTION: Producing Heterologous Antibodies
-; NUMBER OF SEQUENCES: 210
-; CORRESPONDENCE ADDRESS:
-;   ADDRESSEE: Townsend and Townsend Khourie and Crew
-;   STREET: One Market Plaza, Steuart Tower, Suite 200
-;   CITY: San Francisco
-;   STATE: California
-;   COUNTRY: USA
-;   ZIP: 94105
-; COMPUTER READABLE FORM:
-;   MEDIUM TYPE: Floppy disk
-;   COMPUTER: IBM PC compatible
-;   OPERATING SYSTEM: PC-DOS/MS-DOS
-;   SOFTWARE: PatentIn Release #1.0, Version #1.25
-; CURRENT APPLICATION DATA:
-;   APPLICATION NUMBER: US/08/096,762
-;   FILING DATE: 22-JUL-1993
-;   CLASSIFICATION: 800
-; PRIOR APPLICATION DATA:
-;   APPLICATION NUMBER: US 08/053,131
-;   FILING DATE: 26-APR-1993
-; PRIOR APPLICATION DATA:
-;   APPLICATION NUMBER: US 07/990,860
-;   FILING DATE: 16-DEC-1992
-; PRIOR APPLICATION DATA:
-;   APPLICATION NUMBER: US 07/904,068
-;   FILING DATE: 23-JUN-1992
-; PRIOR APPLICATION DATA:
-;   APPLICATION NUMBER: US 07/853,408
-;   FILING DATE: 18-MAR-1992
-; PRIOR APPLICATION DATA:
-;   APPLICATION NUMBER: US 07/810,279
-;   FILING DATE: 17-DEC-1991
-; ATTORNEY/AGENT INFORMATION:
-;   NAME: Smith, William M.
-;   REGISTRATION NUMBER: 30,223
-;   REFERENCE/DOCKET NUMBER: 14643-9-4
-; TELECOMMUNICATION INFORMATION:

```
;    TELEPHONE:  415-326-2400
;    TELEFAX:    415-326-2422
; INFORMATION FOR SEQ ID NO:    61:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:   813 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  241..285
;    FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  373..678
US-08-096-762-61

Query Match        76.3%;     Score 280.8;  DB 1;  Length 813;
Best Local Similarity   96.0%;     Pred. No. 4e-79;
Matches  288;  Conservative   0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT  60
          |||||||||||||| |||||||||||||||||||||||||||||||| ||||| ||||||
Db    386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT  445

Qy     61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC  120
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
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Qy    121 CTGGACAAGGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG  180
          |||||||||||||||||||||||||||||||| ||||| ||||||| ||||  ||||||||
Db    506 CTGGACAAGGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCCTGGTATAGCAAACTACG  565

Qy    181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA  240
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Db    566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA  625

Qy    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG  300
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Db    626 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG  685
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Search completed: July 18, 2003, 19:59:08
Job time : 20.5137 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 18, 2003, 04:46:48 ; Search time 1002.03 Seconds
(without alignments)
10397.705 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 358
1 gtgcagctggtggagtctgg.........cctggtcaccgtctcctca 358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1455102878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_pln:*
34: em_htg_mus:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	267.4	74.7	357	9	HSVH3H2FG	X70485 H.sapiens D
2	264	73.7	1679	9	BC018747	BC018747 Homo sapi
3	263.8	73.7	351	9	HSVH31328	X62965 H.sapiens r
4	262.6	73.4	420	9	AF174030	AF174030 Homo sapi
5	261	72.9	420	9	AF062138	AF062138 Homo sapi
6	260.6	72.8	351	9	HSA300796	AJ300796 Homo sapi
7	259.4	72.5	409	9	HSE55314	Z14189 H.sapiens r
8	258.4	72.2	363	9	AB067237	AB067237 Homo sapi
9	258.4	72.2	372	9	HSVH3I3RM	X63850 H.sapiens D
10	257.4	71.9	351	9	HSA300786	AJ300786 Homo sapi
11	256.6	71.7	375	6	AX061464	AX061464 Sequence
12	256.2	71.6	348	9	HSU80083	U80083 Human immun
13	256.2	71.6	360	9	HSU76679	U76679 Homo sapien
14	255.4	71.3	354	9	HSA300785	AJ300785 Homo sapi
15	254.8	71.1	372	9	AF062188	AF062188 Homo sapi
16	254.6	71.1	814	6	AX001146	AX001146 Sequence
17	254.2	71.0	351	9	HSA300781	AJ300781 Homo sapi
18	253.4	70.8	360	9	AF062241	AF062241 Homo sapi
19	253.2	70.7	459	9	S72729	S72729 IgH=T-cell
20	253	70.7	360	9	U96282	U96282 Homo sapien
21	253	70.7	367	9	HSE55323	Z14175 H.sapiens r
22	252.2	70.4	354	9	HSA300779	AJ300779 Homo sapi
23	251.4	70.2	369	9	AF062119	AF062119 Homo sapi
24	251.2	70.2	375	9	AB067099	AB067099 Homo sapi
25	250.6	70.0	354	9	HSA300783	AJ300783 Homo sapi
26	250.6	70.0	378	9	U00487	U00487 Human immun
27	250.4	69.9	341	9	AF103104	AF103104 Homo sapi
28	250.2	69.9	351	9	AB063892	AB063892 Homo sapi
29	249	69.6	378	9	HSIGVHC01	Z37291 H.sapiens r
30	248.6	69.4	373	9	AB021520	AB021520 Homo sapi
31	247.6	69.2	384	9	AF174118	AF174118 Homo sapi
32	247.4	69.1	354	9	HSA238038	AJ238038 Homo sapi
33	246.6	68.9	360	9	HSU80084	U80084 Human immun
34	246.6	68.9	390	9	AF115121	AF115121 Homo sapi
35	246.4	68.8	423	9	AF062121	AF062121 Homo sapi
36	245.8	68.7	351	9	U00584	U00584 Human immun
37	245.8	68.7	411	9	HSIGHXX14	X65896 H.sapiens m
38	245	68.4	360	9	U96279	U96279 Homo sapien
39	245	68.4	360	9	U96284	U96284 Homo sapien
40	244.8	68.4	363	9	HSVH3DJH4	X61646 Human Ig re
41	244.4	68.3	366	9	AF174095	AF174095 Homo sapi
42	244.4	68.3	405	9	AF174034	AF174034 Homo sapi
43	244	68.2	363	9	AB063913	AB063913 Homo sapi
44	243.8	68.1	357	6	AX300024	AX300024 Sequence
45	243.8	68.1	417	9	HSIGT219	X67908 H.sapiens r

ALIGNMENTS

RESULT 1
HSVH3H2FG

LOCUS   HSVH3H2FG   357 bp   DNA   linear   PRI 17-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody heavy chain variable
            region, subgroup V(H)3 (H2F IgG line).
ACCESSION   X70485
VERSION   X70485.1 GI:38447
KEYWORDS   anti-DNA antibody; complementarity determining region; Ig heavy
            chain; Ig kappa light chain; Ig variable region; IgG;
            immunoglobulin; systemic lupus erythematosus.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 357)

Pred. No. is the number of results predicted by chance to have a

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AUTHORS      Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
             and Diamond,B.
TITLE        Molecular characteristics of antibodies bearing an
             anti-DNA-associated idiotype
JOURNAL      J. Exp. Med. 174 (6), 1639-1652 (1991)
MEDLINE      92078875
PUBMED       1660528
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /isolate="patient HER(SLE)"
                     /db_xref="taxon:9606"
                     /cell_line="EBV-transformed 3I(+) B cell line,H2F IgG"
                     /tissue_type="spleen"
     misc_feature    <1..>357
                     /note="IgG heavy chain variable region"
     misc_feature    88..99
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     misc_feature    145..198
                     /note="complementarity determining region, CDR 2"
BASE COUNT    79 a    91 c    106 g    81 t
ORIGIN

Query Match          74.7%;    Score 267.4;  DB 9;  Length 357;
Best Local Similarity 87.7%;    Pred. No. 1.6e-75;
Matches 315;  Conservative    0;  Mismatches  41;  Indels  3;  Gaps  2;

Qy      1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
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Db      1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60

Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          ||||||||||| |||||||||||||||||||||||  ||||||| |||||||||||||||
Db     61 TGTGCAGCCTCTGGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 120

Qy    120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTCGGAATTGAACCATACTATGCG 179
          ||||||||||||||||||||||||||| ||||  ||||| || ||||||||||||||
Db    121 GGGAAGGGGCTGGAGTGGGTTCATACATTAGTAGTCGTGTAGTACCATATACTACGCA 180

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    181 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 240

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
          |||||||||||||||||||||||||||||||||||||||||||||||||  |||||| |||
Db    241 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA--GATCTGT 298

Qy    300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 357

RESULT 2
BC018747
LOCUS        BC018747         1679 bp    mRNA      linear   PRI 11-DEC-2001
DEFINITION   Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m
             marker), clone MGC:31937 IMAGE:4851063, mRNA, complete cds.
ACCESSION    BC018747
VERSION      BC018747.1   GI:17511791
KEYWORDS     MGC.
SOURCE       Homo sapiens
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 1679)
  AUTHORS    Strausberg,R.
  TITLE      Direct Submission
  JOURNAL    Submitted (07-DEC-2001) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive; Room 11A03, Bethesda, MD 20892-2590,
             USA
  REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT    Contact: MGC help desk
```

```
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 40 Row: i Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis; GenomeScan gene prediction. Similarity but not identity
to protein.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="Primary B-Cells from Tonsils"
                     /clone_lib="NIH_MGC_48"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             63..1475
                     /codon_start=1
                     /product="Similar to immunoglobulin heavy constant gamma 3
                     (G3m marker)"
                     /protein_id="AAH18747.1"
                     /db_xref="GI:17511792"
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                     GFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
                     NSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG
                     GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
                     QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
                     SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                     DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
                     KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
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BASE COUNT     430 a    506 c    452 g    291 t
ORIGIN

Query Match          73.7%;    Score 264;  DB 9;  Length 1679;
Best Local Similarity 86.9%;    Pred. No. 2.4e-74;
Matches 313;  Conservative    0;  Mismatches  45;  Indels  2;  Gaps  2;

Qy      1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 182

Qy     61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db    183 TGTGTAGTCTCTGGATTCACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA 242

Qy    120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTCGGAATTGAACCATACTATGCG 179
          ||||||||||||||||||||||| ||||  ||||| || ||| ||||||||||||||
Db    243 GGGAAGGGGCTGGAGTGGGTGGTTCATACATTAGTAGTCGGCAACATAAAGCAAGATGAGAAAGCCAAGAACTCACTGTATCTG 302

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTGTATTACTGTGCGAGAGATGGCAGC 422
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Qy   299  TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
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Db   423  AGCTGGTACAGGGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  482
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RESULT 3
HSVH31328
LOCUS   HSVH31328   351 bp   mRNA   linear   PRI 02-JUN-1992
DEFINITION H.sapiens rearranged mRNA for fetal IG heavy chain Vh3, an
            unidentified D (or N) region and Jh4 (clone FL13-28).
ACCESSION   X62965
VERSION   X62965.1 GI:37680
KEYWORDS   Ig CDR3 region; Ig heavy chain; Jh element; rearranged gene; Vh
            element.
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 351)
AUTHORS   Raaphorst,F.M., Timmers,E., Kenter,M.J., Van Tol,M.J., Vossen,J.M.
            and Schuurman,R.K.
TITLE   Restricted utilization of germ-line VH3 genes and short diverse
            third complementarity-determining regions (CDR3) in human fetal B
            lymphocyte immunoglobulin heavy chain rearrangements
JOURNAL   Eur. J. Immunol. 22 (1), 247-251 (1992)
MEDLINE   92111633
PUBMED   1730252
REFERENCE   2 (bases 1 to 351)
AUTHORS   Raaphorst,F.M.
TITLE   Direct Submission
JOURNAL   Submitted (31-OCT-1991) F.M. Raaphorst, Division of Immunology,
            Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden,
            Building 1, E3-Q, P.O.Box 9600, 2300 Leiden, THE NETHERLANDS
COMMENT   For related sequences see X62954-X62972, X53612-3, M37277,
            Schroeder H.W. Jr. et al, Proc.Natl.Acad.Sci.USA, 87:6149(1990) &
            Ichihara y. et al, Eur.J. Immunol. 18:649(1988).
FEATURES   Location/Qualifiers
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                     /isolate="Clone FL13-28"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /cell_type="B lymphocyte"
                     /tissue_type="liver"
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     misc_feature   311..351
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BASE COUNT   78 a   83 c   118 g   72 t
ORIGIN

Query Match   73.7%; Score 263.8; DB 9; Length 351;
Best Local Similarity 87.7%; Pred. No. 2.4e-74;
Matches   315; Conservative   0; Mismatches   32; Indels   12; Gaps   2;

Qy   1 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC   60
          ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db   4 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC   63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAAATCCTACGAGCTGGGTACGGCCAGGCTCCA 119
          ||||||||||| ||||||||||||| ||| ||| | ||||||| | |||||||||||||
Db   64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA   123

Qy   120 GGGAAGGGGCTGGAGTGGGTGGTGGGTTAATTAATAATGTAGTCGGAATTGACCATACTATGCG 179
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Db   124 GGGAAGGGGCTGGAGTGGGTGGTGGCCAACATAAAGCAAGATGGAGTGAGAAATACTATGTG   183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG   239
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Db   184  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG   243
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Qy   240  CAAATGAACAGCTGAGAGCCGAGGACACGCCGTGTATTACTGTGCGAGAGGGATCTGT   299
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Db   244  CAAATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------   295

Qy   300  CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   358
              |||  || |  ||  |   |||||||||||||||||||||||||||||||||||||
Db   296  --ATGGGAGGGGGATCCCTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   351
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RESULT 4
AF174030
LOCUS   AF174030   420 bp   mRNA   linear   PRI 08-MAY-2001
DEFINITION Homo sapiens clone 77u-c17 immunoglobulin heavy chain variable
            region precursor (IgH) mRNA, partial cds.
ACCESSION   AF174030
VERSION   AF174030.1 GI:5834019
KEYWORDS   .
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 420)
AUTHORS   Wang,X. and Stollar,B.D.
TITLE   Immunoglobulin VH gene expression in human aging
JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE   99459182
PUBMED   10527689
REFERENCE   2 (bases 1 to 420)
AUTHORS   Wang,X. and Stollar,B.D.
TITLE   Direct Submission
JOURNAL   Submitted (02-AUG-1999) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES   Location/Qualifiers
     source   1..420
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                     /db_xref="taxon:9606"
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                     /cell_type="peripheral blood B lymphocyte"
                     /clone_lib="77u"
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                     /gene="IgH"
     CDS   1..>420
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                     precursor"
                     /protein_id="AAD53776.1"
                     /db_xref="GI:5834020"
                     /translation="MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAAS
                     GFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
                     NSLRAEDTAVYYCARDGDIGDWWFDPWGQGTLVTVSSG"
     sig_peptide   1..57
                     /gene="IgH"
     mat_peptide   58..>420
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                     /product="immunoglobulin heavy chain variable region"
     V_region   58..420
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BASE COUNT   88 a   92 c   143 g   97 t
ORIGIN

Query Match   73.4%; Score 262.6; DB 9; Length 420;
Best Local Similarity 86.9%; Pred. No. 6e-74;
Matches   312; Conservative   0; Mismatches   44; Indels   3; Gaps   2;

Qy   1 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC   60
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Db   61 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 120

Query Match   72.9%; Score 261; DB 9; Length 420;
Best Local Similarity 86.6%; Pred. No. 2e-73;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

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Qy     1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCTGAGACTCTCC   60
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Db    61 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAAACTCTCC  120

Qy    61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCGTCCAGGCTCCA  119
         |||||||||| |||||||||||| ||||| |  ||  ||  |||||||||||||
Db   121 TGTGCAGCCTCTGGATTCACCTTTGGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA  180

Qy   120 GGGAAGGGGCTGGAGTGGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG  179
         |||||||||||||||||| |||  ||||||||| |||   |||||  |||  ||
Db   181 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGTGAGAAACTCACTTCACTGTG  240

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG  239
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Db   241 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  300

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCGT  299
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Db   301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCTGT  360

Qy   300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
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Db   361 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  417

Qy     1 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCGTCCAGGCTCCA  119
         |||||||||| |||||||||||| |||| |  | |    ||||||||||||||
Db   121 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA  180

Qy   120 GGGAAGGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG  239
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGAAGGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  240

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCGT  299
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Db   301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA--GATGGGG  358

Qy   300 CTTATGACAGAGGCTACTTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
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Db   359 ATATCGGTGACTGTGGTTCGACCCCTGGGGGCCAGGGACCCTGGTCACCGTCTCCTCA  417
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RESULT 5
AF062138
LOCUS   AF062138   420 bp   mRNA   linear   PRI 08-MAY-2001
DEFINITION Homo sapiens clone 45u-11 immunoglobulin heavy chain variable
            region (IGH) mRNA, partial cds.
ACCESSION   AF062138
VERSION   AF062138.1 GI:3170738
KEYWORDS   .
SOURCE   Homo sapiens.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 420)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE   Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
  MEDLINE   99459182
   PUBMED   10527689
REFERENCE   2 (bases 1 to 420)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE   Direct Submission
  JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES   Location/Qualifiers
     source   1..420
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.33"
                     /clone="45u-11"
                     /cell_type="peripheral B lymphocyte"
                     /tissue_type="blood"
                     /note="from elderly repertoire 45u"
     gene   1..>420
                     /gene="IGH"
                     58..>420
                     /gene="IGH"
     CDS   1..>420
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC18174.1"
                     /db_xref="GI:3170739"
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                     GFTFGSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
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     sig_peptide   1..57
                     /gene="IGH"
     V_region   58..>420
                     /gene="IGH"
BASE COUNT   89 a   97 c   137 g   97 t
ORIGIN

RESULT 6
HSA300796
LOCUS   HSA300796   351 bp   mRNA   linear   PRI 10-APR-2001
DEFINITION Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
            variable region (IGHV3-7), clone M2-129 (m2hie129), Kawasaki
            disease patient.
ACCESSION   AJ300796
VERSION   AJ300796.1 GI:12733998
KEYWORDS   IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
            variable region.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 351)
  AUTHORS   Leucht,S., Uttenreuther-Fischer,M.M., Gaedicke,G. and Fischer,P.
  TITLE   The B cell superantigen-like interaction of intravenous
            immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
            germline gene origin cloned from a patient with Kawasaki disease is
            enhanced after IVIG therapy
  JOURNAL   Clin. Immunol. 99 (1), 18-29 (2001)
  MEDLINE   21185274
   PUBMED   11286538
REFERENCE   2 (bases 1 to 351)
  AUTHORS   Fischer,P.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
            Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
            Berlin, 10117, GERMANY
FEATURES   Location/Qualifiers
     source   1..351
                     /organism="Homo sapiens"
                     /isolate="Kawasaki disease patient"
                     /db_xref="taxon:9606"
                     /clone="M2-129 (m2hie129)"
                     /cell_type="B cell"
                     /rearranged
     gene   1..351
                     /gene="IGHV3-7"
                     <1..>351
                     /gene="IGHV3-7"
     CDS   1..>351
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                     /function="immune response"
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Left column (RESULT 7)

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V_region
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                /db_xref="GI:12733999"
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                IFDYWGQGTLVTVSS"
                /gene="IGHV3-7"
                /product="immunoglobulin gamma heavy chain variable
                region"
                <1..>351
BASE COUNT      78 a   85 c   113 g   75 t
ORIGIN

Query Match            72.8%;    Score 260.6; DB 9; Length 351;
Best Local Similarity  87.2%;    Pred. No. 2.6e-73;
Matches 313;  Conservative  0;  Mismatches 34;  Indels 12;  Gaps 2;

Qy    1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db    4 GTGCAGCTGCTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          |||||||||||  |||||||||||  |||  || |  | |||||||| ||||||||||||
Db   64 TGTGCAGCCTCTGGATTCACCTTTGGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy  120 GGGAAGGGGCTGGAGTGGGTGGTGTTAATAATGGTAGTCGGAATTGAACCATATACTATGCG 179
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Db  124 GGGAAGGGGCTGGAGTGGGTGGTGGCCAACATAAAGCAAGATGAGAAAATACTACTATGTG 183

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
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Db  184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGCGCCGTGTATTACTGTGCGAGAGGGATCGT 299
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Db  244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTGTATTACTGTGCGAGAG------ 295

Qy  300 CTTATGACAGAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
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Db  296 --ATGACTCTGGGGATCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351

RESULT 7
HSE55314
LOCUS       HSE55314    409 bp    mRNA    linear    PRI 15-MAR-1993
DEFINITION  H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION   Z14189 X65741
VERSION     Z14189.1  GI:31005
KEYWORDS    Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig
            variable region; immunoglobulin.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 409)
AUTHORS     Tonnelle,C.
TITLE       Direct Submission
JOURNAL     Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie
            Marseille-Luminy, Case 906, 13288 Marseille Cedex 9, FRANCE
REFERENCE   2 (bases 1 to 409)
AUTHORS     Cuisinier,A.M., Gauthier,L., Boubli,L., Fougereau,M. and
            Tonnelle,C.
TITLE       Mechanisms that generate human immunoglobulin diversity operate
            from the 8th week of gestation in fetal liver
JOURNAL     Eur. J. Immunol. 23 (1), 110-118 (1993)
MEDLINE     93122076
PUBMED      8419161
FEATURES    Location/Qualifiers
source      1..409
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /chromosome="14"
                /clone="3.14"
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Right column (RESULT 8)

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CDS             /tissue_type="feral liver"
                /clone_lib="E55"
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                FSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSL
                RAEDTAVYYCARGLTGATDAFDIWGQGTMVTVSS"
misc_feature    1..49
                /note="signal peptide"
misc_feature    50..343
                /note="Ig V-segment"
misc_feature    344..362
                /note="Ig D-segment"
misc_feature    363..409
                /note="Ig J-segment"
BASE COUNT      88 a   90 c   134 g   97 t
ORIGIN

Query Match            72.5%;    Score 259.4; DB 9; Length 409;
Best Local Similarity  86.4%;    Pred. No. 6.5e-73;
Matches 310;  Conservative  0;  Mismatches 46;  Indels 3;  Gaps 2;

Qy    1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db   53 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 112

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          ||||||||||| |||||||||||| |||   |  |  | ||||||| |||||||||||||
Db  113 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 172

Qy  120 GGGAAGGGGCTGGAGTGGGTGGTGTTAATAATGGTAGTCGGAATTGAACCATATATGCG 179
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Db  173 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGAGAAATACTATATGTG 232

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
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Db  233 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 292

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCGT 299
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Db  293 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGCTAACT 352

Qy  300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
               |  | |   |  ||||| ||||| |||||||| || |  ||||||||||||||
Db  353 GGGGCCACGGATGCT--TTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCCTCA 409

RESULT 8
AB067237
LOCUS       AB067237    363 bp    mRNA    linear    PRI 02-JUL-2002
DEFINITION  Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
            partial cds, clone:ya016h.
ACCESSION   AB067237
VERSION     AB067237.1  GI:21670530
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:ya016h.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
TITLE       Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 363)
AUTHORS     Kurosawa,Y.
TITLE       Direct Submission
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RESULT 9 (left column)

```
JOURNAL     Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University,
            Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1..363
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="ya016h"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..363
                     /gene="IGH"
     CDS             <1..>363
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                     /codon_start=1
                     /product="immunoglobulin heavy chain VHDJ region"
                     /protein_id="BAC02275.1"
                     /db_xref="GI:21670531"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKG
                     LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREQQL
                     GPHNWFDPWGQGTLVTVSS"
BASE COUNT        82 a       89 c      120 g       72 t
ORIGIN

Query Match      72.2%;  Score 258.4;  DB 9;  Length 363;
Best Local Similarity 86.5%;  Pred. No.1.4e-72;
Matches 308;  Conservative 0;  Mismatches .46;  Indels 2;  Gaps 2;

Qy    1 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGGGGAGGGTCCCTGAGACTCTCC  60
Db    4 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGGGGAGGGTCCCTGAGACTCTCC  63
Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGTCCGGTACGCCAGGCTCCA 119
Db   64 TGTGCAGCCTCTGGATTCACCTTTAGTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123
Qy  120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATGGTGGAATTGAACCATACTACTATGCG 179
Db  124 GGGAAGGGGCTGGAGTGGGTGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183
Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGCAACGCCAAGAACTCACTGTATCTG 239
Db  184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243
Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGGGATCTGT 299
Db  244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGAGCAGCAG 303
Qy  300 CTTATGACAGA-GGCTACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC 354
Db  304 CTGGGACCTCACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTC 359
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RESULT 9 header block

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RESULT 9
HSVH3I3RM
LOCUS       HSVH3I3RM      372 bp    DNA     linear   PRI 17-FEB-1993
DEFINITION  H.sapiens DNA for anti-DNA antibody heavy chain variable
            region,subgroup V(H)3 (III-3R IgM line).
ACCESSION   X63850
VERSION     X63850.1  GI:38346
KEYWORDS    anti-DNA antibody; complementarity determining region; Ig heavy
            chain; Ig kappa light chain; Ig variable region; IgM;
            immunoglobulin; systemic lupus erythematosus.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
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RESULT 9 (right column, continuation of X63850 entry)

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TITLE       and Diamond,B.
            Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype
JOURNAL     J. Exp. Med. 174 (6), 1639-1652 (1991)
MEDLINE     92078875
PUBMED      1660528
FEATURES             Location/Qualifiers
     source          1..372
                     /organism="Homo sapiens"
                     /isolate="patient DIL(SLE)"
                     /db_xref="taxon:9606"
                     /cell_line="EBV-transformed 3I(+) B cell line,III-3R IgM"
                     /tissue_type="spleen"
     misc_feature    <1..>372
                     /note="IgM heavy chain variable region"
     misc_feature    88..99
                     /note="complementarity determining region, CDR 1"
     misc_feature    145..198
                     /note="complementarity determining region, CDR 2"
BASE COUNT        81 a       90 c      126 g       75 t
ORIGIN

Query Match      72.2%;  Score 258.4;  DB 9;  Length 372;
Best Local Similarity 85.2%;  Pred. No.1.4e-72;
Matches 317;  Conservative 0;  Mismatches 41;  Indels 14;  Gaps 2;

Qy    1 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
Db    1 GTGCAGCTGGTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  60
Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGTCCGGTACGCCAGGCTCCA 119
Db   61 TGTGCAGCCTCTGGATTCACCTTTAGTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 120
Qy  120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATGGTGGAATTGAACCATACTACTATGCG 179
Db  121 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 180
Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGCAACGCCAAGAACTCACTGTATCTG 239
Db  181 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 240
Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGGGA----- 294
Db  241 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGAAGGATG 300
Qy  295 --------TCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
Db  301 TGGGAGAGGTGGTTCGGGGAGTCCCGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTC 360
Qy  347 ACCGTCTCCTCA 358
Db  361 ACCGTCTCCTCA 372
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RESULT 10 header block

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RESULT 10
HSA300786
LOCUS       HSA300786      351 bp    mRNA    linear   PRI 10-APR-2001
DEFINITION  Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
            variable region (IGHV3-7), clone M1-45 (mihie45), Kawasaki disease
            patient.
ACCESSION   AJ300786
VERSION     AJ300786.1  GI:12733975
KEYWORDS    IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
            variable region.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Leucht,S., Uttenreuther-Fischer,M.M., Gaedicke,G. and Fischer,P.
  TITLE     The B cell superantigen-like interaction of intravenous
            immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
```

VERSION   AX061464.1   GI:12405599
KEYWORDS
SOURCE   Human immunodeficiency virus type 1.
ORGANISM   Human immunodeficiency virus type 1
             Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
             lentivirus group.
REFERENCE   1 (bases 1 to 375)
AUTHORS   Watkins,B.A. and Reitz,M.S.
TITLE   Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
JOURNAL   Patent: WO 0100678-A 33 04-JAN-2001;
             THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES   Location/Qualifiers
source   1..375
             /organism="Human immunodeficiency virus type 1"
             /db_xref="taxon:11676"
             /note="VH"
BASE COUNT   81 a   90 c   116 g   88 t
ORIGIN

Query_Match   Score 256.6; DB 6; Length 375;
Best Local Similarity 71.7%;   Pred. No. 5.2e-72;
Matches 314; Conservative 0; Mismatches 44; Indels 11; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db   7 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 66

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
        ||||||||||| |||||||||||||| |||| || || ||||||||| ||||||||||||
Db   67 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 126

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
        |||||||||||||||||||||| |||| |||||||||||||||| |
Db 127 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 186

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
        |||||||||||||||||||||||||||||| |||| |||| ||||||||||||||||||||
Db 187 GACTCTGTGAAGGGCCGATTCACCATCTTCAGAAACAACACGCCAAGAACTCACTGTATCTG 246

Qy 240 CAAATGAACAGCTGAGGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCT-- 297
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 247 CAAATGAACAGCTGAGGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGTTGCTACTAT 306

Qy 298 --------GTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC 349
                    |||| ||||| |||||||||||||||||||||||||||||||||||||
Db 307 GGTTCGGGGAGTTATTATTTCTACCCCCTTTGCCTACTGGGGCCAGGGAACCCTGGTCACC 366

Qy 350 GTCTCCTCA 358
        |||||||||
Db 367 GTCTCCTCA 375

RESULT 12
HSU80083
LOCUS   HSU80083   348 bp   DNA   linear   PRI 19-FEB-1997
DEFINITION   Human immunoglobulin heavy chain variable region (V3-07) gene,
             partial cds.
ACCESSION   U80083
VERSION   U80083.1   GI:1791008
KEYWORDS
SOURCE   Homo sapiens.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 348)
AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE   Analysis of rearranged immunoglobulin heavy chain variable region
             genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL   Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE   97182739
PUBMED   9030878
REFERENCE   2 (bases 1 to 348)
AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.B.

JOURNAL   germline gene origin cloned from a patient with Kawasaki disease is
             enhanced after IVIG therapy
             Clin.Immunol. 99 (1), 18-29 (2001)
MEDLINE   21185274
PUBMED   11286538
REFERENCE   2 (bases 1 to 351)
AUTHORS   Fischer,P.
TITLE   Direct Submission
JOURNAL   Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
             Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
             Berlin, 10117, GERMANY
FEATURES   Location/Qualifiers
source   1..351
             /organism="Homo sapiens"
             /isolate="Kawasaki disease patient".
             /db_xref="taxon:9606"
             /clone="M1-45 (m1hie45)"
             /cell_type="B cell"
             /rearranged
gene   1..351
             /gene="IGHV3-7"
CDS   <1..>351
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             /function="immune response"
             /codon_start=1
             /product="immunoglobulin gamma heavy chain variable
             region"
             /protein_id="CAC28891.1"
             /db_xref="GI:12733976"
             /translation="EVQLLESGGGLVQPGESLRLSCAASGFTFSSYGMSWVRQAPGKG
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BASE COUNT   79 a   84 c   114 g   74 t
ORIGIN

Query_Match   Score 257.4; DB 9; Length 351;
Best Local Similarity 71.9%;   Pred. No. 2.9e-72;
Matches 311; Conservative 0; Mismatches 36; Indels 12; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db   4 GTGCAGCTGCTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db   64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
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Db 124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
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Db 184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy 240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCTGT 299
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Db 244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTGTATTACTGTGCGAGAGAGGTGGCT 303

Qy 300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
        || |||||||||||||||||||||||||||||||||||||||
Db 304 --------GGTCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351

RESULT 11
AX061464
LOCUS   AX061464   375 bp   DNA   linear   PAT 22-JAN-2001
DEFINITION   Sequence 33 from Patent WO0100678.
ACCESSION   AX061464

Left column (RESULT 13)

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TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
FEATURES             Location/Qualifiers
     source          1..348
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone="3b2g11"
                     /cell_type="CD19+ B cells"
                     /tissue_type="peripheral blood"
                     /note="CD19+ peripheral blood B cells obtained from a bone
                     marrow transplant recipient 90 days post transplant; clone
                     1 in reference 1"
     gene            1..348
                     /gene="V3-07"
     CDS             <1..>348
                     /gene="V3-07"
                     /note="Ig VH3 heavy chain"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC50998.1"
                     /db_xref="GI:1791009"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKG
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BASE COUNT       79 a     83 c    114 g     72 t
ORIGIN
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Query Match             71.6%;  Score 256.2;  DB 9;  Length 348;
Best Local Similarity   86.6%;  Pred. No. 7e-72;
Matches  311;  Conservative    0;  Mismatches   33;  Indels   15;  Gaps    2;

Qy        1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db        4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy       61 TGTGCAGCCTC--GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCCAGGCTCCA 119
            |||||||||||  |||||||||||||| ||||| |  |  ||||||||| |||||||||||
Db       64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy      120 GGGAAGGGGCTGGAGTGGGTTGGTTAATATAAATGGTAGTCGGAATTGAACCATATATGCG 179
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Db      124 GGGAAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATTACTATGTG 183

Qy      180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACACGCCAAGAACTCACTGTATCTG 243

Qy      240 CAAATGACAGCAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
            ||||||||||||||||||||||||||||||||||| |||||||||||||||  | |||||
Db      244 CAAATGACAGCAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGGGGCTCCAGT 303

Qy      300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
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Db      304 GATATG----------------GACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 348
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RESULT 13
HSU76679
LOCUS       HSU76679      360 bp    mRNA    linear    PRI 14-MAY-2001
DEFINITION  Homo sapiens clone CDC-1hc IgM heavy chain variable region mRNA,
            partial cds.
ACCESSION   U76679
VERSION     U76679.1   GI:1673596
KEYWORDS
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 360)
  AUTHORS   Aguilera,I., Melero,J., Nunez-Roldan,A. and Sanchez,B.
```

Right column (RESULT 14)

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TITLE       Molecular structure of eight human autoreactive monoclonal
            antibodies
JOURNAL     Immunology 102 (3), 273-280 (2001)
MEDLINE     21195372
PUBMED      11298825
REFERENCE   2 (bases 1 to 360)
AUTHORS     Aguilera,I.
TITLE       Direct Submission
JOURNAL     Submitted (30-OCT-1996) Hospital U. Virgen del Rocio, Immunology,
            Manuel Siurot s/n, Seville, Spain, 41013
FEATURES             Location/Qualifiers
     source          1..360
                     /organism="Homo sapiens"
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                     /clone="CDC-1hc"
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                     /product="IgM heavy chain variable region"
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BASE COUNT       74 a     94 c    114 g     78 t
ORIGIN
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Query Match             71.6%;  Score 256.2;  DB 9;  Length 360;
Best Local Similarity   85.8%;  Pred. No. 7e-72;
Matches  308;  Conservative    0;  Mismatches   48;  Indels    3;  Gaps    2;

Qy        1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
            ||||||||||||||||||||||||||||||||| || |||| |||||||||||||||||
Db        4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCGTCCGGGGGGTCCCTGAGACTCTCC 63

Qy       61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCCAGGCTCCA 119
            ||||||||||| |||||||||||||| |||| |   ||  ||||||| |||||||||||
Db       64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTTTTGGCTGAACTGGGTCCGCCAGGCTCCA 123

Qy      120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAAATGGTAGTCGGAATTGAACCATATATGCG 179
            |||||||||||||||||||||| ||   ||||| ||| |   |   |||| |||||||
Db      124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAATTCAAGACGGAAGTGAGAAGTACTATGTG 183

Qy      180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
            |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy      240 CAAATGACAGCAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
            |||||||||||||||||||||| | ||||||||||   ||| ||||||||||  | || 
Db      244 CAAATGACAGCAGCCTGAGAGCGATGACACGGCCGCCATTTATTACTGTGC--GAGGGTTCGG 301

Qy      300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
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Db      302 CTGGTACCTCCCCCCGCCTGACTACTGGGGTCAGGGAACCCTGACTCTGTCACCGTCTCCTCA 360
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RESULT 14
HSA300785
LOCUS       HSA300785      354 bp    mRNA    linear    PRI 10-APR-2001
DEFINITION  Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
            variable region (IGHV3-7), clone M1-40 (m1hie40), Kawasaki disease
            patient.
ACCESSION   AJ300785
VERSION     AJ300785.1   GI:12733973
KEYWORDS    IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
            variable region.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 354)
  AUTHORS   Leucht,S., Uttenreuther-Fischer,M.M., Gaedicke,G. and Fischer,P.
  TITLE     The B cell superantigen-like interaction of intravenous
```

```
JOURNAL    immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
           germline gene origin cloned from a patient with Kawasaki disease is
           enhanced after IVIG therapy
           Clin. Immunol. 99 (1), 18-29 (2001)
MEDLINE    21185274
PUBMED     11285538
REFERENCE  2 (bases 1 to 354)
AUTHORS    Fischer,P.
TITLE      Direct Submission
JOURNAL    Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
           Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
           Berlin, 10117, GERMANY
FEATURES            Location/Qualifiers
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                    /rearranged
     gene           1..354
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     CDS            <1..>354
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                    /function="immune response"
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                    /product="immunoglobulin gamma heavy chain variable
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                    /protein_id="CAC28890.1"
                    /db_xref="GI:12733974"
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                    /product="immunoglobulin gamma heavy chain variable
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BASE COUNT    79 a     86 c    115 g     74 t
ORIGIN

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Matches    309;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    2;

Qy       3  GCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTG  62
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Db       9  GCTGCTCCAGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTG  68

Qy      63  TGCAGCCTC-GGATTCACCTTTACTAGAGAATCTACAGAGTCCTGGGTACGGCCAGGCTCCAGG  121
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Db      69  TGCAGCCCTCTGGATTCACCTTTAGTAGTATTTGGATGAGCTGGGTCCGCCAGGCTCCAGG  128

Qy     122  GAAGGGGCTGGAGTGGGTTGGTTAATAATATGTAGTCGGAATTGAACCATACTATGCGGA  181
            |||||||||||||||||||||| ||| ||| |  |||||| |||||||||||||||||||
Db     129  GAAGGGGCTGGAGTGGGTGGCCAACATAAACAAGATGAAGTGAGAAATACTATGTGCA  188

Qy     182  CTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCA  241
            ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     189  CTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCA  248

Qy     242  AATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCTGTCT  301
            ||||||||||||||||||||||||||||||| ||||||||||||| |
Db     249  AATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGTGGCT--  306

Qy     302  TATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
            |||||||||||                 |||||||||||||||||||||||||||||
Db     307  ------------GGTCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  354

RESULT 15
AF062188
LOCUS       AF062188         372 bp      mRNA      linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 48u-19 immunoglobulin heavy chain variable
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            region (IGH) mRNA, partial cds.
ACCESSION   AF062188
VERSION     AF062188.1    GI:3170838
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 372)
AUTHORS     Wang,X. and Stollar,B.D.
TITLE       Immunoglobulin VH gene expression in human aging
JOURNAL     Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE     99459182
PUBMED      10527689
REFERENCE   2 (bases 1 to 372)
AUTHORS     Wang,X. and Stollar,B.D.
TITLE       Direct Submission
JOURNAL     Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
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                    /note="from elderly repertoire 48u"
     gene           <1..>372
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     CDS            <1..>372
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                    /codon_start=1
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                    /protein_id="AAC18224.1"
                    /db_xref="GI:3170839"
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     V_region       1..>372
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BASE COUNT    82 a     84 c    125 g     81 t
ORIGIN

Query Match          71.2%;    Score 254.8;  DB 9;  Length 372;
Best Local Similarity   85.0%;  Pred. No. 2e-71;
Matches    311;  Conservative    0;  Mismatches   47;  Indels    8;  Gaps    2;

Qy       1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC  60
            |||||||| || |||||||||||||||||| |||||||||||||||||||||||||||||
Db       4  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  63

Qy      61  TGTGCAGCCTC-CGATTCACCTTTACTAGGAAATCCTACGAGTCCAGGCTCCAGGCTCCA  119
            |||||||||||  ||||||||||| |||| |||   |  ||| |||| |||||||||||||
Db      64  TGTGCAGGATCTCGATTCACCTTTAGTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA  123

Qy     120  GGGAAGGGGCTGGAGTGGGTGGGTGTTAATATAATGGTAGTGGTAGTACCATACTATGCG  179
            ||||||||||||||||||||||| | || ||| |  ||  |   |  |   |  | || |
Db     124  GGGAAGGGGCTGGAGTGGGTGGGCAACATAAAGCAAGATGAAGTGAGAAATACTATGTG  183

Qy     180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  239
            |||||||||||||||| ||||||||||||||||||| |||||||||||||||||||||||
Db     184  GACTCTGTGAAGGGCCACCATCTCCAGAGACAACGCCAAGAACTCGCTGTATCTG  243

Qy     240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT  299
            ||||||||||||||||||||||||||||||||||||||||||  |||  |
Db     244  CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGCGAGGGCA  303

Qy     300  CTTATGACAGACAGAGG------CTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC  352
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us-09-627-896b-30.rge

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OM nucleic - nucleic search, using sw model

      Copyright   GenCore version 5.1.6
      Copyright (c) 1993 - 2003 Compugen Ltd.

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Searched: 1615406 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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    22: em_gss_fun:*
    23: em_gss_mam:*
    24: em_gss_mus:*
    25: em_gss_other:*
    26: em_gss_pro:*
    27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	262.4	73.3	704	12	BG759119	BG759119 602710759
2	261	72.9	735	9	AL551886	AL551886 AL551886
3	249	69.6	848	12	BG756291	BG756291 602713609
4	248.2	69.3	904	14	BQ709359	BQ709359 AGENCOURT
5	247.4	69.1	831	12	BG756386	BG756386 602715711
6	247.4	69.1	853	12	BG755960	BG755960 602716437
7	245	68.4	888	14	BQ706683	BQ706683 AGENCOURT
8	244	68.2	950	14	BQ711129	BQ711129 AGENCOURT
9	243.8	68.1	770	12	BG758713	BG758713 602712981
10	243.6	68.0	895	14	BQ710073	BQ710073 AGENCOURT
11	243.6	68.0	934	14	BQ708566	BQ708566 AGENCOURT
12	243.4	68.0	979	14	BQ708029	BQ708029 AGENCOURT
13	243.2	67.9	1164	12	BF974771	BF974771 602245420
14	241.8	67.5	443	10	AW401428	AW401428 UI-HF-BK0
15	241.8	67.5	540	10	AW402648	AW402648 UI-HF-BK0
16	241.8	67.5	938	14	BQ706365	BQ706365 AGENCOURT
17	241.2	67.4	750	12	BG340591	BG340591 602462161
18	240.2	67.1	669	14	BM767227	BM767227 K-EST0049
19	240.2	67.1	920	14	BQ711467	BQ711467 AGENCOURT
20	239	66.8	511	10	AW402613	AW402613 UI-HF-BK0
21	238.8	66.7	942	14	BQ710859	BQ710859 AGENCOURT
22	238.6	66.6	881	12	BG686259	BG686259 602638142
23	238.4	66.6	618	14	BM713479	BM713479 UI-E-EJO-
24	237.4	66.3	436	10	AW402311	AW402311 UI-HF-BK0
25	237.4	66.3	928	14	BQ943156	BQ943156 AGENCOURT
26	237	66.2	999	14	BQ711203	BQ711203 AGENCOURT
27	236.6	66.1	798	12	BF128991	BF128991 60181308
28	235.8	66.1	896	14	BQ717993	BQ717993 AGENCOURT
29	235.8	65.9	984	14	BQ709776	BQ709776 AGENCOURT
30	235.2	65.7	471	10	AW403220	AW403220 UI-HF-BK0
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33	234.6	65.5	447	10	AW403163	AW403163 UI-HF-BK0
34	234.6	65.5	937	14	BQ707419	BQ707419 AGENCOURT
35	233.8	65.3	518	10	AW402029	AW402029 UI-HF-BK0
36	233.8	65.3	1069	14	BM914329	BM914329 AGENCOURT
37	233	65.1	669	12	BG686716	BG686716 602650678
38	232.4	64.9	810	12	BG538620	BG538620 602567352
39	232.2	64.9	834	14	BQ711497	BQ711497 AGENCOURT
40	232	64.8	958	14	BQ709987	BQ709987 AGENCOURT
41	232	64.8	962	14	BQ706534	BQ706534 AGENCOURT
42	231.4	64.6	456	10	AW403059	AW403059 UI-HF-BK0
43	230.8	64.5	518	14	BM708960	BM708960 UI-E-CI1-
44	230.2	64.3	908	12	BG686881	BG686881 602650867
45	229.4	64.1	1000	14	BQ712690	BQ712690 AGENCOURT

ALIGNMENTS

RESULT 1
BG759119

LOCUS   BG759119   704 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602710759F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851063 5',
            mRNA sequence.
ACCESSION   BG759119
VERSION   BG759119.1 GI:14069772
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 704)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1693 row: e column: 16
            High quality sequence stop: 701.
FEATURES   Location/Qualifiers
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FEATURES   Location/Qualifiers
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                /clone_lib="NIH_MGC 113"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."

BASE COUNT   200 a   265 c   254 g   185 t
ORIGIN

Query Match   Best Local Similarity   69.3%;   Score 248.2;   DB 14;   Length 904;
                Pred. No. 7.6e-58;
Matches 303;   Conservative   0;   Mismatches   53;   Indels   3;   Gaps   2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC   60
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Db   128 GTGCGGCTGGTGGAGTCTGGGGGAGGCTTGGTCAGCCTGGGGGGTCCCTGGGGGGTCCCTTAAGACTCTCC   187

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA   119
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Db   188 TGTGCAGCCCTCTGGATTCACGTTTAGTGCCCATTGGATGACCTGGGTGGGTCCGCCAGGCTCCA   247

Qy   120 GGGAAGGGGCTGGAGTGGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG   179
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Db   248 GGGAGGGGGCTGGAGTGGGGTGGTGCCAACATAAAGGACGATGGAAGTGACAAATTCTATGCG   307

Qy   180 GACTCTGTGAAGGGCCGATTCACCATTCACCAGGCAACGCCAAGAACTCACTGTATCTG   239
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Db   308 GACTCACTGAAGGGCCGATTCACCATTCACCAGGCAACGCCAAGAACTCACTGTATCTA   367

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCGT   299
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Db   368 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTTCTGTGCGGGAGA--CATCTGC   425

Qy   300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   358
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Db   426 TAGGGGGTAACAACGACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCCA   484

RESULT 5
BG756386
LOCUS   BG756386   831 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION   602715711F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855682 5',
             mRNA sequence.
ACCESSION   BG756386
VERSION   BG756386.1   GI:14067039
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 831)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1705 row: f column: 03

                /db_xref="taxon:9606"
                /clone="IMAGE:4853667"
                /clone_lib="NIH_MGC 48"
                /tissue_type="primary B-cells from tonsils (cell line)"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."

BASE COUNT   187 a   252 c   236 g   173 t
ORIGIN

Query Match   Best Local Similarity   69.6%;   Score 249;   DB 12;   Length 848;
                Pred. No. 4.4e-58;
Matches 305;   Conservative   0;   Mismatches   45;   Indels   9;   Gaps   2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC   60
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Db   124 GTGCAGCTGGTGGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGGGGGGTCCCTTAAGACTCTCC   183

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA   119
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 TGTGCAGCCCTCTGGATTCACTTTTAGTATCTATTGGATGACCTGGGTGGGTCCGCCAGGCTCCA   243

Qy   120 GGGAAGGGGCTGGAGTGGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG   179
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Db   244 GGGAAGGGGCTGGAGTGGGGTGGTGGCCAATATAAAGGAAGATGAAGTGACAAATACTATGTG   303

Qy   180 GACTCTGTGAAGGGCCGATTCACCATTCACCAGGCAACGCCAAGAACTCACTGTATCTG   239
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Db   304 GACTCTGTGAAGGGCCGATTCACCATTCACCAGGCAACGCCAAGAACTCACTGTATCTG   363

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCGT   299
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Db   364 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCATCTATTACTGTGCGAGAGTAAGTTGG   423

Qy   300 CTTATGACAGAGGCTACTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   358
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Db   424 ATGGTTCAGGGAGTTAGT-------TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   474

RESULT 4
BQ709359
LOCUS   BQ709359   904 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_7983019 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215641
             5', mRNA sequence.
ACCESSION   BQ709359
VERSION   BQ709359.1   GI:21184258
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 904)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2384 row: o column: 02
             High quality sequence stop: 667.

Left column (RESULT 6 / BG755960)

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source          High quality sequence stop: 790.
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                /clone="IMAGE:4855682"
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                /tissue_type="primary B-cells from tonsils (cell line)"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."

BASE COUNT      182 a   244 c   237 g   168 t
ORIGIN

Query Match            69.1%;   Score 247.4;  DB 12;  Length 831;
Best Local Similarity  84.7%;   Pred. No. 1.2e-57;
Matches 304;  Conservative  0;  Mismatches 46;  Indels 9;  Gaps 2;

Qy   1   GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC   60
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Db 123   GTGCAGCTGGTGGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  182

Qy  61   TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACAGAGCTGGTACGCCAGGCTCCA  119
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Db 183   TGTGCAGCCCTCTGGATTCACTTTTAGTATCTATTGGATGACCTGGGTCCGCCAGGCTCCA 242

Qy 120   GGGAAGGGGCTGGAGTGGGTGGTTAATAAATGGTAGTCGGAATTGAACCATATATGCG   179
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Db 243   GGGAAAGGGGCTGGAGTGGGTGGCCAATATAAAGGAAGATGAAGTGACAAATACTATGTG  302

Qy 180   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGCCAAGAACTCACTGTATCTG     239
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Db 303   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  362

Qy 240   CAAATGAACAGCCTGAGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGATCTGT 299
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Db 363   CAAATGAACAGCCTGAGAGAGCCGAGGACACGGCCATCTATTACTGTGCGAGAGTAAGTTGG 422

Qy 300   CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   358
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Db 423   ATGGTTCAGGGACTTAGT------TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA    473
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RESULT 6
BG755960
LOCUS   BG755960   853 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602716437F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855553 5',
            mRNA sequence.
ACCESSION   BG755960
VERSION   BG755960.1 GI:14066613
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 853)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ling Hong/Rubin Laboratory
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be

Right column (RESULT 7 / BQ706683)

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                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLCM1707 row: j column: 10
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FEATURES        Location/Qualifiers
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                /db_xref="taxon:9606"
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                /tissue_type="primary B-cells from tonsils (cell line)"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."

BASE COUNT      183 a   254 c   239 g   177 t
ORIGIN

Query Match            69.1%;   Score 247.4;  DB 12;  Length 853;
Best Local Similarity  84.7%;   Pred. No. 1.2e-57;
Matches 304;  Conservative  0;  Mismatches 46;  Indels 9;  Gaps 2;

Qy   1   GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC   60
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Db 129   GTGCAGCTGGTGGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  188

Qy  61   TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACAGAGCTGGTACGCCAGGCTCCA  119
         |||||||| || |||||||| ||| | ||| |||  |  |||| ||   |||||||||||
Db 189   TGTGCAGCCCTCTGGATTCACTTTTAGTATCTATTGGATGACCTGGGTCCGCCAGGCTCCA 248

Qy 120   GGGAAGGGGCTGGAGTGGGTGGTTAATAATATGGTAGTCGGAATTGAACCATATATGCG   179
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Db 249   GGGAAAGGGGCTGGAGTGGGTGGCCAATATAAAGGAAGATGAAGTGACAAATACTATGTG  308

Qy 180   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGCCAAGAACTCACTGTATCTG     239
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Db 309   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  368

Qy 240   CAAATGAACAGCCTGAGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGATCTGT 299
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Db 369   CAAATGAACAGCCTGAGAGAGCCGAGGACACGGCCATCTATTACTGTGCGAGAGTAAGTTGG 428

Qy 300   CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   358
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Db 429   ATGGTTCAGGGACTTAGT------TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA    479
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RESULT 7
BQ706683
LOCUS   BQ706683   888 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_7976366 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214494
            5', mRNA sequence.
ACCESSION   BQ706683
VERSION   BQ706683.1 GI:21845582
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 888)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory

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                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Agencourt Bioscience Corporation
                 Clone distribution: MGC clone distribution information can be
                 found through the I.M.A.G.E. Consortium/LLNL at:
                 http://image.llnl.gov
                 Plate: LLCM2381  row: o  column: 07
                 High quality sequence stop: 653.
FEATURES         Location/Qualifiers
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                 /db_xref="taxon:9606"
                 /clone="IMAGE:6214494"
                 /clone_lib="NIH_MGC_113"
                 /lab_host="DH10B (phage-resistant)"
                 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                 into EcoRI/XhoI sites using the following 5' adaptor:
                 GGCACGAG(G). Library constructed by Ling Hong in the
                 laboratory of Gerald M. Rubin (University of California,
                 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                 Superscript II RT (Life Technologies). Note: this is a
                 NIH_MGC Library."
BASE COUNT       188 a     259 c     248 g     192 t      1 others
ORIGIN

Query Match            68.4%;  Score 245;  DB 14;  Length 888;
Best Local Similarity  83.8%;  Pred. No. 5.8e-57;
Matches  301;  Conservative   0;  Mismatches  55;  Indels   3;  Gaps   2;

Qy      1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGAGGTCCCTGAGACTCTCC  60
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Db    113 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGACTCTCC 172

Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACCGCCAGGCTCCA 119
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Db    173 TGTGCAGCCTCTGGATTCGCCTTTAGTAGTTTTGGTGATGAGTTTGGTCCGCCAGGCTCCA 232

Qy    120 GGGAAGGGGCTGGGAGTGGGTGGTTAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
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Db    233 GGGAAGGGGCTGGGAGTGGGTGGTTAATAATGGTAGTCGGAATTGAACCATACTATGCG 292

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 GACTCTGTGAAGGGCCGATTCCACCATCTCCAGAGACAACGCCAAGAACTCCTGTTTCTG 352

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    353 CAAATGAACAGCCTGAGAGCCGAGGACACGGCGTGTCTATTATTGTGCGAGA--GTTTATG 410

Qy    300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
          |||||||||||||| || ||||||||||||||||||||||||||||||
Db    411 GTTCGGGGAGGCTATCCAGATGACCACCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 469
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RESULT 8
BQ711129
LOCUS       BQ711129       950 bp    mRNA     linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7977239 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215821
            5', mRNA sequence.
ACCESSION   BQ711129
VERSION     BQ711129.1  GI:21850028
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
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                 cDNA Library Preparation: Rubin Laboratory
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Agencourt Bioscience Corporation
                 Clone distribution: MGC clone distribution information can be
                 found through the I.M.A.G.E. Consortium/LLNL at:
                 http://image.llnl.gov
                 Plate: LLCM2385  row: f  column: 14
                 High quality sequence stop: 398.
FEATURES         Location/Qualifiers
     source      1..950
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:6215821"
                 /clone_lib="NIH_MGC_113"
                 /lab_host="DH10B (phage-resistant)"
                 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                 into EcoRI/XhoI sites using the following 5' adaptor:
                 GGCACGAG(G). Library constructed by Ling Hong in the
                 laboratory of Gerald M. Rubin (University of California,
                 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                 Superscript II RT (Life Technologies). Note: this is a
                 NIH_MGC Library."
BASE COUNT       192 a     259 c     297 g     200 t      2 others
ORIGIN

Query Match            68.2%;  Score 244;  DB 14;  Length 950;
Best Local Similarity  83.2%;  Pred. No. 1.1e-56;
Matches  302;  Conservative   0;  Mismatches  56;  Indels   5;  Gaps   2;

Qy      1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGAGGTCCCTGAGACTCTCC  60
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Db    131 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGACTCTCC 190

Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGGCCAGGCTCCA 119
          ||||||||||| |||||||||||||||| |||||||||||||  ||| |||||||||||
Db    191 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTCGGTCGGCCCAGGCTCCA 250

Qy    120 GGGAAGGGGCTGGGAGTGGGTGGTTAATATAATATGGTAGTCGGAATTGAACCATACTATGCG 179
          |||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db    251 NGGAAGGGGCTGGGAGTGGGTGGTGCCAACATAAAGCAAGCAAGATGGAGAAATACTATGTG 310

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db    311 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 370

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
          ||||||||||||||||||||||||||||||||||||||||| ||||||||| |||||
Db    371 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTGTTATTACTGTGCGAGGTGTGTGGGG 430

Qy    299 ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
                  |||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 GGCTGGTACATCACCTACGGTATGGACGTCTCGGGGCCACGGGACCACTGTCAATATCTCC 490

Qy    356 TCA 358
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Db    491 TCA 493
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RESULT 9
BG758713
LOCUS       BG758713       770 bp    mRNA     linear   EST 15-MAY-2001
DEFINITION  602712981F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852916 5',
            mRNA sequence.
ACCESSION   BG758713
VERSION     BG758713.1  GI:14069379
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
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TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1698 row: b column: 21
            High quality sequence stop: 718.

FEATURES   Location/Qualifiers
     source   1..770
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4852916"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT   168 a   221 c   225 g   156 t
ORIGIN

Query Match   68.1%; Score 243.8; DB 12; Length 770;
Best Local Similarity   84.4%; Pred. No. 1.1e-56;
Matches 303; Conservative 0; Mismatches 0; Indels 14; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC 60
           |||||||||||||||||||||| ||||||||||||| ||| |||||||||||||||||||
Db   125 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTCCGGGGGGTCCCTGAGACTCTCC 184

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db   185 TGTGCAGCCTCTGGATTCACCTTTAGTGATGAGCTATTGGATGAGCTGGGTACGCCAGGCTCCA 244

Qy   120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTGAGAATTGAACCATACATGCG 179
           |||||||||||||||||||| ||| ||| ||||| || |||||||||||||||||||
Db   245 GGGAAGGGGCTGGAGTGGGTGGGTGGTGCCAACATAAAGCCAGATGCAGTGAGAAATACTATGTG 304

Qy   180 GACTCTGTGAAGGGGCCGATTCACCATCTCCAGAGAGCAACGCCAAGAACTCACTGTATCTG 239
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Db   305 GACTCTGTGAAGGGGCCGATTCACCATCTCCAGAGACAACGCCAAAAACTCACTGTCTCTG 364

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Db   365 CAAATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTATTACTGTGCGACGAGATGATCT 424

Qy   300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
           |||||||||||||||||||||||||||||
Db   425 ------------GGCCCTCGACCACCACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 470

RESULT 10
LOCUS   BQ710073
DEFINITION   AGENCOURT_7983184 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215340
             5', mRNA sequence.
ACCESSION   BQ710073
VERSION   BQ710073.1 GI:21848972
KEYWORDS   EST.
SOURCE   Homo sapiens (human).
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE   1 (bases 1 to 895)
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2384 row: b column: 13
             High quality sequence stop: 654.

FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT   193 a   273 c   235 g   194 t
ORIGIN

Query Match   68.0%; Score 243.6; DB 14; Length 895;
Best Local Similarity   83.1%; Pred. No. 1.4e-56;
Matches 304; Conservative 0; Mismatches 0; Indels 54; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC 60
           ||||||||||||||||||||| ||||||||||||| ||| |||||||||||||||||||
Db   106 GTGCCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTCCGGGGGTCCCTGAGACTCTCC 165

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
           ||||||||||| |||||||||||||| ||| ||| |||||| |||||||||||||||||
Db   166 TGTGTAGTCTCTGGATTCACCTTTAGTGATGAGCTATTGGATGAGCTGGGTCCCGCCAGGACCCA 225

Qy   120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTGAGAATTGAACCATACATGCG 179
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Db   226 GTGAAGGGGCTGGAGTGGGTGGGTGGCCACAATAAAGCAAGATGAGAAATACTATGTG 285

Qy   180 GACTCTGTGAAGGGGCCGATTCACCATCTCCAGAGAGCAACGCCAAGAACTCACTGTATCTG 239
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Db   286 GACTCTGTGAAGGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTTTCTG 345

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTATTACTGTGCGA------GAGG 292
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Db   346 CAAATCAACAGCCTGAGAGCCGAGGACACCGCCGTGTATTACTGTGCGAAAAACTAGTAGC 405

Qy   293 GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 352
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   406 GACTATCCACCTACCACTATCCATTACTACTTTGACTACTGGGGCCAGGGAACTGGGGAACTTTGTTTGGTCACCGTC 465

Qy   353 TCCTCA 358
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Db   466 TCCTCA 471

RESULT 11
LOCUS   BQ708566
DEFINITION   AGENCOURT_7975980 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214806
             5', mRNA sequence.
ACCESSION   BQ708566

RESULT 12

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BQ708029
LOCUS       BQ708029
DEFINITION  AGENCOURT_8352453 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277625
            5', mRNA sequence.
ACCESSION   BQ708029
VERSION     BQ708029.1  GI:21846928
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 979)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464 row: e column: 18
            High quality sequence stop: 626.
FEATURES    Location/Qualifiers
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            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH MGC Library."
BASE COUNT      257 a    262 c    279 g    180 t    1 others
ORIGIN

Query Match             68.0%;  Score 243.4;  DB 14;  Length 979;
Best Local Similarity   88.2%;  Pred. No. 1.7e-56;
Matches   276;  Conservative    0;  Mismatches   36;  Indels    1;  Gaps    1;

Qy      1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db    130 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 189

Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCCAGGCTCCA 119
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Db    190 TGTGCAGCCTC-GGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTACGCCCAGGCTCCA 249

Qy    120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGAATTGAACCATACTATGCG 179
          |||||||||||||||||||||||||||||||||| | |||||||||||||||||||||||
Db    250 GGGAAGGGGCTGGAGTGGGTGGTGGCCAACATAAAGCAAGCAAGGAAGTGAGAAATACTATGTG 309

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
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Db    310 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 369

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGA------GAGG 292
          |||||||||||||||||||||||||||||||||||||||||||||||       ||||
Db    370 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 429

Qy    300 CTTATGACAGAGG 312
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Db    430 ATTACGTTTGGGG 442
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(left record)

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VERSION     BQ708566.1  GI:21847465
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 934)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382 row: 1 column: 07
            High quality sequence start: 6
            High quality sequence stop: 653.
FEATURES    Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="IMAGE:6214806"
            /clone_lib="NIH MGC 113"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH MGC Library."
BASE COUNT      203 a    271 c    257 g    200 t    3 others
ORIGIN

Query Match             68.0%;  Score 243.6;  DB 14;  Length 934;
Best Local Similarity   83.1%;  Pred. No. 1.4e-56;
Matches   304;  Conservative    0;  Mismatches   54;  Indels    8;  Gaps    2;

Qy      1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGTCCCTGAGACTCTCC 60
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Db    108 GTGCGGCTGGTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 167

Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCCAGGCTCCA 119
          |||| |||||| ||||||||||||||| ||| ||||  |||||||||| ||||||| |||
Db    168 TGTGTAGTCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTTCGCCAGGCTCCA 227

Qy    120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGAATTGAACCATACTATGCG 179
          |||||||||||||||||||||||  ||| | || || |  ||| |||| || ||||| |
Db    228 GTGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGAGAAGTGAAGTGAGAAATACTATGTG 287

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
          ||||||||||||||||||||||||||||||||||||| ||||||||  ||| ||||| |
Db    288 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAGCTCACTGTTTCTG 347

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGGGCGA------GAGG 292
          ||||||||| |||||||||||||||||||||||||||| |||||| ||
Db    348 CAAATGAACAACAGCCTGAGAGCCGAGGACACGGCCGTGTACTACTGTGCGAAAAACTAGTAGC 407

Qy    293 GATCTGTCTTATGACAGAGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 352
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Db    408 GACTATCCACCTATCCATTACTACTTTGACTACTGGGGGCCAGGGAACTTTGGTCACCGTC 467

Qy    353 TCCTCA 358
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Db    468 TCCTCA 473
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RESULT 13
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LOCUS   BF974771   1164 bp   mRNA   linear   EST 22-JAN-2001
DEFINITION   60224542OF1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335541 5',
               mRNA sequence.
ACCESSION   BF974771
VERSION   BF974771.1 GI:12341986
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1164)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
               National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
               cDNA Library Preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM1209 row: g column: 06
               High quality sequence stop: 696.
FEATURES   Location/Qualifiers
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:4335541"
               /clone_lib="NIH_MGC_48"
               /tissue_type="primary B-cells from tonsils (cell line)"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
               Site_2: EcoRI; cDNA made by oligo-dT priming.
               Directionally cloned into EcoRI/XhoI sites using the
               following 5' adaptor: GGCACGAG(G). Size-selected >500bp
               for average insert size 1.8kb. Library constructed by Ling
               Hong in the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH_MGC Library."
BASE COUNT   284 a   313 c   330 g   236 t   1 others
ORIGIN

Query Match   67.9%;   Score 243.2;   DB 12;   DB 12;   Length 1164;
Best Local Similarity 83.3%;   Pred. No. 2.1e-56;
Matches 300;   Conservative 0;   Mismatches 58;   Indels 2;   Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC   60
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Db   124 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC   183

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCGAGTCGGGTACGGCCAGGCTCCA   119
          ||||||||||| |||||||||||||||||| |||||||||||||||||||||
Db   184 TGTGCAGCCTCTGGATTCACCTTCAGTGACTGACTACTACATGAGCTGGATCCGCCAGGCTCCA   243

Qy   120 GGGAAGGGGCTGGAGTGGGTGGGT   179
          ||||||||||||||||||| |||
Db   244 GGGAAGGGGCTGGAGTGGGTGGGTTTCATACATTAGTAGTAGTAGTTACACAAGCTACGCA   303

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCCAAGAACGCCACTGTATCTG   239
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Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG-GGATCTG   298
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   364 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGATCAGAGG   423

Qy   299 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

Db   424 AACAACCAGCTGGTAGATTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   483
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RESULT 14
AW401428
LOCUS   AW401428   443 bp   mRNA   linear   EST 16-FEB-2000
DEFINITION   UI-HF-BK0-aad-b-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
               IMAGE:3053139 5', mRNA sequence.
ACCESSION   AW401428
VERSION   AW401428.1 GI:6920011
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 443)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
               National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Eco RI site shown at the beginning of the sequence.
               Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
               cDNA Library Preparation: M.B. Soares Lab
               cDNA Library Arrayed by: M.B. Soares Lab
               DNA Sequencing by: M.B. Soares Lab
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
     source   1..443
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:3053139"
               /clone_lib="NIH_MGC_36"
               /tissue_type="lymph"
               /cell_type="germinal center B cells"
               /cell_line="MGC85"
               /lab_host="DH10B (LTI)"
               /note="Vector: pTT3-Pac; Site_1: NotI; Site 2: Eco RI;
               Constructed from size fractionated cytoplasmic mRNA
               (0.5-1.5kb). Directionally cloned. Cells provided by Louis
               M. Staudt, Ph.D. Library preparation by Maria de Fatima
               Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   93 a   116 c   131 g   103 t
ORIGIN

Query Match   67.5%;   Score 241.8;   DB 10;   Length 443;
Best Local Similarity 83.3%;   Pred. No. 2.9e-56;
Matches 299;   Conservative 0;   Mismatches 57;   Indels 3;   Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC   60
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Db   85 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGAGTCTCC   144

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGATCCGGCCAGGCTCCA   119
          ||||||||||| ||||||||||||||| ||||||||||||||||||||||||||
Db   145 TGTGCAGCCTCTGGATTCACCTTCACTACCTACCATGGGCTCCGCCAGGCTCCA   204

Qy   120 GGGAAGGGGCTGGAGTGGGTGGGT   179
          ||||||||||||||||||| ||||
Db   205 GGGAAGGGGCTGGAGTGGGTCTCATCCATCCATGAGTAGTAGTACTTACATATACTACGCA   264

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCCAAGAACGCCACTGTATCTG   239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 GACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG   324

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGGGGATCTGT   299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 CAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTCTTATTACTGTGCGAGAGG--AGTTC   382

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Qy   300  CTTATGACAGAGAGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
          |||    |||||||||||||||||||||||||||||||||||||||||||||||
Db   383  CCATGGTTCAGTTCTACTTTGACTACTGGGGCCAGGGGGAACCCTGGTCACCGTCCTCA 441
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RESULT 15
AW402648
LOCUS       AW402648            540 bp    mRNA     linear    EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aav-b-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3055051 5', mRNA sequence.
ACCESSION   AW402648
VERSION     AW402648.1  GI:6921155
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 540)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..540
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3055051"
                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      120 a    133 c    161 g    126 t
ORIGIN
```

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Query Match        67.5%;    Score 241.8;  DB 10;  Length 540;
Best Local Similarity  82.9%;  Pred. No. 3.3e-56;
Matches  301;   Conservative  0;   Mismatches  57;   Indels  5;   Gaps  2;

Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGGTCCCTGAGACTCTCC  60
         ||||||||||||||||||||||| |||||||||||||||||||  ||||||||||||||||
Db  130  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGACTCTCC 189

Qy   61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGGAGCTGGGTACGCCAGGCTCCA 119
         ||||||||||| |||||||||||||||| || ||||   |||||||||  ||||||||||
Db  190  TGTGCAGCCTCTGGATTCACCTTTAGCAACTATTGATGAGTTGGGTCCGCCAGTCTCCA  249

Qy  120  GGGAAGGGCTGGAGTGGGTGGTGTTAATATAATGGTAGTGGAATTGAACCATACTATGCG 179
         ||||||||||||||||||||||| || |||||||  |||||  |||||||||||||||||
Db  250  GGGAAGGGCTGGAGTGGGTGGTGGCCAACATAAAGGAAGATGGAAGTGAGAAATACTATGTG 309

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
         |||||||||||||||  |||||||||||||  ||||| ||  ||||||||||||||||||
Db  310  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTATATCTG 369

Qy  240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCTGT 299
         ||||||||||||||||||||  |||||||||||| |||| || | || || ||  ||| ||
Db  370  CAAATGAACAGCCTGAGAGTCGAGGACACGGCCGTGTATATTACTTTACTGTGTGAGAGACCATGAT 429
```

```
Qy   300  CTTATGACAGAGAGGCTA----CTTTGACTACTGGGGGCCAGGGGAACCCTGGTCACCGTCTCC 355
          ||       |||||||         ||    |||  || || || || || ||||  ||||
Db   430  ACTAGCAGCTGGTGTATAAACTGGTCGGACCCCTGGGGACCCTGGGCATCGTCTCC 489

Qy   356  TCA 358
          |||
Db   490  TCA 492
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Search completed: July 18, 2003, 09:26:12
Job time : 622.38 secs

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              GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      July 18, 2003, 04:14:58 ; Search time 92.8077 Seconds
                              (without alignments)
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Title:       US-09-627-896b-30
Perfect score: 358
Sequence:    1 gtgcagctggtggagtctgg.........ccctggtcaccgtctcctca 358

Scoring table: IDENTITY.NUC
             Gapop 10.0 , Gapext 1.0

Searched:    2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:       4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
              Maximum Match 100%
              Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result          %      Query
No.    Score  Match  Length  DB   ID         Description
-----  -----  -----  ------  ---  -------    -----------
  1    256.6  71.7    375    22   AAF29077   Human HIV-1 monocl
  2    254.6  71.1    814    20   AAV74274   Human clone A6 fus
  3    243    67.9    675    22   AAH41661   Human interleukin
  4    243    67.9    675    22   AAH30007   Anti-IL8 monoclon
  5    241    67.3    402    24   AAK98398   Human anti-FAPalph
  6    241    67.3    788    24   AAK98407   Anti-FAPalpha anti
  7    240    67.0    792    24   ABK32988   Affinity matured c
  8    240    67.0    794    24   ABK32986   Affinity matured c
  9    240    67.0    795    24   ABK32983   DNA sequence of hu
```

```
 10   240    67.0    240    16   AAQ78945   Human immunoglobul
 11   240    67.0    240    20   AAV72533   Single chain Apo-2
 12   240    67.0    240    24   ABL41734   Nucleotide sequenc
 13   239    66.8    239    16   AAQ89332   DP54 VH gene. Hom
 14   238.6  66.6    366    22   AAF75589   Human anti-HER2/ne
 15   238.6  66.6    366    24   ABK14254   AAV293 anti-(MCP)-
 16   238.2  66.5    366    22   AAS03534   DNA encoding anti-
 17   237.4  66.3   1395    21   AAA46866   DNA encoding the h
 18   237.4  66.3   1395    21   AAA46894   DNA encoding the h
 19   237    66.2    348    24   ABA94334   MAb 27A1 heavy cha
 20   236.8  66.1   1736    22   AAS22532   Human cDNA encodin
 21   235.8  65.9    681    22   AAH30055   TRO005 heavy chain
 22   235.8  65.9    738    21   AAZ55614   Internalising anti
 23   233.6  65.3    659    14   AAQ36131   IN2A8 MAb heavy ch
 24   233.6  65.3   1741    22   AAS22531   Human cDNA encodin
 25   233    65.1   1392    21   AAA46864   DNA encoding the h
 26   233    65.1   1392    21   AAA46870   DNA encoding the h
 27   233    65.1   1392    21   AAA46890   cDNA encoding the
 28   233    65.1   1392    21   AAA46892   DNA encoding the h
 29   233    65.1   1392    21   AAA46896   DNA encoding the h
 30   233    65.1   1999    21   AAA46891   DNA encoding the h
 31   233    65.1   5924    21   AA238921   hCAT1 binding huma
 32   233    65.1    681    21   AAZ38770   HCAT1 clone 25 ant
 33   232.6  65.0    681    22   AAH30056   TRO005 heavy chain
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 35   232.2  64.9    366    22   AAF75587   Human anti-HER2/ne
 36   232.2  64.9    458    22   AAH41153   Human coding seque
 37   232    64.8    363    20   AAV72235   Human anti-GPIIb/I
 38   231.8  64.7    375    22   AAF29079   Human HIV-1 monocl
 39   231.6  64.7    410    24   ABL55674   ACZ885 antibody he
 40   231.6  64.7    519    20   AAZ20407   IgG antibody 2.1.1
 41   231.4  64.6    354    24   ABK88453   Human anti-CD40 mo
 42   231.4  64.6    354    24   ABA94330   MAb 6-2 heavy chai
 43   231.4  64.6    355    22   AAF55226   Nucleotide sequenc
 44   231.4  64.6    355    24   AAF55240   DNA sequence of he
 45   231      64.5    462    24   ABK48972   DNA encoding heavy
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ALIGNMENTS

```
RESULT 1
AAF29077
ID   AAF29077 standard; DNA; 375 BP.
XX
AC   AAF29077;
XX
DT   03-APR-2001  (first entry)
XX
DE   Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 33.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO20010678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US17327.
XX
PR   30-JUN-1999;  99US-0141701.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA,  Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   P-PSDB; AAB62776.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
```

Left column

```
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal -
XX
PS   Claim 4; Page 46; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ   Sequence 375 BP; 81 A; 90 C; 116 G; 88 T; 0 other;
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Query Match             71.7%;  Score 256.6;  DB 22;  Length 375;
Best Local Similarity   85.1%;  Pred. No. 1.7e-61;
Matches 314;  Conservative 0;  Mismatches 44;  Indels 11;  Gaps 2;
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Db    7 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 66

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
        |||||||||||  |||||||||| |||| |  | |  |||||||||| |||||||||||||
Db   67 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 126

Qy  120 GGGAAGGGGCTGGAGTGGGTGGTTAATAAATGTAGTCGGAATTGAACCATACTATGCG 179
        ||||||||||||||||||||||  |  |  |  |   |   ||||  |||||| ||| ||
Db  127 GGGAAGGGGCTGGAGTGGGTGGTGGCAACATAAAGCAAGATGAGAAGTGAGAAATACTATGTG 186

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
        |||||||||||||||||||||||||||| |||||  |||||| ||||||||||||||||||
Db  187 GACTCTGTGAAGGGCCGATTCACCATCTTCAGAAACAACGCCCAAGAACTCACTGTATCTG 246

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCT-- 297
        ||||||||||||||||||||||||||||||||||| |||||||||||||||| | ||||
Db  247 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGTTGCTACTAT 306

Qy  298 -------GTCTTATGACAGAGGCA 349
               |   | |  |||||
Db  307 GGTTCGGGGAGTTATTATTTCTACCCCCTTTGCCTACTGGGGCCAGGGAACCCTGGTCACC 366

Qy  350 GTCTCCTCA 358
        |||||||||
Db  375 GTCTCCTCA 375
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RESULT 2
AAV74274
ID   AAV74274 standard; DNA; 814 BP.
XX
AC   AAV74274;
XX
DT   10-MAY-1999 (first entry)
XX
DE   Human clone A6 fusion protein antibody DNA.
XX
KW   Antibody; human; clone A6; hAb; fusion protein; polyhistidine tag;
KW   Western blot; enzyme-linked immunosorbent assay; ELISA; therapy;
KW   immunofluorescence; immunoprecipitation assay; affinity purification;
KW   diagnosis; vaccine; serum; immune response; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..814
FT                   /*tag= a
FT                   /note= "Partial sequence, no stop codon given"
XX
PN   WO9901475-A2.
XX
PD   14-JAN-1999.
XX
PF   03-JUL-1998; 98WO-DE01882.
XX
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Right column

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PR   04-JUL-1997; 97DE-1028697.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Braunagel M, Doersam H, Kipriyanov S, Kuerschner T;
PI   Little M, Welschof M;
XX
DR   WPI; 1999-106000/09.
DR   P-PSDB; AAW90180.
XX
PT   Human antibody against fusion protein with polyhistidine tag -
PT   useful as standard in immunoassays, for affinity purification,
PT   diagnosis and therapy and for preparing vaccines
XX
PS   Claim 2; Fig 4; 20pp; German.
XX
CC   This invention describes a human antibody (hAb) against a fusion
CC   (poly)peptide or protein that includes a segment of at least 6
CC   consecutive His residues. This antibody is useful in Western blots,
CC   enzyme-linked immunosorbent assay (ELISA), immunofluorescence or
CC   immunoprecipitation assays. Also hAb can be used for affinity
CC   purification of the protein, for in vivo diagnosis or therapy, and
CC   in production of vaccines. hAb are universally applicable
CC   alternatives to human serum. They are specific for the polyhistidine
CC   tag, regardless of the nature of the rest of the protein. Since hAb
CC   are not produced in an animal, they contain no components that can
CC   induce an immune response in humans.
XX
SQ   Sequence 814 BP; 181 A; 228 C; 232 G; 173 T; 0 other;
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Query Match             71.1%;  Score 254.6;  DB 20;  Length 814;
Best Local Similarity   85.1%;  Pred. No. 6.9e-61;
Matches 309;  Conservative 0;  Mismatches 0;  Indels 49;  Gaps 2;
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Qy    1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
        ||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||
Db   12 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 71

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
        |||||||||||  |||||||||| |||| |  | |  |||||||||| |||||||||||||
Db   72 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 131

Qy  120 GGGAAGGGGCTGGAGTGGGTGGTTAATAAATGGTAGTCGGAATTGAACCATACTATGCG 179
        ||||||||||||||||||||||  |  |  |  |   |   ||||  |||||| ||| ||
Db  132 GGGAAGGGGCTGGAGTGGGTGGCGCAACATAAAGCAAGATGAGAAGTACTATGTG 191

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
        |||||||||||||||||||||||||||| |||||  |||| | |||||||||||||||||
Db  192 GACTCTGTGAAGGGCCGATTCACCATCTTCAGAGACAACACGCCAAGAACTCACTGTATCTG 251

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATTACTGTGCGAGAGGGGATCTG- 298
        ||||||||||||||||||||||||||||||||||| ||||||||||||||
Db  252 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAAAAGCAGC 311

Qy  299 ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
            |  | |  | |  |  |  |          ||  |   |||||  |||||||  ||
Db  312 AGCTGGTATCTTGGGGATGCTTTTGATATCTGGGGCCAAGGGACCAATGTCACCGTCTCT 371

Qy  356 TCA 358
        |||
Db  372 TCA 374
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```
RESULT 3
AAH41661
ID   AAH41661 standard; DNA; 675 BP.
XX
AC   AAH41661;
XX
DT   28-AUG-2001 (first entry)
XX
DE   Human interleukin 8 antibody nucleotide sequence M1-23H.
XX
```

```
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO20140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US33042.
XX
PR   06-DEC-1999; 99US-0456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding
PT   to nonhuman-antibodies, involves contacting sample with human antibody
PT   which binds to antibodies from nonhuman species and detecting binding
PT   -
XX
PS   Example 22; Page 88; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the
CC   amount of target antigen in a sample in a semi-quantitative or relative
CC   sense. Quantification of one or more target antigens in a sample can
CC   also be carried out using (I). AAH41612 to AAH41686, and AAB99361 to
CC   AAB99399, represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;

Query Match             67.9%;  Score 243;  DB 22;  Length 675;
Best Local Similarity   84.1%;  Pred. No. 1.1e-57;
Matches  302;  Conservative   0;  Mismatches  45;  Indels  12;  Gaps   2;

Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCTGAGACTCTCC   60
         |||||||| |||||||||||||||||| || ||||||||||||| |||||||||||||
Db    4  GTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC   63

Qy   61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
         ||||||| |  |||||||||| || ||  ||    || ||||| |||||||| |||||
Db   64  TGTGCAGCCTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA  123

Qy  120  GGGAAGGGGCTGGAGTGGGTGGTTAATATAATAATGGTAGTCGGAATTGAACCATATGCG  179
          ||||||||||| ||||||||| |||  ||| ||  || ||| || ||| || || |
Db  124  GGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGGTATGATGAAGTAAAAACATACAATGCA  183
```

```
Qy  180  GACTTCTGTGAAGGGCCGATTCACCATTCCAGAGGCAACGCCAAGAACTCACTGTATCTG  239
         |||| ||||||||||||||||||| |||||||| || |||   ||| ||||||||||
Db  184  GACTTCCGTGAAGGGCCGATTCACCATTCCAGAGACAATTCCAAGAACACACGCTGTATCTG  243

Qy  240  CAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCTGT  299
         ||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  244  CAAATGAACAGCCGAGGACCGAGGACACGGCCGTGTGTGTATTACTGTGCGGAGAG-------  295

Qy  300  CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCA  358
         |||  ||||||  |||||||||||||||||||||  ||||||||||||||||||||||
Db  296  ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  351


RESULT 4
AAH30007
ID   AAH30007 standard; DNA; 675 BP.
XX
AC   AAH30007;
XX
DT   19-JUL-2001 (first entry)
XX
DE   Anti-IL8 monoclonal antibody nucleotide fragment M1-23H.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US27237.
XX
PR   02-OCT-1999;   99US-0157415.
PR   01-DEC-1999;   99US-0453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells -
XX
PS   Example 22; Page 92; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (III) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;

Query Match             67.9%;  Score 243;  DB 22;  Length 675;
Best Local Similarity   84.1%;  Pred. No. 1.1e-57;
```

Left column

Matches 302; Conservative 0; Mismatches 45; Indels 12; Gaps 2;

```
Qy    1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
          ||||||||||| |||||||||||||||| ||||| |||||| |||||||||||||||||||
Db    4 GTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC  63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          ||||||| || ||||||||||||  ||    || ||  ||||||||| ||||||||||||
Db   64 TGTGCAGCGTCTGGATTCACCTTTCAGTGACTACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy  120 GGGAAGGGGCTGGAGTGGGTGGTGTTAATATAATGTGAGTCGGAATTGAACCATACTATGCG 179
          ||||||||||||||||||||||||
Db  124 GGCAGGGGCTGGAGTGGGTGGTGGCAGCTATATGATGTATGATGGAAGCATACAATGCA 183

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACACACGCTGTGTCTG 243

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  244 CAAATGAACAGCCTGAGAGCCGAGGACACGCGCTGTGTATTACTGTGCCGAGAG-------- 295

Qy  300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
           ||  ||     |||||||||||||||||||||||||||||||||||||||||||||||
Db  296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351
```

RESULT 5
AAK98398
ID   AAK98398 standard; DNA; 402 BP.
XX
AC   AAK98398;
XX
DT   08-AUG-2002 (first entry)
XX
DE   Human anti-FAPalpha antibody fragment VH50 DNA.
XX
KW   Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;
KW   gene therapy; cancer; wound healing; inflammation; cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20016708-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-EP04716.
XX
PR   17-MAR-2000; 2000DE-1013286.
PR   11-SEP-2000; 2000GB-0022216.
XX
PA   (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI   Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;
PI   Schmidt A;
XX
DR   WPI; 2002-041180/05.
DR   P-PSDB; AAO14049.
XX
PT   New human humanized antibody that specifically binds to fibroblasts
PT   activating protein alpha, useful for treating cancer or tumor, and for
PT   imaging tumors associated with activated stromal fibroblasts, e.g. lung
PT   or breast cancer -
XX
PS   Claim 20; Page 43; Page 20; 109pp; English.
XX
CC   The present invention relates to a human or humanised antibody (Ab) which
CC   specifically binds to fibroblast activating protein alpha (FAPalpha). The
CC   antibodies are useful for preparing a composition for the treatment of
CC   cancer, and for imaging tumours associated with activated stromal
CC   fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
CC   breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
CC   cancer, pancreatic cancer and metastatic brain cancer, and diseases

Right column

CC   associated with the same, such as inflammation and wound healing. The
CC   present sequence is a coding sequence described in the exemplification of
CC   the invention.
XX
SQ   Sequence 402 BP; 92 A; 105 C; 124 G; 81 T; 0 other;

Query Match 67.3%; Score 241; DB 24; Length 402;
Best Local Similarity 82.1%; Pred. No. 3.5e-57;
Matches 308; Conservative 0; Mismatches 50; Indels 17; Gaps 2;

```
Qy    1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
          || ||||||||||||||||||||||||||||||||  |||||| |||||||||||||||||
Db    4 GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          ||||||| || |||||||||||||  ||   || |  ||||||||| ||||||||||||
Db   64 TGTGCAGCGTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy  120 GGGAAGGGGCTGGAGTGGGTGGTGTTAATATAATGTGAGTCGGAATTGAACCATACTATGCG 179
          |||||||||||||||||||||||||
Db  124 GGGAAGGGGCTGGAGTGGGTGGTGGCCAACATAAAGCAAGATGAGAAATACTATGTG 183

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGCAGAGG------- 292
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGCAGAGTTCACTC 303

Qy  293 -------GATCTGCTTATGCAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTG 343
                 |||||  |||  ||||  ||||||||||||||||||||||||||||||||
Db  304 TGTACTGATGGTAGCTGCTGCCCCACCATAGGGCCTGGGCAAACTGGGGCCAGGGAACCCTG 363

Qy  344 GTCACCGTCTCCTCA 358
          |||||||||||||||
Db  364 GTCACCGTCTCCTCA 378
```

RESULT 6
AAK98407
ID   AAK98407 standard; DNA; 788 BP.
XX
AC   AAK98407;
XX
DT   08-AUG-2002 (first entry)
XX
DE   Anti-FAPalpha antibody fragment VH50YOLVLIII25 DNA.
XX
KW   Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;
KW   gene therapy; cancer; wound healing; inflammation; cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20016708-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-EP04716.
XX
PR   17-MAR-2000; 2000DE-1013286.
PR   11-SEP-2000; 2000GB-0022216.
XX
PA   (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI   Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;
PI   Schmidt A;
XX
DR   WPI; 2002-041180/05.
DR   P-PSDB; AAO14058.
XX
PT   New human humanized antibody that specifically binds to fibroblasts
PT   activating protein alpha, useful for treating cancer or tumor, and for

PT   imaging tumors associated with activated stromal fibroblasts, e.g. lung
PT   or breast cancer -
XX
PS   Claim 90; Page 46-47; 109pp; English.
XX
CC   The present invention relates to a human or humanised antibody (Ab) which
CC   specifically binds to fibroblast activating protein alpha (FAPalpha). The
CC   antibodies are useful for preparing a composition for the treatment of
CC   cancer, and for imaging tumours associated with activated stromal
CC   fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
CC   breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
CC   cancer, pancreatic cancer and metastatic brain cancer, and diseases
CC   associated with the same, such as inflammation and wound healing. The
CC   present sequence is a coding sequence described in the exemplification of
CC   the invention.
XX
SQ   Sequence 788 BP; 191 A; 212 C; 212 G; 173 T; 0 other;

Query Match   67.3%; Score 241; DB 24; Length 788;
Best Local Similarity 82.1%; Pred. No. 4e-57;
Matches 308; Conservative 0; Mismatches 50; Indels 17; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         |||||||||||||||||| ||||||||||||| ||||||| ||||||||||||||||||
Db   4 GTACAGCTGGTGGAGTCGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
         ||||||||||| ||||||||||| || || || | ||||||| ||||||||||||
Db   64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGTGAGTCGGAATTGAACCATACTATGCG 179
         |||||||||||||||||||||| | | || | | ||| || ||| |||||||| |
Db 124 GGGAAGGGGCTGGAGTGGGTGGTGGCCAACATAAAGCAAGATGGAGTGAGAAATACTATGTG 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy 240 CAAATGAACAGCTGAGAGCGCCGAGGACACGGCCGTGTATTACTGTGCCAGAGAG------ 292
         ||||||||||||||||||| ||||||||||||||||| ||||||||| | ||
Db 244 CAAATGAACAGCTGAGAGCGCCGAGGACACGGCCGTGTGTTATTACTGTGCCGAGAGTTCACTC 303

Qy 293 -------GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTG 343
                 || | ||| ||||||||||||||||||||
Db 304 TGTACTGATGGTAGCTGCCCCACCATAGGGCCTGGGCCAAACTGGGGCCAGGGAACCCTG 363

Qy 344 GTCACCGTCTCCTCA 358
         |||||||||||||||
Db 364 GTCACCGTCTCCTCA 378

RESULT 7
ABK32988
ID   ABK32988 standard; DNA; 792 BP.
XX
AC   ABK32988;
XX
DT   23-APR-2002 (first entry)
XX
DE   Affinity matured clone M36-12 DNA from anti-IL8 scFv clone 123-36.
XX
KW   Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
KW   variable light-chain; VL; anti-IL8; interleukin-8; scFV clone; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200200729-A2.
XX
PD   03-JAN-2002.
XX
PF   25-JUN-2001; 2001WO-US20542.
XX

PR   23-JUN-2000; 2000US-0602373.
PR   23-JUN-2000; 2000US-0602972.
PR   23-JUN-2000; 2000US-0603658.
PR   23-JUN-2000; 2000US-0603663.
XX
PA   (GENE-) GENETASTIX CORP.
XX
PI   Zhu L, Hua SB;
XX
DR   WPI; 2002-090521/12.
DR   P-PSDB; AAU75154.
XX
PT   Screening libraries of tester proteins against protein, peptide or
PT   nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT   generating recombinant human antibodies and screening for their
PT   affinity binding with target antigens -
XX
PS   Example 8; Fig 20; 251pp; English.
XX
CC   The present invention relates to compositions and methods for high
CC   throughput generation and screening of a human antibody or immunoglobulin
CC   (Ig) library in yeast. The method comprises expressing a library of
CC   tester fusion proteins in yeast cells, each tester fusion protein
CC   comprising either an activation domain or a DNA binding domain of a
CC   transcription activator and a tester protein having a large diversity
CC   within the library. The tester protein comprises a first polypeptide
CC   subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC   within the library, a second polypeptide subunit (e.g. human variable
CC   light-chain, VL) whose sequence varies within the library independently
CC   of the first polypeptide, and a linker peptide which links the first and
CC   second polypeptide subunits. The method is useful for generating
CC   recombinant human antibodies and screening for their affinity binding
CC   with target antigens. The present DNA sequence represents an anti-IL8
CC   scFv clone as described in the methods of the present invention.
XX
SQ   Sequence 792 BP; 166 A; 210 C; 247 G; 169 T; 0 other;

Query Match   67.0%; Score 240; DB 24; Length 792;
Best Local Similarity 81.5%; Pred. No. 7.5e-57;
Matches 313; Conservative 0; Mismatches 45; Indels 26; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         |||||||||||||||||| ||||||||||||| ||||||| ||||||||||||||||||
Db   4 GTACAGCTGGTGGAGTCCGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
         ||||||||||| ||||||||||| || | | | ||||||| ||||||||||||
Db   64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAAATGTGAGTCGGAATTGAACCATACTATGCG 179
         |||||||||||||||||||||| | | | | | || || || |||||||| |
Db 124 GGGAAGGGGCTGGAGTGGGTGGTGGCCTACATAAAGCAAGATGGAGTGAGAAATACTATGTG 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCCAAGAACTCACTGTATCTG 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCCAAGAACTCATTGTATCTG 243

Qy 240 CAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGGGATCTGT 299
         |||||||||||||||||||||||||||||||||||| ||||||||| ||||||
Db 244 CAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTGTTATTACTGTGCGAGGGAGTAAAGAGT 303

Qy 300 ------------------CTTATGACAGAGGCTACTACTTTGACTACTGGGGCCAG 334
                           |||| | | || | ||||||||||||||||||
Db 304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGCCAG 363

Qy 335 GGAACCCTGGTCACCGTCTCCTCA 358
         ||||||||||||||||||||||||
Db 364 GGAACCCTGGTCACCGTCTCCTCA 387

RESULT 8
ABK32986
ID   ABK32986 standard; DNA; 794 BP.

```
XX
AC  ABK32986;
XX
DT  23-APR-2002  (first entry)
XX
DE  Affinity matured clone M36-8 DNA from anti-IL8 scFv clone 123-36.
XX
KW  Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
KW  variable light-chain; VL; anti-IL8; interleukin-8; scFv clone; ds.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO200200729-A2.
XX
PD  03-JAN-2002.
XX
PF  25-JUN-2001; 2001WO-US20542.
XX
PR  23-JUN-2000;  2000US-0602373.
PR  23-JUN-2000;  2000US-0602972.
PR  23-JUN-2000;  2000US-0603658.
PR  23-JUN-2000;  2000US-0603663.
XX
PA  (GENE-) GENETASTIX CORP.
XX
PI  Zhu L,  Hua SB;
XX
DR  WPI; 2002-090521/12.
DR  P-PSDB; AAU75152.
XX
PT  Screening libraries of tester proteins against protein, peptide or
PT  nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT  generating recombinant human antibodies and screening for their
PT  affinity binding with target antigens -
XX
PS  Example 8; Fig 20; 251pp; English.
XX
CC  The present invention relates to compositions and methods for high
CC  throughput generation and screening of a human antibody or immunoglobulin
CC  (Ig) library in yeast. The method comprises expressing a library of
CC  tester fusion proteins in yeast cells, each tester fusion protein
CC  comprising either an activation domain or a DNA binding domain of a
CC  transcription activator and a tester protein having a large diversity
CC  within the library. The tester protein comprises a first polypeptide
CC  subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC  within the library, a second polypeptide subunit (e.g. human variable
CC  light-chain, VL) whose sequence varies within the library independently
CC  of the first polypeptide, and a linker peptide which links the first and
CC  second polypeptide subunits. The method is useful for generating
CC  recombinant human antibodies and screening for their affinity binding
CC  with target antigens. The present DNA sequence represents an anti-IL8
CC  scFv clone as described in the methods of the present invention.
XX
SQ  Sequence 794 BP; 166 A; 213 C; 247 G; 168 T; 0 other;

Query Match        67.0%;  Score 240;  DB 24;  Length 794;
Best Local Similarity  81.5%;  Pred. No. 7,5e-57;
Matches  313;  Conservative  0;  Mismatches  45;  Indels  26;  Gaps  2;

Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
         |||||||||||||||  ||||||||||||||||||||  || || |||||||||||||||
Db    4  GTGCAGCTGGTGAGTCCGGGGGAGGCTTGGTCCAGCCCGGGGGGTCCCTGAGACTCTCC  63

Qy   61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
         ||||||||||| ||||||||||||| |||| ||   |||||| ||  |||||||||||||
Db   64  TGTGCAGCCTCTGGATTCACCTTTAGTAGTACTATTGGATGAGCTGGGTCCGGCAGGCTCCA  123

Qy  120  GGGAAGGGGCTGGAGTGGGTGGTTAATTAATAATGTAGTCGGAATTGAACCATACTATGCG  179
         ||||||||||||||||||||||||   || || |||  || |||||||||  |||||||||
Db  124  GGGAAGGGGCTGGAGTGGGTGGGTGGCCTACATAAAGCAAGATGAAGTGAAGATACTACTGTG  183

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  239
```

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                           |||||||||||||||||||||||  |||||||||||||||||||  |||||||
Db  184  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCATTGTATCTG  243

                           |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Qy  240  CAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGATCTGT  299
         |||||||||||||||||||  ||||||| ||||||||||||||||||||| ||||| 
Db  244  CAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAAGAGT  303

Qy  300  --------------------CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG  334
                             |||||||||||||||||||||||||||||||
Db  304  AGCAGTAGCTGGTCTTACTATGATAGTAGTGTTATTACTACCCTGACTACTGGGGCCAG  363

Qy  335  GGAACCCTGGTCACCGTCTCCTCA  358
         |||||||||||||||||||||||
Db  364  GGAACCCTGGTCACCGTCTCCTCA  387
```

```
RESULT 9
ABK32983
ID  ABK32983 standard; DNA; 795 BP.
XX
AC  ABK32983;
XX
DT  23-APR-2002  (first entry)
XX
DE  DNA sequence of human anti-IL8 scFv clone 123-36.
XX
KW  Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
KW  variable light-chain; VL; anti-IL8; interleukin-8; scFV clone; ds.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO200200729-A2.
XX
PD  03-JAN-2002.
XX
PF  25-JUN-2001; 2001WO-US20542.
XX
PR  23-JUN-2000;  2000US-0602373.
PR  23-JUN-2000;  2000US-0602972.
PR  23-JUN-2000;  2000US-0603658.
PR  23-JUN-2000;  2000US-0603663.
XX
PA  (GENE-) GENETASTIX CORP.
XX
PI  Zhu L,  Hua SB;
XX
DR  WPI; 2002-090521/12.
DR  P-PSDB; AAU75149.
XX
PT  Screening libraries of tester proteins against protein, peptide or
PT  nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT  generating recombinant human antibodies and screening for their
PT  affinity binding with target antigens -
XX
PS  Example 8; Fig 16; 251pp; English.
XX
CC  The present invention relates to compositions and methods for high
CC  throughput generation and screening of a human antibody or immunoglobulin
CC  (Ig) library in yeast. The method comprises expressing a library of
CC  tester fusion proteins in yeast cells, each tester fusion protein
CC  comprising either an activation domain or a DNA.binding domain of a
CC  transcription activator and a tester protein having a large diversity
CC  within the library. The tester protein comprises a first polypeptide
CC  subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC  within the library, a second polypeptide subunit (e.g. human variable
CC  light-chain, VL) whose sequence varies within the library independently
CC  of the first polypeptide, and a linker peptide which links the first and
CC  second polypeptide subunits. The method is useful for generating
CC  recombinant human antibodies and screening for their affinity binding
CC  with target antigens. The present DNA sequence represents an anti-IL8
CC  scFv clone as described in the methods of the present invention.
XX
```

SQ Sequence 795 BP; 166 A; 211 C; 247 G; 171 T; 0 other;

Query Match
Best Local Similarity   67.0%;   Score 240; DB 24;   Length 795;
                        81.5%;   Pred. No. 7.5e-57;
Matches 313; Conservative 0; Mismatches 45; Indels 26; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCGCCAGGCTCCA 119
         |||||||||| |||||||||||||| ||||| |||||||||||||||||||||
Db   64 TGTGCAGCCTCTGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATGTAGTCGGAATTGAACCATACTATGCG 179
         ||||||||||||||||||||||||| ||| || |||||| ||||||||||||||
Db 124 GGGAAGGGGCTGGAGTGGGTGGCTACATAAAGCAAGATGAAGATGAGAAATACTATGTG 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCATTGTATCTG 243

Qy 240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAAGAGT 303

Qy 300 -----------------CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG 334
                          |||| |||||||||||||||||||||||||
Db 304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCGTGACTACTGGGGCCAG 363

Db 335 GGAACCCTGGTCACCGTCTCCTCA 358

Db 364 GGAACCCTGGTCACCGTCTCCTCA 387

RESULT 10
AAQ78945
ID AAQ78945 standard; DNA; 877 BP.
XX
AC AAQ78945;
XX
DT 01-AUG-1995 (first entry)
XX
DE Human immunoglobulin Vh gene #7.
XX
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   184..638
FT   /*tag= a
FT   /product= Human immunoglobulin Variable heavy chain
FT intron   229..331
FT   /*tag= b
FT misc_signal   638..640
FT   /*tag= c
FT   /note= "miscellaneous signal, does not conform to
FT   terminator or splice site sequence"
XX
PN WO9426895-A.
XX
PD 24-NOV-1994.
XX
PF 10-MAY-1993; 93WO-JP00603.
XX
PR 10-MAY-1993; 93WO-JP00603.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
PI Honjo T; Matsuda F;
XX

DR WPI; 1995-006791/01.
DR P-PSDB; AAR66301.
XX
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
XX
PS Claim 16; Page 39-40; 130pp; Japanese.
XX
CC A series of genes (AAQ78939-79002) encoding human immunoglobulin
CC variable heavy chains. The genes were isolated and cloned from a series
CC of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131,
CC by PCR amplification using primers AAQ78917-38. The genes are subdivided
CC into 5 families of Vh genes. The fragments cover a region of 800 kb.
CC The DNA fragments were isolated from high molecular weight DNA from
CC human placenta. The DNA was partially digested with TaqI restriction
CC enzyme. The fragments were separated by gel electrophoresis and 35-45 kb
CC fractions were collected. The fragments were ligated with ClaI-digested
CC cosmid vector pJB81. The ligation products were in vitro packed and
CC infected into E.coli 490A. The Vh genes and the DNA fragments encoding
CC hybridisation. The fragments were then subcloned by colony
CC useful in producing human immunoglobulin in mammalian hosts.
XX
SQ Sequence 877 BP; 198 A; 207 C; 258 G; 214 T; 0 other;

Query Match
Best Local Similarity   67.0%;   Score 240; DB 16;   Length 877;
                        91.1%;   Pred. No. 7.6e-57;
Matches 266; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 347 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAGACTCTCC 406

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTATTGGATGAGCTGGGTC 119
         |||||||||| ||||||||||||| ||||| |||||||||||||||||||||||||||
Db 407 TGTGCAGCCTCTGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 466

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
         |||||||||||||||||||||||| ||||| || |||||| ||||||||||||||
Db 467 GGGAAGGGGCTGGAGTGGGTGGCTACATAAAGCAAGATGAAGATGAGAAATACTATGTG 526

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 527 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 586

Qy 240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 587 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 638

RESULT 11
AAV72533
ID AAV72533 standard; cDNA; 939 BP.
XX
AC AAV72533;
XX
DT 16-MAR-1999 (first entry)
XX
DE Single chain Apo-2 antibody 20E6 encoding cDNA.
XX
KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW TNF cytokine; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..939
FT   /*tag= a
XX
PN WO9851793-A1.
XX
PD 19-NOV-1998.
XX

PF 14-MAY-1998;   98WO-US09704.
XX
PR 09-FEB-1998;   99US-0020746.
PR 15-MAY-1997;   97US-0857216.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
DR WPI; 1999-045228/04.
DR P-PSDB; AAW83323.
XX
PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
PT conditions linked with decreased apoptosis e.g. cancer, and produce
PT antibodies to increase or decrease apoptosis
XX
PS Example 14; Fig 15B; 134pp; English.
XX
CC The present invention describes human Apo-2. Apo-2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and so is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs and Apo-2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo-2, useful to treat
CC mammalian cancer cells, and to produce Apo-2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC tag polypeptide allow Apo-2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmaceutically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric molecules
CC comprising first and second Apo-2 antibodies). Agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC antibodies may also be used diagnostically e.g. to detect Apo-2
CC expression in cells/tissues and in Apo-2 purification. The present
CC sequence encodes a single chain Apo-2 antibody, designated 20E6.
XX
SQ Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;

Query Match   67.0%; Score 240; DB 20; Length 939;
Best Local Similarity   91.1%; Pred. No. 7.7e-57;
Matches 266; Conservative   0; Mismatches 25; Indels   1; Gaps   1;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 180

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          |||||||||| ||||||||||||||||||||||||| ||||||| |||||||||||||
Db   181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240

Qy   120 GGGAAGGGGCTGGAGTGGGTGGCCAACATCTCCAGAGGACAACGCCAAGACCATACTATGCG 179
          |||||||||||||||||||||| ||||| |||||||||||||| ||||| ||||||||
Db   241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
          |||||||||||| ||||||||||||||||||||||| ||||||||||| |||||||||
Db   301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 412

RESULT 12
ABL41734
ID ABL41734 standard; DNA; 939 BP.
XX
AC ABL41734;
XX

DT 29-MAY-2002 (first entry)
XX
DE Nucleotide sequence of single-chain Apo-2 antibody 20E6.
XX
KW Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
KW caspase; apoptosis; cancer; antibody; ss.
XX
OS Bacteriophage.
XX
FH Key   Location/Qualifiers
FT CDS   1..939
FT   /*tag= a
FT   /product= "single-chain Apo-2 antibody 20E6"
XX
PN US6342369-B1.
XX
PD 29-JAN-2002.
XX
PF 14-MAY-1998;   98US-0079029.
XX
PR 15-MAY-1997;   97US-046615P.
PR 09-FEB-1998;   98US-074119P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 2002-224941/28.
DR P-PSDB; ABB09604.
XX
PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
PT stimulating apoptosis in cancer cells, thus especially useful in the
PT treatment of cancer, or in enhancing immune-mediated cell death -
XX
PS Example 14; Fig 15B; 68pp; English.
XX
CC The present sequence encodes a single-chain Apo-2 antibody, designated
CC 20E6, which is isolated from a phage library. It is believed that
CC Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
CC family. Apo-2 polypeptide is capable of triggering caspase-dependent
CC apoptosis and activating nuclear factor-kappa B. A soluble
CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
CC antibodies may be used to activate or stimulate apoptosis in cancer
CC cells. They are therefore especially useful in the treatment of cancer,
CC to enhance immune-mediated cell death in cells expressing Apo-2, to
CC detect expression of Apo-2 in specific cells, tissues or serum, and in
CC affinity purification of Apo-2 from recombinant cell culture or natural
CC sources.
XX
SQ Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;

Query Match   67.0%; Score 240; DB 24; Length 939;
Best Local Similarity   91.1%; Pred. No. 7.7e-57;
Matches 266; Conservative   0; Mismatches 25; Indels   1; Gaps   1;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 180

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
          |||||||||| ||||||||||||||||||||||||| ||||||| |||||||||||||
Db   181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240

Qy   120 GGGAAGGGGCTGGAGTGGGTGGCCAACATCTCCAGAGGACAACGCCAAGAACCATATATGCG 179
          |||||||||||||||||||||| ||||| |||||||||||||| ||||| ||||||||
Db   241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
          |||||||||||||||||||||||||||||||||||||||||||||||||||

Db   361 CAAATGAACAGCCTGAGAGCCGAGGACGGCTGTGTATTACTGTGCGAGAG 412

RESULT 13
AAQ89332
ID   AAQ89332 standard; DNA; 294 BP.
XX
AC   AAQ89332;
XX
DT   26-SEP-1995 (first entry)
XX
DE   DP54 VH gene.
XX
KW   Graves ophthalmopathy associated immunoglobulin protein;
KW   orbital antigen; monoclonal antibody; heavy chain; H chain;
KW   variable region; autoimmunity; ss.
XX
OS   Homo sapiens.
XX
PN   WO9508336-A.
XX
PD   30-MAR-1995.
XX
PF   22-SEP-1994; 94WO-US10756.
XX
PR   22-SEP-1993; 93US-0124469.
XX
PA   (NICH-) NICHOLS INST DIAGNOSTICS.
XX
PI   Mclachlan SM, Rapoport B;
XX
DR   WPI; 1995-139383/18.
DR   P-PSDB; AAR72074.
XX
PT   Graves' ophthalmopathy-associated monoclonal antibody - produced
PT   by molecular cloning of immunoglobulin genes by PCR
XX
PS   Disclosure; Page 72; 94pp; English.
XX
CC   L- and H-chain DNA was amplified by PCR from Graves' orbital
CC   tissue and clones encoding autoimmune-associated immunoglobulin
CC   fragments were obtained. 2/15 clones of H chain (IgG1) genes
CC   showed homology to the germline gene DP54 (AAQ89332). The DNA
CC   (AAQ89333) and corresp. amino acid (AAR72075) sequences of the VH
CC   region of a representative clone, OF7H1.19, are provided.
XX
SQ   Sequence 294 BP; 69 A; 66 C; 98 G; 61 T; 0 other;

Query Match   66.8%; Score 239; DB 16; Length 294;
Best Local Similarity 91.1%; Pred. No. 1.2e-56;
Matches 265; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACAGCTCCAGGCTCCA 119
         |||||||||| | |||||||||||| | | | ||||||| ||||||||
Db   64 TGTGCAGCCTCTCGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy   120 GGGAAGGGGCTGGAGTGGGTTGTTAATAATGGTAGTCGGAACCATACTATGCG 179
         |||||||||||||||||||||| | || | | | | || || || ||
Db   124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGAAGTGAGAAATACTATGTG 183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA 290
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA 294

RESULT 14.
AAF75589
ID   AAF75589 standard; DNA; 366 BP.
XX
AC   AAF75589;
XX
DT   10-MAY-2001 (first entry)
XX
DE   Human anti-HER2/neu antibody 2-E8 heavy chain coding sequence.
XX
KW   Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
KW   3-F2; 1-D2; 2-E8; growth factor receptor; ds.
XX
OS   Homo sapiens.
XX
PN   WO200109187-A2.
XX
PD   08-FEB-2001.
XX
PF   25-JUL-2000; 2000WO-US20272.
XX
PR   29-JUL-1999; 99US-0146313.
PR   10-MAR-2000; 2000US-0188539.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T, Deo Y;
XX
DR   WPI; 2001-168698/17.
DR   P-PSDB; AAB72883.
XX
PT   New human monoclonal antibody that specifically binds to growth factor
PT   receptor HER2/neu, for treating, preventing or diagnosing diseases
PT   characterized by aberrant HER2/neu expression e.g. cancers
XX
PS   Disclosure; Page 108; 113pp; English.
XX
CC   The present invention provides the protein and coding sequences for human
CC   monoclonal antibodies which bind specifically to the HER2/neu growth
CC   factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
CC   and 2-E8. They can be used in the immunotherapy-based treatment and
CC   prognosis of cancers, particularly adenocarcinomas such as salivary
CC   gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
CC   and ovarian cancer. The present sequence is a coding sequence of an
CC   antibody of the invention.
XX
SQ   Sequence 366 BP; 80 A; 87 C; 114 G; 85 T; 0 other;

Query Match   66.6%; Score 238.6; DB 22; Length 366;
Best Local Similarity 82.4%; Pred. No. 1.6e-56;
Matches 299; Conservative 0; Mismatches 59; Indels 5; Gaps 2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTCCAGGCTCCA 119
         ||||||||||| | ||||||||| | | | ||| |||| ||||||||||
Db   64 TGTGCAGCCTCTCGATTCACCTTTCAGTAGCTATGTCATGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy   120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
         ||||||||||||||||||||| | || | | | | ||| | | |||||| || ||
Db   124 GGCCAAGGGGCTGGAGTGGGTGGCAGTTATATGATGATGGAAGTAATAAATACTATGCA 183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCACGCCTGTATCTG 239
         ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||
Db   184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACACCAAGAACACGCTGTATCTG 243

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGATCTG- 298
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTGTATTACTGTGCGCTTATGGTTCGG 303

Qy   299 ---TCTTATGACAGAGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355

```
Db   304 GGACTTATTATAACGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 363
             | |  |||||||||||||||||||||||||||||||||||||||||||||
Qy   356 TCA 358
             |||
Db   364 TCA 366

RESULT 15
ABK14254
ID   ABK14254 standard; cDNA; 366 BP.
XX
AC   ABK14254;
XX
DT   08-MAY-2002  (first entry)
XX
DE   AAV293 anti-(MCP)-1 antibody heavy chain cDNA sequence.
XX
KW   Human; antibody; MCP; monocyte chemoattractant; antiasthmatic;
KW   antiallergic; antiinflammatory; idiopathic thrombocytopaenia;
KW   immunosuppressive; cytostatic; vasotropic; antiarteriosclerotic;
KW   antirheumatic; antiarthritic; osteopathic; antigen-binding site;
KW   immunoglobulin heavy chain; monocyte migration; T cell migration;
KW   CC-type chemokine; eotaxin; allergy; allergic rhinitis; cancer;
KW   hypersensitivity response; allergic contact dermatitis; gene;
KW   inflammatory disease; asthma; psoriasis; COPD; osteoporosis;
KW   inflammatory bowel disease; multiple sclerosis; autoimmune disease;
KW   rheumatoid arthritis; diabetes; systemic lupus erythematosus;
KW   bone disease; osteoporosis; osteoarthritis; periodontal disease;
KW   haematological disorder; haemolytic anaemia; graft rejection;
KW   leucocyte infiltration; restenosis; arteriosclerosis; AAV293; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..366
FT                  /*tag= a
FT                  /product= "AAV293 heavy chain protein"
FT                  /transl_except= (pos:142..144, aa:Val)
FT                  /partial
FT                  /note= "No start or stop codon shown"
XX
PN   WO200202640-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-EP07468.
XX
PR   30-JUN-2000; 2000GB-0016138.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Hiestand P, Hofstetter H, Payne TG, Urfer R, Di Padova FE;
XX
DR   WPI; 2002-164525/21.
DR   P-PSDB; AAU75737.
XX
PT   New compound that binds human monocyte chemoattractant protein-1,
PT   useful e.g for treating inflammation, comprises immunoglobulin chains
PT   with specific hypervariable regions -
XX
PS   Example 1; Page 21; 42pp; English.
XX
CC   This invention relates to a molecule that binds MCP-1 (human monocyte
CC   chemoattractant protein-1). The molecule has at least one antigen
CC   -binding site comprising at least one immunoglobulin (Ig) heavy and/or
CC   light chain variable domain (Vh, Vl). The antibody of the invention
CC   inhibits binding of MCP-1 (and also eotaxin) to specific receptors, so
CC   preventing migration of monocytes and T cells. These are human
CC   antibodies with very high affinity for MCP-1, but no significant
CC   reaction with other human CC-type chemokines or MCP-1 from other
CC   species. The MCP-1 binding molecules, specifically antibodies that cross
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CC   -react with eotaxin, are used to prevent or treat MCP-1 or eotaxin-
CC   mediated disorders, particularly those that involve migration or
CC   activation of monocytes and T cells, e.g. allergies (allergic rhinitis,
CC   hypersensitivity responses, allergic contact dermatitis, inflammatory
CC   diseases (asthma, psoriasis, COPD, inflammatory bowel disease,
CC   multiple sclerosis) autoimmune disease (rheumatoid arthritis; diabetes,
CC   systemic lupus erythematosus), diseases of bone and cartilage
CC   (osteoporosis, osteoarthritis, periodontal disease) haematological
CC   disorders (haemolytic anaemia, idiopathic thrombocytopaenia) graft
CC   rejection, cancers that include leucocyte infiltration, (re)stenosis,
CC   arteriosclerosis, osteoporosis and many other diseases listed in the
CC   specification. The present sequence represents the human AAV293
CC   anti-(MCP) antibody heavy chain cDNA sequence of the invention.
XX
SQ   Sequence 366 BP; 78 A; 87 C; 118 G; 83 T; 0 other;

Query Match             66.6%;  Score 238.6; DB 24;  Length 366;
Best Local Similarity   82.4%;  Pred. No. 1.6e-56;
Matches  299;  Conservative  0;  Mismatches  59;  Indels  5;  Gaps  2;

Qy     1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCTGAGACTCTCC  60
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Db     4 GTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  63

Qy    61 TGTGCAGCCTC-CGGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db    64 TGTGCAGCCTCTGGATTCACCTTTAGTCACTACTGGATGCACTGGGTCCGCCAGGCTCCA 123

Qy   120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTGTCGGAATTGAACCATACTATGCG 179
           ||||| |||||||||||||||| |||  |||| |||||||||||||| |||||||||||
Db   124 GGGAAGGGCTGGAGTGGGTGGCTGGCCAACATAGACAAGATGAAGATACTATGTG 183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
           |||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||||
Db   184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACACACGCCAAGAATTCACTGTATCTG 243

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGGAGAG---GGAT 295
           |||||||||||||||||||||||||||||||||||||| ||||||| |||||||    |
Db   244 CAAATGAACAGTCTGAGAGCCGAGGACACGGCCGTGTATTCTGTGCGGAGGATCTTGAA 303

Qy   296 CTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
           |||||||  |||||||||||||||||  ||||||||||||||||||||||||||||||||
Db   304 GGTCTACATGGGGATGGGGTACTTCGATCTCTGGGGCCACCCTGGTCACCGTCTCT 363

Qy   356 TCA 358
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Db   364 TCA 366

Search completed: July 18, 2003, 06:44:07
Job time : 93.8077 secs
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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        July 18, 2003, 06:19:39 ; Search time 86.5438 Seconds
                                          (without alignments)
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Title:         US-09-627-896B-30
Perfect score: 358
Sequence:      1 gtgcagctggtggagtctgg.........ccctggtcaccgtctcctca 358

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters:    2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications_NA:*
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               2:  /cgn2_6/ptcdata/1/pubpna/PCT_NEW_PUB.seq:*
               3:  /cgn2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*
               4:  /cgn2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*
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               8:  /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*
               9:  /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq:*
               10: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq1:*
               11: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq2:*
               12: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq3:*
               13: /cgn2_6/ptcdata/1/pubpna/US09_PUBCOMB.seq:*
               14: /cgn2_6/ptcdata/1/pubpna/US10_NEW_PUB.seq:*
               15: /cgn2_6/ptcdata/1/pubpna/US10_PUBCOMB.seq:*
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               17: /cgn2_6/ptcdata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	243	67.9	675	12	US-09-453-234-67	Sequence 67, Appl
2	241	67.3	402	10	US-09-811-737-7	Sequence 7, Appli
3	241	67.3	788	10	US-09-811-737-24	Sequence 24, Appli
4	240	67.0	939	15	US-10-052-798-7	Sequence 7, Appli
5	239	66.8	294	12	US-09-995-529-7	Sequence 7, Appli
6	237.6	66.4	672	12	US-09-972-656-67	Sequence 67, Appl
7	237.4	66.3	1395	15	US-10-153-382-8	Sequence 8, Appl
8	237	66.2	348	15	US-10-324-493-15	Sequence 15, Appli
9	236	65.9	375	15	US-10-172-317-1	Sequence 1, Appli
10	233	65.1	1392	15	US-10-153-382-1	Sequence 1, Appli
11	233	65.1	1392	15	US-10-153-382-4	Sequence 4, Appli
12	233	65.1	1392	15	US-10-153-382-12	Sequence 12, Appli
13	233	65.1	1999	15	US-10-153-382-2	Sequence 2, Appli
14	231.4	64.6	354	15	US-10-324-493-7	Sequence 7, Appli
15	231	64.5	357	15	US-10-073-644C-1	Sequence 1, Appli
16	231	64.5	630	11	US-09-844-684-14	Sequence 14, Appl

No.	Score		% Match	Length	DB	ID	Description
c 17	231	230.6	64.5	630	15	US-10-040-244-14	Sequence 14, Appl
c 18	230.6	230.6	64.4	9182	12	US-09-927-122-41	Sequence 41, Appl
c 19	230.6	230.6	64.4	9182	12	US-09-927-121B-89	Sequence 89, Appl
20	230.2	230.2	64.3	675	12	US-09-453-234-59	Sequence 59, Appl
21	230.2	230.2	64.3	675	12	US-09-453-234-91	Sequence 91, Appl
22	230.2	230.2	64.2	677	12	US-09-453-234-55	Sequence 55, Appl
23	230	230	64.2	1798	10	US-09-925-299-230	Sequence 230, App
24	230	230	64.1	1798	12	US-09-925-299-230	Sequence 230, App
25	229.4	229.4	64.1	580	11	US-09-884-684-12	Sequence 12, Appl
26	229.4	229.4	64.1	580	15	US-10-040-244-12	Sequence 12, Appl
27	228.2	228.2	63.7	669	12	US-09-972-656-85	Sequence 85, Appl
28	228	228	63.7	375	12	US-09-848-798-89	Sequence 89, Appl
29	226.6	226.6	63.3	411	11	US-09-423-800-58	Sequence 58, Appl
30	226.6	226.6	63.3	411	15	US-10-182-018-58	Sequence 58, Appl
31	226.6	226.6	63.3	411	15	US-10-169-003-58	Sequence 58, Appl
32	226.4	225.4	63.2	375	12	US-09-848-798-90	Sequence 90, Appl
33	225.4	225.4	63.0	351	15	US-10-324-493-23	Sequence 23, Appl
34	225.4	225.4	63.0	375	12	US-09-848-798-91	Sequence 91, Appl
35	225.4	225.4	63.0	675	12	US-09-453-234-107	Sequence 107, App
36	224.8	224.8	62.8	375	12	US-09-848-798-77	Sequence 77, Appl
37	223.8	223.8	62.5	675	12	US-09-453-234-105	Sequence 105, App
38	223.6	223.6	62.5	381	12	US-09-848-798-88	Sequence 88, Appl
39	223.4	223.4	62.4	660	12	US-09-791-153A-56	Sequence 56, Appl
40	223.2	223.2	62.3	363	11	US-09-822-698A-4	Sequence 4, Appli
41	223.2	223.2	62.3	1143	11	US-09-822-698A-6	Sequence 6, Appli
42	223.2	223.2	62.3	1356	11	US-09-822-698A-27	Sequence 27, Appl
43	222.2	222.2	62.1	675	12	US-09-453-234-61	Sequence 61, Appl
44	222.2	222.2	62.1	675	12	US-09-453-234-69	Sequence 69, Appl
45	222.2	222.2	62.1	675	12	US-09-453-234-99	Sequence 99, Appl

ALIGNMENTS

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RESULT 1
US-09-453-234-67
; Sequence 67, Application US/09453234
; Publication No. US2003009199SAl
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT: Valkirs, Gunars
;  APPLICANT: Gray, Jeff
;  APPLICANT: Lonberg, Nils
;  APPLICANT: Biosite Diagnostics, Inc.
;  APPLICANT: GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-0001l0US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;  LENGTH: 675
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: M1-23H
;  NAME/KEY: CDS
;  LOCATION: (1)..(675)
US-09-453-234-67

  Query Match             67.9%;     Score 243;  DB 12;  Length 675;
  Best Local Similarity   84.1%;     Pred. No. 3.3e-73;
  Matches  302;  Conservative  0;  Mismatches  45;  Indels  12;  Gaps  2;

Qy    1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
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Db    4 GTCCAGCTGGTGGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  63

Qy   61 TGTGCAGCCTC-CGGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
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Db    64 TGTGCAGCCTCTGGATTCACCTTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy   120 GGGAAGGGGCTGGAGTGGGTGTTAATATAATGTGAGTCGGAATTGAACCATACTATGCG 179
           ||||||||||||||||||||||  |||| |||  ||||||||| || |||||||||||
Db   124 GGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAACATACAATGCA 183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
           |||| ||||||||||  ||||| ||| || |||||  |||  ||||| |||||||||
Db   184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCGCGTATCTG 243

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Db   244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG------- 295

Qy   300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
           ||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351

RESULT 2
US-09-811-737-7
; Sequence 7, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Human FAP-alpha-specific antibodies
; FILE REFERENCE: 1-1129
; CURRENT APPLICATION NUMBER: US/09/811,737
; CURRENT FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-811-737-7

Query Match           67.3%;  Score 241;  DB 10;  Length 402;
Best Local Similarity 82.1%;  Pred. No. 1.4e-72;
Matches  308;  Conservative   0;  Mismatches  50;  Indels  17;  Gaps   2;

Qy    1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCTGAGACTCTCC 60
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Db    4 GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db   64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy  120 GGGAAGGGGCTGGAGTGGGTGTTAATATAATGTGAGTCGGAATTGAACCATACTATGCG 179
          |||||||||||||||||||||  |||| ||| ||||||||| || |||||||||||
Db  124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGAGAAAATACTATGTG 183

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
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Db  184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGG------ 292
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Db  244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG------- 303

Qy  293 -------GATCTGTCTTATGACAGAGGCTACTACTGGGGCCAGGGAACCCTG 343
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Db  304 TGTACTGATGGTAGCTGCCCCACCATAGGGGCCTGGGCCAAACTGGGGCCAGGGAACCCTG 363

Qy  344 GTCACCGTCTCCTCA 358
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Db  364 GTCACCGTCTCCTCA 378

RESULT 3
US-09-811-737-24
; Sequence 24, Application US/09811737
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Db    64 TGTGCAGCCTCTGGATTCACCTTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy   120 GGGAAGGGGCTGGAGTGGGTGTTAATATAATGTGAGTCGGAATTGAACCATACTATGCG 179
           ||||||||||||||||||||||  |||| |||  ||||||||| || |||||||||||
Db   124 GGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAACATACAATGCA 183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db   184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACACGCGTGTATCTG 243

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
           ||||||||||||||||||| |||| |||||||| || |||||||| |||||||||
Db   244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG------- 295

Qy   300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
           ||| |||||||||||||| |||||||||| |||||||||||||||||||||||||||||
Db   296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351

RESULT 4
US-10-052-798-7
; Sequence 7, Application US/10052798
; Publication No. US2002015098A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
;            Ashkenazi, Avi J.
;            Chuntharapai, Anan
;            Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech).
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/052,798
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;     FILING DATE: 02-No. US20020150985A1-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/079,029
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Marschang, Diane L.
;     REGISTRATION NUMBER: 35,600
;     REFERENCE/DOCKET NUMBER: P1101R2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650/225-5416
;     TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 939 base pairs
;     TYPE: Nucleic Acid
;     STRANDEDNESS: Single
;     TOPOLOGY: Linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-052-798-7

Query Match      67.0%;  Score 240;  DB 15;  Length 939;
Best Local Similarity  91.1%;  Pred. No. 4e-72;
Matches  266;  Conservative  0;  Mismatches  25;  Indels  1;  Gaps  1;

Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC   60
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Db  121  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC  180

Qy   61  TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACAGCTGGGTACGCCAGGCTCCA  119
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Db  181  TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATTGAGTGGATGAGCTGGGTCGGCCAGGCTCCA  240

Qy  120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTGCGAATTGAACCATACTATGCG  179
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Db  241  GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAGTGAGAAATACTATGTG  300

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGGCAACGCCAAGAACTCACTGTATCTG  239
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  301  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  360

Qy  240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG  291
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG  412


RESULT 5
US-09-995-529-7
; Sequence 7, Application US/09995529
; Publication No. US2003009965A1
; GENERAL INFORMATION:
;   APPLICANT: Watkins, Jeffry D.
;   APPLICANT: Huse, William D.
;   APPLICANT: Tang, Ying
;   TITLE OF INVENTION: Humanized Collagen Antibodies and
;   TITLE OF INVENTION: Related Methods
;   FILE REFERENCE: P-IX 4976
;   CURRENT APPLICATION NUMBER: US/09/995,529
;   CURRENT FILING DATE: 2001-11-26
;   NUMBER OF SEQ ID NOS: 358
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-995-529-7

Query Match      66.8%;  Score 239;  DB 12;  Length 294;
Best Local Similarity  91.1%;  Pred. No. 6e-72;
Matches  265;  Conservative  0;  Mismatches  25;  Indels  1;  Gaps  1;

Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC
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Db    4  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC   63

Qy   61  TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
         ||||||||||  ||||||||||||| ||  ||||||||||| ||||||||||||||||||
Db   64  TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATTGGATGAGCTGGGTCGGCCAGGCTCCA  123

Qy  120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTGCGAATTGAACCATACTATGCG  179
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Db  124  GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAGTGAGAAATACTATGTG  183

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGGCAACGCCAAGAACTCACTGTATCTG  239
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Db  184  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  243

Qy  240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA  290
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Db  244  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA  294


RESULT 6
US-09-972-656-67
; Sequence 67, Application US/0972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
;   APPLICANT: Deshpande, Rajendra
;   APPLICANT: Tsai, Mei-Mei
;   TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;   TITLE OF INVENTION: Neutralizing Activity
;   FILE REFERENCE: A-799
;   CURRENT APPLICATION NUMBER: US/09/972,656
;   CURRENT FILING DATE: 2001-10-05
;   NUMBER OF SEQ ID NOS: 135
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
;   LENGTH: 672
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(672)
US-09-972-656-67

Query Match      66.4%;  Score 237.6;  DB 12;  Length 672;
Best Local Similarity  82.9%;  Pred. No. 2.4e-71;
Matches 295;  Conservative  0;  Mismatches  59;  Indels  2;  Gaps  2;

Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC   60
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    4  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC   63

Qy   61  TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTAC      AGCTGGGTACGCCAGGCTCCA  119
         ||||||||||  ||||||||||||||||          |||||||| |||||||||||||
Db   64  TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCGGCCAGGCTCCA  123

Qy  120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTGCGAATTGAACCATACTATGCG  179
         ||||||||||||||||||||  | |                ||||||||||||||||||
Db  124  GGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGGTAGTAGCAGACCATACCGA  183

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGGCAACGCCAAGAACTCACTGTATCTG  239
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  184  GACTCCGTGAAGGGCCGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG  243

Qy  240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG-GGATCTG  298
         |||||||||||||||||| |  ||       |||||||||| |||        |||||||
Db  244  CAAATGAACAGCCTGAGAGCCCTGTCTTGTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC  303


RESULT 7
US-10-153-382-8
```

; Sequence 8, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-8

Query Match 66.3%; Score 237.4; DB 15; Length 1395;
Best Local Similarity 82.7%; Pred. No. 3.5e-71;
Matches 297; Conservative 0; Mismatches 56; Indels 6; Gaps 2;

Qy 1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
Db 61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120

Qy 61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
Db 121 TGTACAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 180

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTATGGTAGTCGGAATTGAACCATATGCGG 179
Db 181 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGAGGAAGTAATAAACACTATGGA 240

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
Db 241 GACTCCGTGAAGGGCCGATTCACCATCTCCAGTGACAATTCCAAGAACACGCTGTATCTG 300

Qy 240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
Db 301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGAGAGAGA 360

Qy 300 CTTATGACAGAGCTACTTTGACTACTGGGCCCAGGAACCCTGGTCACCGTCTCCTCA 358
Db 361 CTGGGGTC-----CTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 414

RESULT 8
US-10-324-493-15
; Sequence 15, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
; APPLICANT: Pluenneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 3005-C
; CURRENT APPLICATION NUMBER: US/10/324,493
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/847,816
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/579,808
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/665,343
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/785,934
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)..(348)
US-10-324-493-15

Query Match 66.2%; Score 237; DB 15; Length 348;
Best Local Similarity 83.3%; Pred. No. 3.1e-71;
Matches 299; Conservative 0; Mismatches 45; Indels 15; Gaps 2;

Qy 1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
Db 4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy 61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
Db 64 TGTACAGCGTCTGGATTCACCTTCAGTAGATATGGCACTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATATGCGG 179
Db 124 GGCAAGGGGCTGGAGTGGGTGGCAATTATATGTTTGAAGGAAATATCAATACTATGCA 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
Db 184 GACTCCGTGAAGGGCCGATTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy 240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
Db 244 GAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGGAGAGGGAAGT-- 301

Qy 300 CTTATGACAGAGCTACTTTGACTACTGGGCCCAGGAACCCTGGTCACCGTCTCCTCA 358
Db 302 --------ACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 348

RESULT 9
US-10-172-317-1
; Sequence 1, Application US/10172317
; Publication No. US20030091561A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus A.
; APPLICANT: Halk, Edward
; APPLICANT: Gerritsen, Arnout F.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
; FILE REFERENCE: GMI-020
; CURRENT APPLICATION NUMBER: US/10/172,317
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/298,172
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-317-1

Query Match 65.9%; Score 236; DB 15; Length 375;
Best Local Similarity 81.5%; Pred. No. 6.9e-71;
Matches 303; Conservative 0; Mismatches 55; Indels 14; Gaps 2;

Qy 1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
Db 4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy 61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
Db 64 TGTGCAGCGTCTGGATTCACCTTCAGTACCTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATATGCGG 179
Db 124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGGTATATGGGATGATGAGAAGTTATAAATACTATGGA 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239

RESULT 10
US-10-153-382-1
; Sequence 1, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-1

Query Match   65.1%;   Score 233; DB 15; Length 1392;
Best Local Similarity   82.2%;   Pred. No. 1.1e-69;
Matches 295; Conservative   0; Mismatches   55; Indels   9; Gaps   2;

```
Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC   60
         |||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db   61  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGAGGTCCCTGAGACTCTCC  120

Qy   61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTCAGGCCAGGCTCCA   119
         |||| || || ||||||||||||| ||| |||           |||||||||||||
Db  121  TGTGTAGCGTCTGGATTCACCTTTCAGTAGCACTAGCCATGGCATGCCAGGCTCCA   180

Qy  120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG  179
         || |||||||||||||||||||
Db  181  GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGATGTATATGATGGAAGAAATAAATACTATGCA  240

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGCAACGCCAAGAACTCACTGTATCTG  239
         || |||||||||||||||||||||||||||||
Db  241  GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACAATTCCAAGAACACGCTGTTTCTG  300

Qy  240  CAAATGAACAGCCTGAGACGCCGAGGACACGGCCGTGTGTATTACTGTGTATTACTGTGT  299
         ||||||||||||||||||||   || |||||||||||||||||||||||||||||||
Db  301  CAAATGAACAGCCTGAGAGCACGGCCGTGTGTATTACTGTGTATTACTGTGCGAGAGG-------  353

Qy  300  CTTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  354  -AGGTCACTTCGGTCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   411
```

RESULT 11
US-10-153-382-4
; Sequence 4, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-4

Query Match   65.1%;   Score 233; DB 15; Length 1392;
Best Local Similarity   82.2%;   Pred. No. 1.1e-69;
Matches 295; Conservative   0; Mismatches   55; Indels   9; Gaps   2;

```
Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC   60
         |||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db   61  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGAGGTCCCTGAGACTCTCC  120

Qy   61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTCAGGCCAGGCTCCA   119
         |||| || || ||||||||||||| ||| |||           |||||||||||||
Db  121  TGTGTAGCGTCTGGATTCACCTTTCAGTAGCACTAGCCATGGCATGCCAGGCTCCA   180

Qy  120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG  179
         || |||||||||||||||||||
Db  181  GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGATGTATATGATGGAAGAAATAAATACTATGCA  240

Qy  180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGCAACGCCAAGAACTCACTGTATCTG  239
         || |||||||||||||||||||||||||||||
Db  241  GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACAATTCCAAGAACACGCTGTTTCTG  300

Qy  240  CAAATGAACAGCCTGAGACGCCGAGGACACGGCCGTGTGTATTACTGTGTATTACTGTGT  299
         ||||||||||||||||||||   || |||||||||||||||||||||||||||||||
Db  301  CAAATGAACAGCCTGAGAGCACGGCCGTGTGTATTACTGTGTATTACTGTGCGAGAGG-------  353

Qy  300  CTTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  354  -AGGTCACTTCGGTCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   411
```

RESULT 12
US-10-153-382-12
; Sequence 12, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-12

Query Match   65.1%;   Score 233; DB 15; Length 1392;
Best Local Similarity   82.2%;   Pred. No. 1.1e-69;
Matches 295; Conservative   0; Mismatches   55; Indels   9; Gaps   2;

```
Qy    1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGTCCCTGAGACTCTCC   60
         |||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db   61  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGAGGTCCCTGAGACTCTCC  120

Qy   61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTCAGGCCAGGCTCCA   119
         |||| || || ||||||||||||| ||| |||           |||||||||||||
Db  121  TGTACAGCGTCTGGATTCACCTTTCAGTAGTTATGGCATGCCAGTAGCACTAGCCATGGCATGCCAGGCTCCA  180
```

Qy 120 GGGAAGGGGCTGGTGAGTGGGTGGTGTTAATATAAATTGAACCATACTATGCG 179
         |||||||||||||||||||||||||||||| || || ||||||||||||
Db 181 GGCAAGGGGCTGGTGAGTGGGTGGCAGTTATATGGTATGGAAGCAATAAACACTATGCA 240

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
         ||||| | |||||||||||||||||||||||||||||||||||||||||| ||||||||
Db 241 GACTCCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAGACACGCGTGTATCTG 300

Qy 240 CAAATGAACAGCCTGAGAGCCTGATTACTGTCGCGAGAGGGGATCTGT 299
         |||||||||||||||||||||| |||||| ||||||||||||||||
Db 301 CAAATGAACAGCCTGAGAGCCTGAGAGCACGCTGTGTATTACTGCGAGAGGGGACTCTG 360

Qy 300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCA 358
         || |||||||||||||||||||||||||||||||||||||||
Db 361 CT--------GGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 411

RESULT 13
US-10-153-382-2
; Sequence 2, Application US/10153382
; Publication No. US2003008693OA1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-2

Query Match   65.1%; Score 233; DB 15; Length 1999;
Best Local Similarity   82.2%; Pred. No. 1.3e-69;
Matches 295; Conservative   0; Mismatches   55; Indels   9; Gaps   2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         |||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||
Db   61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGGTCCCTGAGACTCTCC 120

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTTACGAGCTGGGTACGCCAGGCTCCA 119
         |||||||| | ||||||||||||| || || | ||||||||||| ||||||||
Db 121 TGTGTAGCGTCTGGATTCACCTTCAGTGAGCCATGGCATGGCTGTATTCAGTGGGTCCGCCAGGCTCCA 180

Qy 120 GGGAAGGGGCTGGTGAGTGGGTGGTGTTAATATAAATTGAACCATACTATGCG 179
         |||||||||||||||||||||||||||| || || ||||||||||||
Db 181 GGCAAGGGGCTGGTGAGTGGGTGGCAGTTATATGGTATGGAAGAAATAAATACTATGCA 240

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
         ||||| | |||||||||||||||||||||||||||||||||||||||||| ||||| ||
Db 241 GACTCCCGTGAAGGGCCGATTCACCATCTCCAGAGACACACGCTGTGTTTCTG 300

Qy 240 CAAATGAACAGCCTGAGAGCCTGATTACTGTCGCGAGAGGGGATCTGT 299
         |||||||||||||||||||||||| |||||| ||||||||||||||
Db 301 CAAATGAACAGCCTGAGAGCCTGTATTACTGTGCGAGAGG-------- 353

Qy 300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCA 358
         | ||||||||||||||||||||||||||||||||||||||
Db 354 -AGGTCACTTCGTCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 411

RESULT 14
US-10-324-493-7
; Sequence 7, Application US/10324493
; Publication No. US2003012412A1
; GENERAL INFORMATION:
; APPLICANT: Pluenneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF

; FILE REFERENCE: 3005-C
; CURRENT APPLICATION NUMBER: US/10/324,493
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/847,816
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/579,808
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/665,343
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/785,934
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(354)
US-10-324-493-7

Query Match   64.6%; Score 231.4; DB 15; Length 354;
Best Local Similarity   81.9%; Pred. No. 2.6e-69;
Matches 294; Conservative   0; Mismatches   56; Indels   9; Gaps   2;

Qy   1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
         |||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||
Db   4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTTACGAGCTGGGTACGCCAGGCTCCA 119
         |||||||| | ||||||||||||| || || | ||||||||||| ||||||||
Db   64 TGTGCAGCCTCTGGATTCGCCTTCAGTGATTAGCTATTCAGTGGGTCCGCCAGGCTCCA 123

Qy 120 GGGAAGGGGCTGGTGAGTGGGTGGTGTTAATATAAATTGAACCATACTATGCG 179
         |||||||||||||||||||||||||||| || || ||||||||||||
Db 124 GGCAAGGGGCTGGTGAGTGGGTGGCAGTTATATCATATGATGGAGCAAGAAATACTATGCA 183

Qy 180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
         ||||| | |||||||||||||||||||||||||||||||||||||||||| ||||||||
Db 184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAGACAATTCCAAGACAATTCCAAGAGATACGCGTGTATTTG 243

Qy 240 CAAATGAACAGCCTGAGAGCCTGTTATTACTGTGCGAGAGGGATCGT 299
         |||||||||||||||||||||| |||||| ||||||||||||||
Db 244 CAAATGAACAGCCTGAGAGCCTGAGAGCGACGCTGTGTATTACTGCGAGAGGGGAGA 303

Qy 300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCA 358
         | ||||||||||||||||||||||||||||||||||||||
Db 304 C-------GTGGGTCGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 354

RESULT 15
US-10-073-644C-1
; Sequence 1, Application US/10073644C
; Publication No. US2003008264A1
; GENERAL INFORMATION:
; APPLICANT: Hudson, Debra
; APPLICANT: van de Winkel, Jan
; APPLICANT: van Dijk, Marc
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO FC ALPHA
; TITLE OF INVENTION: RECEPTOR (CD89)
; FILE REFERENCE: MXI-211
; CURRENT APPLICATION NUMBER: US/10/073,644C
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/338,956
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/268,075
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 357
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-073-644C-1

```
Query Match        64.5%;   Score 231;   DB 15;   Length 357;
Best Local Similarity   81.6%;   Pred. No. 3.6e-69;
Matches  293;   Conservative   0;   Mismatches   60;   Indels   6;   Gaps   2;

Qy     1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
         ||||| |||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db     4 GTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGGTCCCTGAGACTCTCC  63

Qy    61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
         |||||||||||  |||||||||| |||| ||| |   | ||||||||| |||||||||||
Db    64 TGTGCAGCCTCTGGATTCACCTTCAGTAGTTATGTTCTGCACTGGGTCCGCCAGGCTCCA  123

Qy   120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAAATGGTAGTCGGAATTGAACCATACTATGCG  179
         |||||||||||||||||||||||| |  |   | ||| || ||| |      | | |||
Db   124 GGCAAGGGGCTGGATTGGGTGGCAGTGATTATCAGAGATGATGGAAGGAATAAATACTTCGCA  183

Qy   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACGCCAAGAACTCACTGTATCTG  239
         |||| |||||||||||||||||||||||||| |   ||  | |||||| |||||||||
Db   184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG  243

Qy   240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT  299
         |||||||||||||||||||||||||||  |||| |||||||||| |||| ||||   |||
Db   244 CAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGTGAGAG----AAG  298

Qy   300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
         ||  |||||||| ||| ||||||||||||||||||||||| |||||||||||||||||
Db   299 GGTATAGCGGCAGCTGGTTTGACTACTGGGGCCAGGGAACCCCGGTCACCGTCTCCTCA  357
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Search completed: July 18, 2003, 15:38:41
Job time : 87.5438 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 09:26:19 ; Search time 18.9834 Seconds
(without alignments)
5783.490 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 1 gtgcagctggtggagtctgg.........cctggtcaccgtctcctca 358

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	240	67.0	877	3	US-08-545-809A-7	Sequence 7, Appli
2	240	67.0	939	4	US-09-079-029-7	Sequence 7, Appli
3	228	63.7	375	4	US-09-240-274-89	Sequence 89, Appl
4	226.4	63.2	375	4	US-09-240-274-90	Sequence 90, Appl
5	225.8	63.1	1350	1	US-08-157-101A-9	Sequence 9, Appl
6	225.8	63.1	1576	1	US-08-157-101A-6	Sequence 6, Appl
7	225.4	63.0	375	4	US-09-240-274-91	Sequence 91, Appl
8	224.8	62.8	375	4	US-09-240-274-77	Sequence 77, Appl
9	223.6	62.5	381	4	US-09-240-274-88	Sequence 88, Appl
10	223.4	62.4	354	2	US-08-652-816A-22	Sequence 22, Appl
11	223	62.3	363	4	US-09-202-181-3	Sequence 3, Appl
12	222.6	62.2	432	1	US-08-026-320A-1	Sequence 1, Appl
13	222.2	62.1	892	4	US-09-273-839A-11	Sequence 11, Appl
14	221.6	61.9	375	4	US-09-240-274-92	Sequence 92, Appl
15	220.4	61.6	381	4	US-09-240-274-87	Sequence 87, Appl
16	219.4	61.3	360	5	US-08-428-197-21	Sequence 21, Appl
17	219.4	61.3	360	5	PCT-US93-10555-21	Sequence 21, Appl
18	218.4	61.0	363	3	US-08-599-226-37	Sequence 37, Appl
19	218.4	61.0	363	4	US-09-125-098-37	Sequence 37, Appl
20	217.8	60.8	360	2	US-08-428-197-19	Sequence 19, Appl
21	217.8	60.8	360	2	US-08-958-201-7	Sequence 7, Appl
22	217.8	60.8	360	4	US-08-958-201-9	Sequence 9, Appl
23	217.8	60.8	360	5	PCT-US93-10555-19	Sequence 19, Appl
24	217.6	60.8	715	3	US-08-545-809A-11	Sequence 11, Appl
25	216.8	60.6	375	4	US-09-240-274-78	Sequence 78, Appl
26	216.6	60.6	375	4	US-09-240-274-93	Sequence 93, Appl
27	216.2	60.4	360	2	US-08-428-197-23	Sequence 23, Appl
28	216.2	60.4	360	2	US-08-428-197-25	Sequence 25, Appl
29	216.2	60.4	360	2	US-08-428-197-27	Sequence 27, Appl
30	216.2	60.4	360	5	PCT-US93-10555-23	Sequence 23, Appl
31	216.2	60.4	360	5	PCT-US93-10555-25	Sequence 25, Appl
32	216.2	60.4	360	5	PCT-US93-10555-27	Sequence 27, Appl
33	215.4	60.2	417	4	US-08-134-346A-49	Sequence 49, Appl
34	215.2	60.1	908	4	US-09-273-839A-9	Sequence 9, Appli
35	214.8	60.0	360	2	US-08-428-197-29	Sequence 29, Appl
36	214.8	60.0	360	2	US-08-428-197-31	Sequence 31, Appl
37	214.8	60.0	360	5	PCT-US93-10555-29	Sequence 29, Appl
38	214.8	60.0	360	5	PCT-US93-10555-31	Sequence 31, Appl
39	214.8	60.0	378	5	US-09-240-274-192	Sequence 192, App
40	214.6	59.9	389	5	PCT-US93-08435-11	Sequence 11, Appli
41	214.6	59.9	423	1	US-08-259-372A-1	Sequence 1, Appli
42	214.6	59.9	423	1	US-08-468-671-1	Sequence 1, Appli
43	214.4	59.9	519	3	US-08-545-809A-21	Sequence 21, Appl
44	214.4	59.9	743	3	US-08-545-809A-48	Sequence 48, Appl
45	214.2	59.8	351	4	US-09-240-274-184	Sequence 184, App

ALIGNMENTS

RESULT 1
US-08-545-809A-7
; Sequence 7, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 877 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-7

Query Match   67.0%;   Score 240;   DB 3;   Length 877;

Best Local Similarity   91.1%;   Pred. No. 1.4e-63;
Matches 266; Conservative   0; Mismatches 25; Indels   1; Gaps   1;

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Db    347 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAGACTCTCC 406

Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGATGAGCTGGCTCCA 119
          |||||||||||  ||||||||||||||||| ||| |||||||||||||||||||||||||
Db    407 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTTCCGGCCAGGCTCCA 466

Qy    120 GGGAAGGGGCTGGAGTGGGTGGCAACTAAAGCAAGATGGAGTGAGAAATACTATGCG 179
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    467 GGGAAGGGGCTGGAGTGGGTGGCAACTAAAGCAAGATGGAGTGAGAAATACTATGCG 526

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db    527 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAACAACGCCAAGAACTCACTGTATCTG 586

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
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Db    587 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 638
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RESULT 2
US-09-079-029-7
; Sequence 7, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
;   APPLICANT: Adams, Camilia W.
;   APPLICANT: Ashkenazi, Avi J.
;   APPLICANT: Chuntharapai, Anan
;   APPLICANT: Kim, Kyung J.
;   TITLE OF INVENTION: Apo-2 Receptor
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/079,029
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Marschang, Diane L.
;   REGISTRATION NUMBER: 35,600
;   REFERENCE/DOCKET NUMBER: P1101R2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-5416
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 939 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-09-079-029-7

Query Match   67.0%;   Score 240; DB 4; Length 939;
Best Local Similarity   91.1%;   Pred. No. 1.4e-63;
Matches 266; Conservative   0; Mismatches 25; Indels   1; Gaps   1;

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Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGATGAGCTGGCTCCA 119
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Db    181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTTCCGGCCAGGCTCCA 240

Qy    120 GGGAAGGGGCTGGAGTGGGTGGTGGTGCCAACATAAAGCAAGATGAAGTGAGAAATACTATGCG 179
          |||||||||| |||||||||||||  ||| ||  |  ||||  |   |||||||||||||||
Db    241 GGGAAGGGGCTGGAGTGGGTGGTGCCAACATAAAGCAAGATGAAGTGAGAAATACTATGTG 300

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
          ||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db    301 GACTCTGTGAAGGGCCCGATTCACCATCTCCAGAGACACGCCAAGAACTCACTGTATCTG 360

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 412
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RESULT 3
US-09-240-274-89
; Sequence 89, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-89

Query Match   63.7%;   Score 228; DB 4; Length 375;
Best Local Similarity   80.1%;   Pred. No. 4.6e-60;
Matches 298; Conservative   0; Mismatches 60; Indels 14; Gaps   2;

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Qy     61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGATGAGCTGGCTCCA 119
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Db     64 TGTGTAGTGTCTGGATTCACCTTTCATAACTATGGCATGCACTGGGTTCGCCAGGCTCCA 123

Qy    120 GGGAAGGGGCTGGAGTGGGTGGTGGTGCCAACATAAAGCAAGATGAAGTGAGAAATACTATGCG 179
          |||||||||| ||||||||| |||| ||| ||||  ||  |  | |||  || |||||||||
Db    124 GGCAAGGGGCTGGAGTGGGTGGGTGGCAGTTATTTGTTGTTGATGAAGTAATAAATACTATGCA 183

Qy    180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
          |||| || |||||||||||||||||||||||||||  | | ||||| ||  || ||||||
Db    184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243

Qy    240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC--- 296
          ||||||||||||| ||||||||||||||||||||| ||||| |||||||| || |    |
Db    244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATATTACTGTGCGAGAGAACCAG 303

Qy    297 --------TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                  ||  | | ||||  ||| | || |||||  || ||||  || |   |||||
Db    304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGTCAGGGAACCCTGGTC 363

Qy    347 ACCGTCTCCTCA 358
          ||||||||||||
Db    347 ACCGTCTCCTCA 358
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Db   364 ACCGTCTCCTCA 375

RESULT 4
US-09-240-274-90
; Sequence 90, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 0596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-90

Query Match   63.2%; Score 226.4; DB 4; Length 375;
Best Local Similarity 79.8%; Pred. No. 1.4e-59;
Matches 297; Conservative 0; Mismatches 61; Indels 14; Gaps 2;

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Db    4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy   61 TGTGCGACCTC-GGATTCACCTTACTAGGAATCCTACGAGCTGGTACGCCAGGCTCCA  119
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Db   64 TGTGTAGTGTCTGGTTTCACCTTCAACTAATATAATGGCATGGGTCGGCCAGGCTCCA  123

Qy  120 GGGAAGGGGCTGGAGTGGGTGTTAATAAATGTAGTCGGAATTGAACCATACTATGCG  179
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Db  124 GCCAAGGGGCTGGAGTGGGTGGCAGTTATTTGATGAAGTAATAAATACTATGCA  183

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
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Db  184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACACACTGTACCTG 243

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATC-- 296
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Db  244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGAGAACCAG 303

Qy  297 --------TGTCTTATGACAGAGGCTACTTTGACTCTGGGGGCCAGGGAACCCTGGTC  346
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Db  304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTCTGGGGGCCAGGGAACCCTGGTC 363

Qy  347 ACCGTCTCCTCA 358
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Db  364 ACCGTCTCCTCA 375
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RESULT 5
US-08-157-101A-9
; Sequence 9, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
;   APPLICANT: KURIHARA, TATSUYA
;   APPLICANT: MATSUKURA, SHIGEKAZU
;   APPLICANT: TSURUOKA, NOBUO
;   APPLICANT: ARIMA, KENJI
;   APPLICANT: NISHIHARA, TATSURO
;   TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
;   TITLE OF INVENTION: PLASMIDS THEREFOR

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
  ADDRESSEE: PILLSBURY, MADISON & SUTRO
  STREET: 1100 NEW YORK AVENUE, N.W.
  CITY: WASHINGTON
  STATE: D.C.
  COUNTRY: USA
  ZIP: 20005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/157,101A
  FILING DATE: 05-APR-1994
  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
  NAME: TITUS, MARLANA K
  REGISTRATION NUMBER: 35843
  REFERENCE/DOCKET NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-861-3711
  TELEFAX: 202-822-0944
  TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1350 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
US-08-157-101A-9

Query Match   63.1%; Score 225.8; DB 1; Length 1350;
Best Local Similarity 80.5%; Pred. No. 3.1e-59;
Matches 289; Conservative 0; Mismatches 67; Indels 3; Gaps 2;

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Qy    1 GTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
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Db    4 GTGCAGCTGGTGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC  63

Qy   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db   64 TGTGCAGCTCTGGATTCACCTTCAGTAGCAATTCTATGCACTGGGTCGCCCAGGCTCCA  123

Qy  120 GGGAAGGGGCTGGAGTGGGTGTGGTTAATAATGGTAGTGAGTTGAACCATACTATGCG  179
        |||||||||||||||||||||  || |||| || || || |||||||| |||| ||||
Db  124 GGCAAGGGGTTGGAGTGGGTGGCAGTTATATTATGATGAAATCATAAATTCTACGCA  183

Qy  180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 239
        ||||| |||||||||||||||||||| |||||||||  |  |||| | |||||| |||||
Db  184 GACTCCGTGAAGGGCCGATTCACCATTCCAGAGACAACAATTCCAAGAACACACTGTACTG 243

Qy  240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGATCGT 299
        |||||||||||||||||||||||||||||||| |||  || |||||||| || |  |
Db  244 GAGTGAAGAGCTGCAAACTGAGGACACGGGGGTGTCTATTACTGTATAAGA--GATCAA  301

Qy  300 CTTATGACAGAGGCTACTTTGACTCTGGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
        |||  || |  || |||||||||||| |||||||||||||||||||||||||||||||
Db  302 CTTACGGAGTCCACAGATTTGACTCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 360
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RESULT 6
US-08-157-101A-6
; Sequence 6, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
;   APPLICANT: KURIHARA, TATSUYA
;   APPLICANT: MATSUKURA, SHIGEKAZU
;   APPLICANT: TSURUOKA, NOBUO
;   APPLICANT: ARIMA, KENJI
;   APPLICANT: NISHIHARA, TATSURO

US-09-240-274-77

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Query Match        62.8%;  Score 224.8;  DB 4;  Length 375;
Best Local Similarity   79.6%;  Pred. No. 4.3e-59;
Matches  296;  Conservative   0;  Mismatches   62;  Indels  14;  Gaps    2;

Qy      1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGGTCCCTGAGACTCTCC    60
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Db      4  GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC    63

Qy     61  TGTGCAGCCTC-GGATTCACCTTACTAGGAATCCTACGAGCTGGGTACGCCAGGGCTCCA   119
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Db     64  TGTGTAGTGTCTGGTTTCACCTTCACAATAACTATGGCATGCACTGGGTCCGCCAGGCTCCA   123

Qy    120  GGGAAGGGGCTGGAGTGGGTGGTTAATAATAATGGTAGTCGGAATTGAACCATACTATGCG   179
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Db    124  GGCAAGGGGCTGGAGTGGGTGGTGCAGTTTATATGTTTGATGATGGAAGTAAGAGACTATGCA   183

Qy    180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG   239
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Db    184  GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACACTTCCAGAGAACACACTGTATCTG   243

Qy    240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA--------   296
           |||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    244  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAAAATGTG   303

Qy    297  --------TGTCTTATGACAGAGGCTACTTTGACTACTTTGACTTTGATTACTGGGGCC   346
                   ||| |||||||||||||||||| ||||||||||||||||||||||||
Db    304  ATAAAGCTATGGTCCCGATACCTTTACTACTTTGATTACTGGGGCCAGGGAACCCTGGTC   363

Qy    347  ACCGTCTCCTCA   358
           |||||||||||
Db    364  ACCGTCTCCTCA   375
```

RESULT 9
US-09-240-274-88

```
; Sequence 88, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 0596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D14
US-09-240-274-88

Query Match        62.5%;  Score 223.6;  DB 4;  Length 381;
Best Local Similarity   79.1%;  Pred. No. 1e-58;
Matches  299;  Conservative   0;  Mismatches   59;  Indels  20;  Gaps    2;

Qy      1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGAGGGGTCCCTGAGACTCTCC    60
           ||||||||||||||||||||||||||| |||||||| || |||||||||||||||||||||
Db      4  GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC    63

Qy     61  TGTGCAGCCTC-GGATTCACCTTACTAGGAATCCTACGAGCTGGGTACGCCAGGGCTCCA   119
           |||||||| || ||||||||||| | ||    ||||||||||||||  |||||||||||||
Db     64  TGTGCAGCGTCTGGATTCACCTTCAGTACTTATGGCATGCACTGGGTCCGCCAGGCTCCA   123

Qy    120  GGGAAGGGGCTGGAGTGGGTGGTTAATAATAATGGTAGTCGGAATTGAACCATACTATGCG   179
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;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 22:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 354 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-652-816A-22

Query Match         62.4%;  Score 223.4; DB 2; Length 354;
Best Local Similarity 80.5%;  Pred. No. 1.1e-58;
Matches 289;  Conservative 0;  Mismatches 61;  Indels 9;  Gaps 2;

Qy   1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC    60
        |||||| ||||||||||||||||||||  ||||  |||||||| |||| ||||||||||||
Db   4  GTACACCTGGTGGAGTCTGGGGGAGGCCTTGGTCAGCCTGGGGGGTCCCTGAGACTCTCC    63

Qy  61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGTACGCCAGGCTCCA   119
        |||||| ||||  || |||||||||||||||| |||||||||||| |||||||||||||
Db  64  TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGCACTGGGTCCGCCAGGCTCCA   123

Qy 120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG   179
        ||||||||||| ||||||||| |  |||||||||||||||| ||||| ||||||||||
Db 124  GGGAAGGGGCTTGAGTGGGTGTCTCAGCTATTAGTGGTAGTGGTAGCACATACTACGCA   183

Qy 180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCGTGTATTACTGTGCGAGA   239
        ||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db 184  GACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG   243

Qy 240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA-------   295
        |||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 244  CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------   295

Qy 300  CTTATGACAGAGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   358
        |||   |||   |  ||||||| ||||||||||||||||||||||||||||||||||||
Db 296  CTTTGGTTCGGGGAGTTATAAAGGACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   354
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Qy  61  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGTACGCCAGGCTCCA   119
        |||||| |||  || |||| |||| ||||| ||  ||||| ||||||||| |||||||||
Db  64  TGTGCACCGTCTGGATTCGTCTTCAGCAGTTATGGCATGCACTGGGTCCGCCAGACTCCA   123

Qy 120  GGGAAGGGGCTGGAGTGGGTGTTAATATAATGGTAGTCGGAATTGAACCATACTATCGCG   179
        || ||||||| ||||||||||  | | |||| |||| |||| ||| |  || | ||||
Db 124  GGCAAGGGGCTTGAGTGGGTGTCACTTTATATGCATGATGGAAGTAATAGATTCTATGCA   183

Qy 180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG   239
        ||||| |||||||||||||||||||||||||||||||  |||||||||  |||||| |||
Db 184  GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACATTGTATTTG   243

Qy 240  CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT   299
        |||||||||||||||||||||||||||||||| ||||| ||||| ||||||||
Db 244  CAAATGAACAGCCTGAGAGCCGAGGACACGGCTATGTACTTCTGTGCGAGAGAGGCTG   303

Qy 300  CTTATGACAGAGCT-ACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC   357
        |||||||||||||   ||||||| ||||||||||||||||||||||||||||||||||
Db 304  ATTGCAGCACCTGCTGCCTTTTGACCCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC   362
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RESULT 11
US-09-202-181-3
; Sequence 3, Application US/09202181
; Patent No. 6254867
; GENERAL INFORMATION:
;  APPLICANT: REISNER, Yair et al.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO THE HEPATITIS B SURFACE
;  TITLE OF INVENTION: ANTIGEN
;  FILE REFERENCE: REISNER=5
;  CURRENT APPLICATION NUMBER: US/09/202,181
;  CURRENT FILING DATE: 1998-12-10
;  PRIOR APPLICATION NUMBER: 118625
;  PRIOR FILING DATE: 1996-06-11
;  PRIOR APPLICATION NUMBER: IL97/00184
;  PRIOR FILING DATE: 1997-06-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;  LENGTH: 363
;  TYPE: DNA
;  ORGANISM: human
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(363)
US-09-202-181-3

Query Match         62.3%;  Score 223; DB 4; Length 363;
Best Local Similarity 79.9%;  Pred. No. 1.5e-58;
Matches 287;  Conservative 0;  Mismatches 70;  Indels 2;  Gaps 2;

Qy   1  GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC    60
        |||||| |||||||||||||||||||| ||||||||||||| |||| ||||||||||||
Db   4  GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC    63
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RESULT 12
US-08-026-320A-1
; Sequence 1, Application US/08026320A
; Patent No. 5419904
; GENERAL INFORMATION:
;  APPLICANT: Irie, Reiko F
;  TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
;  TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
;  NUMBER OF SEQUENCES: 11
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Poms, Smith, Lande & Rose
;   STREET: 2029 Century Park East, Suite 3800
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 90067
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WordPerfect 5.1
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/026,320A
;   FILING DATE: 26-FEB-1993
;   CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/609803
;   FILING DATE: 05-NOV-1990
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Oldenkamp, David J
;   REGISTRATION NUMBER: 29421
;   REFERENCE/DOCKET NUMBER: 94268
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 3107885046
;   TELEFAX: 3102771297
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 432 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
;  ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;   CELL TYPE: Epstein Barr Virus Transformed B cell
;   CELL LINE: L612
;  FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..432
;   OTHER INFORMATION: /function= "Heavy Chain"
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;   OTHER INFORMATION:  /product= "Immunoglobulin Variable Region"
;   OTHER INFORMATION:  /standard_name= "HuMab L612 Heavy Chain Variable
;   OTHER INFORMATION:  Region Sequence"
;   FEATURE:
;   NAME/KEY:  misc_feature
;   LOCATION: 148..162
;   OTHER INFORMATION:  /function= "Complementary
;   OTHER INFORMATION:  determining region 1 (CDR1)"
;   FEATURE:
;   NAME/KEY:  misc_feature
;   LOCATION: 271..300
;   OTHER INFORMATION:  /function= "Complementary
;   OTHER INFORMATION:  determining region 2 (CDR2)"
;   FEATURE:
;   NAME/KEY:  misc_feature
;   LOCATION: 397..429
;   OTHER INFORMATION:  /function= "Complementary determining
;   OTHER INFORMATION:  region 3 (CDR3)"
US-08-026-320A-1

Query Match             62.2%;  Score 222.6;  DB 1;  Length 432;
Best Local Similarity   79.9%;  Pred. No. 2.1e-58;
Matches  287;  Conservative   0;  Mismatches   69;  Indels   3;  Gaps   2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         61 GTGCAGCTGTTGGATTCTGGATTCACCTTGGTACAGCCTGGGGGTGCCCAGGCTCTCC  120

Qy         61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
              ||||||||||  ||||||||||||   || | |||||||||||||||||||||||||||
Db        121 TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGGCATGCACTGGGTCCGCCAGGCTCCA  180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATAAATGGTAGTGGAATTGAACCATACTATGCG  179
              ||||||||||||||||||||||| ||||||| | ||||||||||| ||||||||||
Db        181 GGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTAGCACATACTACGCA  240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  239
              |||||||||||||||||||||||   |||||  |||||||||||||  |||||||||||
Db        241 GACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGGTGTATCTG  300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCGT  299
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTATTACTGTGCGAAAGTGGCAAC  360

Qy        300 CTTATGACAGAGAGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
              ||||   |||| | | ||||||||     ||||||||||||||||||||||||||||||
Db        361 GATATTTTGACTGGTTATTATGCT--TCGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  417
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RESULT 13
US-09-273-839A-11
; Sequence 11, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
;   APPLICANT: Cirino, Nick M
;   APPLICANT: Jackson, Paul J
;   APPLICANT: Lehnert, Bruce E
;   TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
;   TITLE OF INVENTION: Receptors
;   FILE REFERENCE: S-89,662
;   CURRENT APPLICATION NUMBER: US/09/273,839A
;   CURRENT FILING DATE: 1999-03-22
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 892
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-273-839A-11

Query Match   62.1%; Score 222.2; DB 4; Length 892;
Best Local Similarity   80.5%; Pred. No. 3.4e-58;
Matches 289; Conservative   0; Mismatches   58; Indels 12; Gaps   2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  165

Qy         61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
              ||||||||||  ||||||||||   || | ||||||||||||||||||| |||||||||
Db        166 TGTGCAGCCTCTGGATTCACCTTCAATACCATGTATGGAATGCACTGGGTCCGCCAGGCTCCA  225

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATAAATGGTAGTGGAATTGAACCATACTATGCG  179
              ||  |||||||||||||||| ||| |||| | ||||||||| | |||||||||||
Db        226 GGCAAGGGGCTGGAGTGGGTCTCTGGTATTAATTGGGATGGTGGTAGCACAGGTTATGCA  285

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  239
              ||||||||||||||||||||||||||||||   |||| | ||||||  |||||||||||
Db        286 GACTCTGTGAAGGGCCGATTCGCCGTCTCCAGAGACAACACCAAGAACTCCCTGTATCTG  345

Qy        240 CAAATGAACAGCCTGAGAGACGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCGT  299
              ||||||||||||||||| | |||||| |||||| |||||||| |||
Db        346 CAAATAAACAGTCTGAGAGCTGAGGACACTGTGTATTACTGTGCGAGAG----------  397

Qy        300 CTTATGACAGAGAGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  358
              ||         |||| |||||||||||    |||| ||| ||||||||||||||||||
Db        398 ---CTAACTGGGGACGCCATTGACTACTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCA  453
```

RESULT 14
US-09-240-274-92
; Sequence 92, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-42U2
;   CURRENT APPLICATION NUMBER: US/09/240,274
;   CURRENT FILING DATE: 1999-01-29
;   EARLIER APPLICATION NUMBER: 60/081,380
;   EARLIER FILING DATE: 1998-04-10
;   EARLIER APPLICATION NUMBER: 60/028,550
;   EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D18
US-09-240-274-92

Query Match   61.9%; Score 221.6; DB 4; Length 375;
Best Local Similarity   79.0%; Pred. No. 4e-58;
Matches 294; Conservative   0; Mismatches   64; Indels 14; Gaps   2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCCAGCCTGGGAGGTCCCTGAGACTCTCC  63

Qy         61 TGTGCAGCCTC-CGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
              ||||||||||  ||||||||||   || | ||||||||||||||||||| |||||||||
Db         64 TGTGTAGTGTCTCTGGTTCACCTTCAATACTACTGCCATGTCGTGGTTTGATGAGTAATAAATACTACTGCA  123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATAAATGGTAGTGGAATTGAACCATACTATGCG  179
              ||  |||||||||||||||| ||| | || | ||||||||| | |||||||||||
Db        124 GGCAAGGGGTTGGAGTGGGTGGCAGTTATTTGGTTTGATGAAGTAATAAATACTACTATGCA  183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG  239
              ||||||||||||||||||||||||||||   |  |||| | ||||||  ||||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACACTGTACCTG  239

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC  296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    244  CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGAACCAG  303

Qy    297  --------TGTCTTATGACAGAGAGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC   346
                   |||||| |||||||||||||||||||||
Db    304  ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC  363

Qy    347  ACCGTCTCCTCA  358
           ||||| |||||
Db    364  ACCGTGTCCTCA  375
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RESULT 15
US-09-240-274-87
; Sequence 87, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D13
US-09-240-274-87

  Query Match   61.6%; Score 220.4; DB 4; Length 381;
  Best Local Similarity   78.6%; Pred. No. 9.3e-58;
  Matches 297; Conservative   0; Mismatches 61; Indels 20; Gaps   2;

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Qy     1  GTGCAGCTGGTGGTGAGTCGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTTCTCC   60
          |||||| |||||| |||||||||||||||||| |||||||||||||||||||||||||
Db     4  GTGCAGCTGCTCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC   63

Qy    61  TGTGCAGCCTC-GGATTCACCTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA  119
          |||||||||||  ||| |||||||||||| |||||||||||||||||||||||||
Db    64  TGTGCAGCGTCTGGATTCACCTTCAGTACTTATGGCATGCACTGGGTCCGCCAGGCTCCA  123

Qy   120  GGGAAGGGGCTGGAGTGGGTTAATATAATGTAGTCGGAATTGAACCATACTATGCG  179
          |||||||||| ||||||||||||||    ||||||     | |||||
Db   124  GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGTTTGATGGAAGTAACAGAGACTATGCA  183

Qy   180  GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACCAACGCCAAGAACTCACTGTATCTG  239
          |||| || ||||| |||| ||||| ||||||| |||||| |||| |||| |||
Db   184  GAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAGTCCAAGAACACACTGTATCTG  243

Qy   240  CAAATGAACAGCCTGAGAGCCGAGGACACGCGCCGTGTATTACTGTGCGAGA--------  290
          ||||||||||||||||||| ||||||| |||  || |   |||||||||||
Db   244  CAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTATTGTGCGAGAAAATGTG  303

Qy   291  --------GGGATCTGTCTTATGACAGAGAGCTACTTTGACTACTGGGGCCAGGGAACC  340
                  ||  |   |||||||||  || |||||||||||||||||||||||||
Db   304  GCTCGTGTGGGGGGGGGCGTTCGATACAAGTACTTTGACTACTTTGACTACTGGGGCCAGGGAACC  363

Qy   341  CTGGTCACCGTCTCCTCA  358
          ||||||||||| |||||
Db   364  CTGGTCACCGTCCCTCA  381
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Search completed: July 18, 2003, 19:59:09
Job time : 29.9834 secs